



111th Annual Meeting of the German Zoological Society

10 - 15 September 2018 | Greifswald

Abstracts

(sorted by presenter)





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Main Meeting, FG Evolutionary Biology
Oral Presentation

A colourful mystery: Insights into the *Cepaea nemoralis* banding pattern mechanism

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The terrestrial gastropod species *Cepaea nemoralis* has been the focus of morphological, population genetic, molecular and evolutionary research for over 70 years. Scientists and collectors alike are interested in the different shell background colours ranging from light yellow over pink to brown. But it is the near Mendelian inheritance pattern of zero to five brown bands, which can be interrupted or merged, that initiated a new wave of research into the underlying molecular mechanisms. In the last years transcriptomic and proteomic approaches yielded first insights into the mechanisms patterning these gastropod shells. They verified the previously known supergene arrangement of loci responsible for shell background colour and banding pattern. Furthermore they revealed that the pigment used by *C. nemoralis* is not bound to a carrier protein like in juvenile *Haliotis asinina*. But the specific genes responsible for patterning *C. nemoralis* shells remained unknown. We here present an approach using transcriptome based differential gene expression between mantle regions with pigmented bands and background colour to gain candidate genes for shell patterning in *C. nemoralis*. The addition of *in situ* gene expression analyses (qPCR and slide *in situ* hybridisation) allows us to quantitatively and qualitatively validate these candidate genes. Additionally, analytical chemistry finally brings to light which pigments are responsible for the shell colours, further enhancing our understanding for banding and colouration mechanisms in *C. nemoralis*.



Symposium: 5th Meeting of the Arthropod Neuroscience Network
Oral Presentation

Input and output connections of the circadian clock of the Madeira cockroach *Rhyparobia (Leucophaea) maderae* with specific layers of lamina and medulla

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The accessory medulla in the brain's optic lobes is the circadian clock of the Madeira cockroach that controls sleep-wake rhythms. To examine input and output circuits of the clock we performed immunocytochemical and histochemical analysis of the neuroanatomy of optic lobe neuropils. Since previous studies determined that the compound eye only enables photic entrainment of the cockroach circadian clock, we examined the connections between the clock and photoreceptor axon termination sites in lamina and medulla. Furthermore, we specified the number of layers in lamina and medulla, as possible input and output regions of the circadian clock. Enzymatic staining with acetylcholinesterase histochemistry distinguished ten layers of the medulla and three layers of the lamina. Neurobiotin backfills from the contralateral optic stalk identified contralateral inputs. Antisera against the neurotransmitters histamine, GABA, and serotonin, and against the neuropeptides pigment-dispersing factor, corazonin, orcokinin, myoinhibitory peptides, FMRFamides, and allatotropin allowed to further define these layers. We found that only the neuropeptidergic anterior fiber fan connects the circadian clock to possible light input sites in the proximal lamina and the accessory laminae. In contrast, the GABAergic distal tract connects the clock to different layers in the medulla only. Strongest connectivity was observed between medulla layer 4 (ME4) and the clock. ME4 is innervated by neurobiotin backfills and contains all neuroactive substances tested. We conclude that ME4 serves as main input and output region of the cockroach circadian clock to control rhythms in physiology and behavior. [Supported by DFG grants STE531/18-2, 18-3 and STE 531/25-1 to MS]



Main Meeting, FG Behavioural Biology

Poster: Behav 1

Discrimination of temporal patterns of electric communication signals in the weakly electric fish, *Mormyrus rume proboscirostris*

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The weakly electrical mormyrid fish *Mormyrus rume proboscirostris* constantly emits series of electric pulses by discharging an electrical organ in its tail. These electric organ discharges (EODs) are used for active electrolocation and for electro-communication with conspecifics. While EOD waveform and amplitude stay constant, the inter-discharge intervals (IDI) can vary depending on the behavioural context. Natural IDI patterns are highly variable and fluctuate between 20 and several hundred ms. Here, we tested whether fish recognize certain temporal IDI patterns and can discriminate them from other patterns presented simultaneously. IDI patterns were pre-recorded from *M. rume* siblings, while they engaged in various defined behavioural contexts, e.g. feeding, resting or exploring. Four *M. rume* were trained to discriminate between two IDI-patterns emitted by two sender dipoles located at opposite ends of an aquarium. Fish were rewarded for approaching the dipole which played back an IDI pattern recorded from another fish during feeding (S+). The negative stimuli were regular, synthetic IDI-patterns starting with a low frequency of 5 Hz. In transfer tests, we test whether fish can discriminate between their S+ and various natural IDI patterns, and whether they can recognise feeding patterns recorded from different individuals. When two stimulus sequences were presented simultaneously, the fish could discriminate successfully between the S+ and the S-. We will present the results of further tests revealing whether fish can distinguish natural IDI sequences from different behaviours and whether they are able to recognize IDI patterns recorded in the same behavioural context but from different individuals.



Workshop: Animal Welfare
Oral Presentation

Animal experimentation under the requirements of biological safety levels BSL-3 and BSL-4

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The Friedrich Loeffler-Institute, Federal Research Institute for Animal Health, performs in vitro and in vivo experiments to improve our understanding of viral and bacterial infections in animals and humans, and to evaluate possible candidates for future vaccines and therapeutics. Working with experimental animals using disease agents harboring a highly pathogenic zoonotic potential is regulated by the legal requirements regarding work safety, protection from infection, genetic engineering and animal welfare. This results in the critical evaluation of the partially diverse protection aims of these regulations, which is performed in close cooperation with the relevant authorities. In general, work in such facilities requires a specific and thorough training as well as a very cautious and reliable work style of all staff involved. This task is complicated by the fact that an increasing number of challenge experiments is not only performed in the so-called dead end host species but also in the putative reservoir hosts or even in endangered wildlife species. While farm or companion animals usually tolerate being handled by humans, putative reservoir hosts may include species that are more difficult to handle under experimental conditions. Nevertheless, adequate husbandry and proper handling of such animals is essential, and needs to be ensured by the building infrastructure and by the recruitment and development of specific expertise among the staff involved in this work. This presentation will highlight the aforementioned aspects by presenting different examples of our experimental animal work.



Main Meeting, FG Ecology

Poster: Ecol 3

Stage-specific expression of blue-, UV- and long wavelength-sensitive opsins in the freshwater crustacean *Daphnia*

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Light is one of the major abiotic factors, influencing the behaviour of diverse organisms. In the freshwater crustacean *Daphnia*, which is a zooplanktonic primary consumer serving as an important link between trophic levels, light plays a special role as the different species show a strong phototactic behaviour. Genome sequencing of *D. pulex* and *D. magna* revealed a vast repertoire of opsins. In *D. pulex* 48 and in *D. magna* 33 opsins were found and categorised as ciliary opsins group4-opsins, and rhabdomeric-opsins. These r-opsins are responsible for visual light perception: ultraviolet-sensitive (UVOP), blue sensitive (BLOP) and two long wavelength-sensitive opsins (LOPA and LOPB). We investigated the expression of BLOP, LOPA and UVOP in a wavelength dependent manner during different developmental stages using RT-qPCR. Individuals of *D. pulex* and *D. magna* in the first juvenile instar were exposed to different wavelengths between 400-500 nm (blue), 450-550 nm (green) 600-700 nm (red). Additionally, controls were kept under white light and in the dark for 24 h and 48 h. LOPA is independently expressed from wavelength and exposure time, while BLOP and UVOP showed differences in their expression. Furthermore, we investigated the expression of UVOP under UV-light during embryo development. We see an upregulation of UVOP in UV exposed embryos. Our study provides first insights into the expression of opsins in *D. pulex* und *D. magna* and their resting eggs.



Main Meeting, FG Behavioural Biology

Poster: Behav 4

Harbour porpoises (*Phocoena phocoena*) show significantly decreased source levels of echolocation in shallow waters of the Wadden Sea

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Recent studies gave evidence that Harbour Porpoises adapt their source level to the environmental characteristics in different habitats during echolocation. The Wadden Sea is characterised by canyon-like underwater structures within flat and shallow waters with high tidally driven particle resuspension – unique in European waters. In this study echolocation clicks of free-ranging harbour porpoises in the German Wadden Sea were recorded with a vertical linear six-element hydrophone array. To estimate source levels of these porpoise clicks, time-of-arrival-differences (TOAD) were used. The calculated distances of porpoises to the array led to a back-calculated mean source level of 169 ± 5 dB re $1 \mu\text{Pa}$ pp. This is significantly lower than reported for free-ranging harbour porpoises from Inner Danish Waters (+20 dB) and British Columbia (+9 dB). This study confirms that porpoises adapt their source parameters to different acoustic habitats with large implications for acoustic monitoring. Static acoustic monitoring represents a good method to receive long term information about migratory behaviour, abundance and population density of echolocating odontocetes by recording their clicks in defined distances. Since these loggers have only one hydrophone, their detection range depends on the sensitivity of the hydrophone, but also the source level of the clicks. A decreased source level of 20 dB may, in the worst case, result in a 90% reduction in the effective detection radius. Further studies on population density should take account of the habitat dependent source levels to reliably estimate abundance and derive the correct comparisons on porpoise occurrence rates between areas.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral Presentation

The earliest ants: diversity and extinction illuminated by amber

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Today, ants are ubiquitous components of terrestrial ecosystems worldwide and exhibit significant diversity. The over 13,000 described extant ant species range from nomadic army ants and leaf-harvesting fungus farmers to species of social parasites incapable of feeding themselves and seed-milling specialists. The morphology of today's ants mirrors their extreme ecological diversity, and this is amplified by intraspecific caste specialization; there are in effect tens of thousands of ant morphotypes with a wide array of optimized arms and armors. Even still, the earliest ant fossils from the Cretaceous reveal additional ancient diversity that is now lost. Through combined morphological and molecular phylogenetic analysis, as well as CT-scanning and functional morphology, the oldest ant fossils from 78-100-million-year-old amber are described and contextualized, providing insight into the evolutionary history of one of the Earth's most prolific and ecologically impactful lineages. Fossils reveal early adaptive radiations, extinction, and subsequent faunal turnover, indicating that the ants of today are in effect echoes of their Cretaceous counterparts.



Main Meeting, FG Physiology

Poster: Phy 1

Toxic cargo? Organic anion transporting polypeptides (Oatp) in a cardenolide-sequestering leaf beetle

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The evolutionary seesaw between selective pressure and adaptation can be vividly observed in the chemical arms race between plants and insects. One famous class of specialized plant metabolites developed as defense against herbivores, are the cardiac glycosides (cardenolides and bufadienolides). Their ability to inhibit the ubiquitous Na⁺/K⁺-ATPase leads to a high potential toxicity throughout the animal kingdom. But numerous insects from different orders are not only able to tolerate cardenolides, but to sequester them and use them for their own defense against predators. The dogbane leaf beetle *Chrysochus auratus* does so by sequestering cardenolides from its apocynaceous host plants into its own defensive glands. The mechanisms by which the toxins are transported and concentrated are to date unknown. There is evidence of members of the ABC transporter family expressed in *C. auratus* capable of transporting cardenolides (Kowalski et al., in preparation), but these membrane proteins are exclusively known to export substances from cells in eukaryotes. Transcellular transport of substances across epithelia, as assumed here, requires import and export carriers, though. Members of the Organic anion transporting polypeptides (Oatps) are reported to transport cardenolides into human, rat and fruit fly cells and are therefore a promising candidate for being involved in cardenolide transport in *C. auratus*. Three SLCO genes encoding Oatps in *C. auratus* were identified from transcriptomic data, cloned and – together with their orthologues from the non-sequestering *Chrysochus asclepiadeus* – functionally tested in *Xenopus* oocytes.



Main Meeting, FG Physiology

Poster: Phy 4

Clock genes expression in the red flour beetle, *Tribolium castaneum*

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Circadian rhythms are driven by cell located mechanism called molecular clock. Its core is composed of the clock proteins that control expression of own genes (clock genes) in a form of the transcriptional-translational feedback loops (TTFLs). The best known TTFLs of the molecular oscillator is described in the fruit fly, *Drosophila melanogaster*. However, in other insects (including many model species) structure of the TTFs, and even daily profiles of clock genes/proteins expression, are very poorly characterized. Here, we ask the question whether in the red flour beetle, *Tribolium castaneum*, canonical clock genes orthologs are rhythmically expressed and whether expression of these genes is entrainable by day-night and temperature cycles. In addition to the data on the expression profiles of the canonical clock genes, that have been identified in the *Tribolium* genome, we present results of an analysis of the core clock proteins expression in the brains and peripheral organs (fat body, gut and Malpighian tubules) of adult beetles. We also showed that expression of core clock genes and proteins in peripheral organs are maintained in vitro. It supports our hypothesis that these organs contain a self-sustaining, entrainable circadian oscillators. Our data showed that both, light and temperature, seem to be equal Zeitgebers for molecular oscillator of *Tribolium* beetles. Supported by NCN grant No. 2013/11/B/NZ4/03310 to PB.



Main Meeting, FG Morphology

Poster: Morph 14

The effects of head appendages on the brain anatomy of Eunicida (Polychaeta)

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Eunicida is a taxon of errant Polychaetes which consist of highly mobile hunters and possess a sophisticated nervous system and different kinds of sensory structures. The brain is well developed, shows different tracts and is located inside the prostomium. A nuchal organ, to detect chemical traces, is present and may be paired or a single groove located dorsally to the brain. Most remarkable are the different amounts of eyes or antenna/palps present on the head of species of the five major taxa of Eunicida. There are species with 5, 3, 1 or none antenna, species with one or two pair of eyes or species which lack eyes. That makes Eunicida an ideal group to study the effects of head appendages and eyes on the anatomy of the brain. We therefore performed Immunohistochemistry, μ CT, TEM, paraffin- histology (5 μ m) and semithin sectioning (1 μ m) to investigate the nervous system of Eunicida. Our results show that complexity of the brain is not affected by the amount of sensory structures located on the head. Moreover in species lacking antenna we found nerves which are most likely homologous to the nerves innervating the antenna in species which possess frontal head appendages. These findings argue for a reduction and not a gain of head appendages during radiation of Eunicida.



Symposium: 5th Meeting of the Arthropod Neuroscience Network
Oral Presentation

The circadian clock network in bees

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Bees, like many other organisms, evolved an endogenous circadian clock, which enables them to foresee daily environmental changes and exactly time foraging flights to periods of floral resource availability. The basis of time keeping in the bee is a molecular feedback loop, which includes the central clock genes period, cryptochrome, clock and cycle. But also the neuropeptide Pigment Dispersing Factor (PDF) seems to play an important role as communication factor between different clock centers, as this has been demonstrated before in other insects. We characterized in detail the localization of the circadian clock in the honey bee (*Apis mellifera*) brain via immunocytochemical labeling of two clock components, namely PERIOD (PER) and PDF. PER is localized in four lateral and dorsal neuron clusters, many glia cells and photoreceptor cells. This expression pattern is similar to the one in other insect species and indicates a common ground plan of clock cells among insects. In one neuron cluster with cell bodies located in the lateral brain, PER is co-expressed with PDF. These cells build a complex arborization network throughout the brain and provide the perfect infrastructure to convey time information to brain centers, where complex behavior, e.g. sun-compass orientation and time memory, is controlled. By comparing the honey bee clock network with the one in other insects, our research aims to improve the understanding of neuroanatomical adaptations in the evolution of insect circadian clocks.



Symposium: Adaptations to Hematophagy in Blood-feeding Parasites
Oral Presentation

An updated check-list of marine and freshwater leeches (Annelida: Clitellata: Hirudinida) of Tunisia

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Available informations on the distribution, taxonomy, and ecology of leeches in Tunisia have been scattered throughout various historical as well as recent papers, but none of these have focused on the country's fauna as a whole. Freshwater leeches (Annelida: Clitellata: Hirudinida) of Tunisia were studied on the basis of old literature information, the MNHN (muséum national d'Histoire naturelle de Paris) collection and results of recent surveys conducted by the authors. The objectives of this study were to summarize recent taxonomic information, and to update the check-list of leeches using records collected during the period extending from 2006 through 2016. Altogether, 13 species representing 11 genera and 4 families are reported for Tunisia, including 8 first reports for the country (*Theromyzon tessulatum*, *Alboglossiphonia hyalina*, *Helobdella stagnalis*, *Erpobdella testacea*, *Trocheta tunisiana*, *Dina punctata punctata*, *Dina punctata maroccana* and the marine leech *Trachellobdella lubrica*). Except the representatives of the Erpobdellidae family which are carnivorous, all the recorded leeches are ectoparasitic hematophagous. A detailed description of the distributions of rare species and characterization of localities from which they are reported are presented.



Main Meeting, FG Physiology

Poster: Phy 7

The glutton's secret weapon: The gut microbiome in the sea urchin *Strongylocentrotus droebachiensis*

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The sea urchin *Strongylocentrotus droebachiensis* can destructively graze down large areas of marine vegetation such as kelp forests resulting in so-called barren grounds. Kelps are otherwise avoided by grazers due to low protein content, thick leaf structure and grazing deterrents. The surprising ability to consume kelp might be caused by a bacterial symbiosis in the sea urchin gut, whereby bacteria contribute to the degradation of structural components and provide nutrients through nitrogen fixation. We analyzed sea urchin gut bacterial diversity and community composition in a no-choice feeding experiment with the algal diets: *Saccharina latissima* (kelp), *Fucus serratus* (wrack) and *Palmaria palmata* (red alga). Starved urchins served as a control, and urchins collected from the Oslo fjord prior to the experiment served as a reference for natural microbiomes. Illumina MiSeq PCR amplicon sequencing of 16S rRNA gene fragments revealed 614 amplicon sequence variants (ASVs). One ASV (related to *Psychromonas marina*) accounted for 44 % of the total sequence reads and was present in all samples, thereby representing a main symbiont in these sea urchins. The urchins given uniform algal diets had a significantly lower ASV diversity compared to the control and reference urchins indicating that algal ingestion promotes certain dominant bacterial taxa. Several ASVs were related to bacteria that can degrade structural components like alginate, and to nitrogen-fixing taxa. These findings provide a better understanding of how sea urchins are able to survive on high-carbon food sources like kelp and provide ideas on how to mitigate catastrophic sea urchin grazing events.



Main Meeting, FG Behavioural Biology*

Poster: Behav 5

Evidence for a contribution of sensory feedback from leg chordotonal organs to speed-dependent inter leg coupling in *Drosophila*

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Amputation experiments in *Drosophila* revealed that single leg stumps oscillate rhythmically during walking, with an oscillatory period independent of the step period of the remaining intact legs during slow walking, but phase-coupled to the walking legs at higher walking speeds. Here we investigate if this phase coupling is dependent on sensory feedback from the leg's chordotonal organs. We compared leg oscillation periods, phases, and absolute inter-leg movement intervals during walking between middle leg amputees of CS WT flies and flies of the nan[36a] mutant, which has defective chordotonal organs. Single middle leg stumps of nan[36a] mutant flies showed the same high frequency oscillations that were found during experiments with wild type flies. The stumps oscillated almost independent of walking speed with a movement period of about 100 ms. Contradictory to results from wild type flies the stump oscillations in the mutant flies failed to entrain to the stepping behavior of the intact legs at high walking speeds. Also the absolute time intervals between liftoff events in intact legs and subsequent onset of levation or depression in the stump were found to be more variable compared to findings in wild type animals. These results suggest an important role for sensory feedback from chordotonal organs in inter leg coordination.

*Contribution also presented in: *Symposium: 5th Meeting of the Arthropod Neuroscience Network*
(Poster: ANN 1)



Main Meeting, FG Morphology
Poster: Morph 23

Differential habitat utilisation in two sympatric tamarins (Callitrichidae, Primates) in Amazonian Peru: Leaping behavior and implications for morpho-functional adaptations in the hindlimbs

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Different species of tamarins in Amazonian Peru build mixed-species troops during daily forages in the rain forest. These sympatric and closely-related species have previously been documented to exhibit behavioural differences which may also be reflected in their postcranial morphology. To further investigate this system, we quantified habitat utilisation as with a focus on leaping behavior in free-ranging *Saguinus mystax* and *Leontocebus nigrifrons*. The aim of the work was to determine the relationship of leaping behavior with habitat use and how this is determined by the properties of the habitat. The data were analysed by using the Mann–Whitney U test and the T test. We collected data on the leaping behavior, support properties, and foraging height of the monkeys during a 5-month field study in the Amazonian in northeastern Peru at the Estacion bioloquica quebrada blanco (EBQB). The instantaneous-scan-sampling method and the focal-animal-scan-method were used. Our results showed that *S. mystax* spends significantly more time in the upper forest strata (< 15m, with mostly horizontal, thin and thus flexible terminal branches) and uses the predominant supports at a noticeably higher rate than *L. nigrifrons*. In contrast, *L. nigrifrons* is predominantly active in the lower forest strata (with a higher proportion of vertical tree trunks) and accordingly exhibits a high number of trunk-to-trunk leaps. Generally, *L. nigrifrons* is leaping at a higher rate than *S. mystax*. We hypothesize that these observed behavioral differences also involve differential functional demands caused by kinematic and dynamic differences in horizontal and vertical leaps, respectively.



Main Meeting, FG Physiology
Oral Presentation

Algae affect rhythms in *Daphnia*

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Molecular oscillator in animals is composed of genes and proteins that interact with each other in a form of transcriptional-translational feedback loops (TTFLs). The main players of these TTFLs are negative and positive regulators of transcription. In the fruit fly, *Drosophila melanogaster*, PER and TIM proteins negatively regulate expression of own genes. It is achieved by interaction of PER:TIM and CLK:CYC heterodimers. PER:TIM as negative regulators bind to CLK:CYC factors leading to repression on *per*, *tim* and clock controlled genes. Molecular clock of the fruit fly is entrainable due to activity of the CRY protein, which binds to TIM protein causing its light-dependent degradation. TTFLs structure of *Daphnia* molecular oscillator remains to be elucidated. However, rhythmic expression of canonical clock genes orthologs has been described in *Daphnia*. Moreover, there is no information about factors (other than light) which may entrain the oscillator and activity it controls in *Daphnia*. We aimed to answer the question whether the green algae *Scenedesmus* provided as a food source can serve as Zeitgeber for *Daphnia*. For *Daphnia* kept in light:dark conditions light seems to be a main Zeitgeber. In animals kept in darkness, algae affect the profile and phase of their activity rhythm. Under continuous light *Daphnia*'s clock seems to be desynchronized and cannot be entrained by other factors (algae). These changes also reflect in the daily profiles of *per*, *cyc* and *cry* genes expression in *Daphnia* bodies. Supported by NCN grant No. 2013/11/B/NZ4/03310 to P.



Main Meeting, FG Physiology
Oral Presentation

Fluorescence measurements of the marine flatworm *Macrostomum lignano* during exposure to the TNT derivatives 2ADNT and 4ADNT

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The most significant explosive of conventional munition dumped in the sea is 2,4,6-trinitrotoluene (TNT). Two main metabolites of TNT are 2-amino-4,6-dinitrotoluene (2ADNT) and 4-amino-2,6-dinitrotoluene (4ADNT). The toxicity of both compounds was tested on the marine flatworm *Macrostomum lignano* raised in the laboratory. The tested concentrations of both derivatives were in the μM to the nM range. After several days the mortality of the flatworms exposed to both derivatives at the concentration of $169\mu\text{M}$ increased. In addition, the influence of temperature and UV-radiation was determined. The solutions of 2ADNT and 4ADNT with the concentration of $169\mu\text{M}$ were irradiated by UV-light for 4 hours. After that, the worms were exposed to this solution, which induced a slightly increased mortality after one week at 21C° . By increasing the temperature from 21C° to 30C° , the toxicity of both derivatives was strongly increased. Using sub-lethal concentrations the defense mechanisms of exposed worms, namely drug and xenobiotic transporters, expelling toxic compounds from the cytosol, were strongly enhanced. Also measurements of auto-fluorescence showed distinct alterations. (in part financed by EU Interreg Project DAIMON)



Main Meeting, FG Systematics, Biogeography and Diversity
Oral Presentation

Neuropeptide precursor sequences provide comprehensive data to elucidate phylogenetic relationships within Blattodea

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Neuropeptides are the most diverse group of intercellular signaling molecules within multi-cellular animal organisms (Metazoa). They represent key players in information transfer and act as important regulators of development, growth, metabolism, and reproduction. In Insects, these short protein-like substances show a high degree of structural variability, although they are under a high stabilizing evolutionary pressure, due to co-evolution with their respective receptor. In previous studies, sequences of selected neuropeptides were used to reconstruct phylogenetic relationships within various insect groups. Thereby, merely the sequences of single or multiple bioactive neuropeptides have been used. With unprecedented access to transcriptome data it is now possible to not only incorporate the sequence of expressed neuropeptides but of the whole neuropeptide precursor. This not only extends the length of the alignment, but also enables the incorporation of previously unstudied sequences with diverse evolutionary pressures, such as sequences of the signal peptide or potentially non-bioactive precursor-peptides. Here we show results of analyses of the cryptic phylogenetic relationships within Blattodea based on sequences of 17 neuropeptide precursors. In addition, we analyzed in detail to which extent the functionally different parts of neuropeptide precursors provided phylogenetic information to recover inter-familial relationships. Our work stands as the first comprehensive utilization of neuropeptide precursors of arthropods for solely phylogenetic purposes. It serves as logical successor of previous studies incorporating neuropeptide sequences in phylogenetic analysis and indorses the increased phylogenetic information that is obtained by integrating complete precursor sequences instead of merely sequences of expressed neuropeptides.



Main Meeting, FG Behavioural Biology

Poster: Behav 6

The corona ciliata in arrow worms: functional implications of flow measurements

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Arrow worms (Chaetognatha) are planktonic or benthic Metazoa that prey on a variety of organisms. They possess a corona ciliata, a ciliated organ on the head, neck and / or trunk, which is specific to the phylum. Various functions have been hypothesized to be the main purpose of the corona, including respiration, excretion, mechanoreception, or chemoreception. As the cilia are known to be motile and beat actively, we measured the water flow that is produced by the corona and draw conclusions as to its relevance and fitness for different possible functions. In *Spadella cephaloptera*, a benthic chaetognath, water is drawn towards the corona ciliata in a funnel-shaped pattern from dorsal and slightly rostral of the head and neck (Bleich et al. (2017), *Zoology* 125, 79). Maximal flow velocities were 140 $\mu\text{m s}^{-1}$, velocities averaged over the area of the corona were 104 $\mu\text{m s}^{-1}$, and volumetric flow rate was 0.0026 $\mu\text{l s}^{-1}$. We assessed Péclet numbers of $Pe=2.6$ for oxygen and $Pe=5.82$ for proline. This indicates that advection prevails over diffusion in the transport of chemicals in the influx zone of the corona already in light molecules, and consequently more so in heavier molecules. Together with morphological evidence that speaks against excretion as a main function of the corona, we conclude that it mainly functions as a chemosensory organ. The funnel-shaped water flow towards the corona potentially enables directional chemosensation, as an odour source above the chaetognath's head, where prey is attacked, will be highlighted.



Symposium: Adaptations to Hematophagy in Blood-feeding Parasites
Oral Presentation

Characterization of IrSPI, an *Ixodes ricinus* serine protease inhibitor involved in tick feeding and in bacterial infection of salivary glands

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Ixodes ricinus ticks are important vectors of pathogens affecting both animal and human health. To replace the use of acaricides, new environmentally sustainable approaches providing broad protection against tick-borne pathogens (TBP) are urgently needed. Such development requires improved understanding of the biology of ticks and more particularly of their interactions with vertebrate hosts and TBP. Tick saliva is an essential biofluid for ticks, its proteolytic, anticoagulant, immunomodulatory, and anti-inflammatory activities allowing ticks to acquire their blood meal under optimal conditions. Moreover, injection of saliva during blood feeding represents the principal route by which TBP are transmitted. To understand the molecular mechanisms involved in TBP transmission, as well as to identify putative vaccine candidates from *I. ricinus* saliva, salivary glands from bacteria infected and uninfected ticks were compared by high throughput transcriptomics. The most up-regulated transcript following infection was IrSPI, which belongs to the Kunitz/BPTI inhibitor family. Functional analyses via RNAi knockdown experiments revealed that IrSPI enhances both blood feeding and bacterial burden in the salivary glands. The presented work concerns the structural and functional characterization of IrSPI. The dynamics of IrSPI expression were evaluated during both tick feeding and colonization of ticks by TBP. Antibodies were generated against recombinant IrSPI protein and used to establish its presence in tick salivary secretion. While IrSPI had no impact on coagulation, as determined by analysis of thrombin generation time, it inhibited the proliferation of mitogen-stimulated CD4⁺ lymphocytes. IrSPI may thus play a role in modulating the host immune response during blood feeding.



Symposium: 5th Meeting of the Arthropod Neuroscience Network
Oral Presentation

Developmental neurotoxicity testing for axonal navigation defects in an intact locust embryo

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Developmental neurotoxicity (DNT) poses a serious threat to the health of children. However, far too few industrial chemicals have yet been tested, mainly because current assays require the use of high numbers of laboratory animals. The formation of a functional brain requires the precisely timed navigation of axons. We address this complexity by monitoring defects in axonal navigation of pioneer neurons of intact locust embryos after exposure to chemicals. Mechanisms of axonal guidance, such as growth cone navigation along molecular semaphorin gradients are evolutionary conserved. Thus, assays monitoring axonal navigation in insects will be indicative for the DNT potential of industrial chemicals in humans. Locust embryos are kept in culture overnight in the presence of test chemicals, followed by biochemical viability measurement and immunolabeling of leg bud pioneer neurons. Defects in axonal outgrowth and navigation of pioneer axons are detected via fluorescence microscopy. Currently, the assay is being calibrated against a range of positive compounds with known DNT potential, and negative compounds, which are toxic, but have no specific DNT potential. For example, the mitochondrial respiratory chain inhibitor rotenone inhibited both pioneer neuron growth and correct pathfinding in the same concentration range as found in human neurons. The signaling pathways that transduce the extracellular semaphorin guidance cues into correct axonal navigation are unknown. Application of channel blockers and intracellular store releasers provide evidence for calcium-mediated signaling mechanisms in growth cone behavior. This insect assay will serve as complementary test system to other alternative DNT testing methods. (Funded by BMBF 031L0062A)



Main Meeting, FG Neurobiology

Poster: NB 16

The influence of learning conditions on a learned, multimodal object detection task

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The nocturnal weakly electric fish *Gnathonemus petersii* uses self-generated electric organ discharges (EOD) for sensing nearby objects. In addition to active electrolocation, fish can detect objects especially at larger distances also with their visual sense. Here we tested under which conditions *G. petersii* uses either active electrolocation, vision or both senses when detecting a metal object in a learned detection task. In particular, the role of training distance on multimodal sensing was investigated. Six fish were trained to detect a metal cube (S+) at a distance of 1 cm or 2.5 cm. After successful learning, fish were tested in transfer tests at different object distances when they could use either only vision, only active electrolocation or both. Fish learned the detection task on average after 32 training sessions. When only vision was available, only 1 of 3 fish trained at 1cm could detect the object, while all fish trained at 2.5 cm were successful. With only their electric sense functioning, 5 of 6 fish detected the object, while one fish trained at 2.5 cm did not. Fish's performance was always better, when both senses could be used simultaneously (synergy). Fish trained at 2.5 cm could detect the object up to longer distances than fish trained at 1 cm. We confirmed that active electrolocation works as a nearfield sense, while vision is mainly used at longer distances. Our results show that multimodal sensing depends on the conditions, under which a sensory task is acquired, i.e., learning can influence multisensory integration.



Main Meeting, FG Morphology
Oral Presentation

Nobodies or Somebodies? - Exploring the unexplored potential of sea spiders (Pycnogonida) to inform on arthropod evolution

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Sea spiders (Pycnogonida) are commonly regarded as rather bizarre arthropods. Owing to an unusually high ratio of leg length to body size, pycnogonids have been even unflatteringly coined the arthropod "nobodies". However, as likely sister group of all other chelicerates (Euchelicerata), these "nobodies" are a crucial taxon to study in order to unravel evolutionary transformations near the base of the chelicerate tree. Beyond that, I will exemplarily outline and illustrate why pycnogonids hold potential to inform on different aspects of arthropod evolution. At the adult morphological level, especially the three pycnogonid "head" appendages have been a playground for evolution, unparalleled by any other euchelicerate taxon. The numerous combinations of appendage presence/absence and structure in the extant "families" afford an excellent opportunity for comparative studies on the evolutionary stability vs. plasticity of affiliated internal organ systems, such as the brain and subesophageal ganglion. Further, the pycnogonid ventral nerve cord with its plesiomorphic array of separate segmental ganglia is unique among chelicerates and provides a perfect basis for unbiased segment-specific analyses down to the level of individually identifiable neurons. In contrast to the fused euchelicerate synganglion, this enables more straightforward comparisons to important mandibulate taxa, such as myriapods. Lastly, the recent discovery of a putative system of adult neurogenesis in each ventral pycnogonid ganglion paved the way for initial studies of this phenomenon in a non-mandibulate group. Comparison to decapod crustaceans and insects allow first conclusions concerning the cellular system(s) underlying this aspect of adult neural plasticity in the arthropod stem species.



Workshop: From Gene to Function: Using CRISPR/Cas9 in Zoology
Oral Presentation

Genome editing - the basics

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Genome editing is opening new avenues for the study of gene function in non-model organisms. As introduction to the workshop “CRISPR/Cas9 – Applications in Zoology” I will review the basics of CRISPR/Cas9 genome editing and its application in animals. Further, I will present selected kinds of manipulations by genome editing that target certain questions in Zoological research.



Symposium: Phenotypic Plasticity - RESPONSES of Animals to
Environmental Change
Oral Presentation

Developmental phenotypic plasticity helps bridge stochastic weather events associated with climate change

Warren W. Burggren

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Global climate change is often described in terms of the slow, inexorable rise in annual average global temperatures and acidification of the oceans. However, a differentiation must be made between “weather” and “climate”. Many environmental changes, especially weather-related, are often extreme, variable and stochastic. This is especially true of temperate terrestrial and freshwater habitats. Yet, the protocols for studies of animal and plant phenotypic plasticity rarely use short-term, stochastic environmental change – i.e. realistic conditions of weather, as opposed to climate. The frequently abrupt environmental changes in weather (days, weeks, months) accompanying much longer-term general climate change (e.g. global warming over decades or centuries) demand that the true nature of environmental change (as opposed to statistical mean values) be coupled to an expansion of focus on developmental phenotypic plasticity. Such developmental plasticity can be obligatory/facultative and/or beneficial/deleterious, all depending upon the rate and degree of environmental variability during specific points of organismal development. To summarize, as important as adult phenotypic plasticity is, such plasticity will be irrelevant if the developing offspring are insufficiently plastic to develop alternative phenotypes aiding survival during stochastic weather events.



Main Meeting Keynote Lectures
Oral Presentation

Developmental plasticity, epigenetics and evolution: a comparative physiological perspective

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Developmental plasticity, epigenetics and evolution are often treated as separate phenomena by biologists, yet in fact may be all closely interrelated. Yet, understanding how this triad of interacting biological concepts can affect survival and reproduction (while also creating unwanted variation in our data sets) can lead to greater insights into the evolution of physiological and other adaptations. This keynote address discusses data from both vertebrate (humans, fish, birds) and invertebrate models (brine shrimp, flatworms, insects) to reveal the often complex yet subtle interactions between developmental plasticity and epigenetics. Also discussed is how such interactions may actually affect species evolution. It is posited that epigenetically-based short-term modifications in phenotype lasting at most a few generations may be as or more effective than evolutionary, gene-modification based change for surviving shorter term environmental stressors. Epigenetic inheritance may be especially important as increasingly harsh and stochastic weather events associated with long term climate change become more prevalent, and so more challenging, to both terrestrial and aquatic organisms.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral Presentation

Turing pattern diversity and the rapid evolution of tarsal adhesive microstructures in stick and leaf insects (Phasmatodea)

Thies Henning Büscher¹; Mikhail Kryuchkov²; Vladimir L. Katanaev²; Stanislav N. Gorb¹

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The mesodiverse lineage of stick and leaf insects (Phasmatodea) has undergone a rapid evolutionary radiation during the Eocene. Phasmids evolved specialised attachment organs on their tarsi and pretarsi in order to adhere to different surfaces they face in the specific ecological environment. Due to geographically isolated adaptive radiations these insects developed numerous forms of convergent ecological specialisations. The tarsal attachment pads (euplantulae) of different ecological forms possess a high diversity of adhesive microstructures on their cuticle surface. These adhesive microstructures are suggested to reflect ecological adaptations of particular species, but their origin and development remain largely unknown. We approached the outstanding diversity of euplantular surfaces of Phasmatodea using scanning electron microscopy and a mathematical Turing-model generating various types of pad surface microstructures. Using the reaction-diffusion-model by Alan Turing that explains pattern formation in nature we identified eight principal patterns and were able to simulate the transitions between these. Furthermore the model predicts intermediate patterns, which we described on the adhesive surfaces on phasmid euplantulae. The fast and easy transformations between the patterns suggest a notable adaptability of adhesive microstructures which possibly potentiates the rapid evolution of different microstructures of euplantulae and might explain the scattered occurrence of the different types of microstructures within the phasmatodean phylogeny. The functional significance and potential benefits of different adhesive microstructures in context of the species' ecology are discussed.



Main Meeting, FG Morphology

Poster: Morph 19

The functional organization of the sclerome of five species of *Acanthogorgia* (Octocorallia, Holaxonia)

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Soft corals are usually characterized by their colony structures and sclerite morphologies. Specimens of the genus *Acanthogorgia* (Acanthogorgiidae, Octocorallia) show different sclerite types in the colony parts like axis coenenchym, polyps and tentacles. In order to understand how these sclerites interact for mobilization of the colony and the polyps we investigated the spatial arrangement and interaction of sclerites and tissues using non-destructive X-ray microscopy. We compared the functional organization of the sclerome of five *Acanthogorgia* species (*A. aspera*, *A. armata*, *A. granulata*, *A. hirta*, *A. muricata*) from the North Atlantic ocean. Our results show differences between these species in forms, sizes and arrangements of the sclerites. The general spatial organization closely relates to the function of the body parts and is the same in all investigated taxa. As a basis, the rigid axial skeleton allows gentle elastic swaying of the colonies to prevent breakage in strong currents. The tissue reinforced by skeleton structures enables the upright movement of tentacles as well as the expansion and contraction of the polyps. The basal parts of the polyps are anchored in the axial coenenchym, but the polyps of this genus cannot retract into the coenenchym. Our study provides a detailed insight into the various dynamic interactions within the sclerome providing a first view in the biomechanics of sclerite structures.



Main Meeting, FG Morphology
Oral Presentation

Biomechanics of the predatory strike in dragonfly larvae (Insecta: Odonata)

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Odonata larvae are often key predators in their aquatic biotopes. They catch their prey with a unique and highly efficient apparatus, the so-called prehensile labial mask, a strongly modified and extensible mouthpart. The main driving force and underpinning biomechanics of this movement remain still questionable. We used various techniques, such as micro computed tomography (μ CT), scanning electron microscopy (SEM), confocal laser scanning microscopy (CLSM), force measurements and high-speed videography combined with manipulation experiments to gain insights into the biomechanics of the predatory strike of Odonata larvae. Our results suggest a catapult system as driving force for this prey capturing process. We could identify two resilin-dominated sclerites (T-rod and premental sclerite) and two accessory muscles 0la5 and 0hy7 responsible for the mechanism. Here the resilin-containing structure is strained by slow muscle action and thereby energy is stored. To allow for this energy storage in spring-loaded catapult systems, locks are needed to prevent the spring from untimely release. Two locks are identified as muscle 0la8 and a latch system consisting of interlocking sclerites. To ensure the simultaneity of the predatory strike the trigger muscle 0la15 unlocks the mentioned latch mechanism after relaxation of the muscle 0la8. Furthermore, the hypothesis that hydraulic pressure is the driving force of the striking process, as suggested by former investigations, could be refuted by manipulation experiments, where we used $MgCl_2$ as muscle relaxant agent, and high-speed videography. We suggest that hydraulic pressure is most likely used for recoil-preventing jet propulsion during the prey capturing process.



Main Meeting, FG Morphology

Poster: Morph 24

Histological analysis of cartilages from *Raja undulata* (Rajidae)

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Elasmobranch fishes (sharks and rays) have a cartilaginous skeleton unique among living vertebrates, formed by an unmineralized matrix surrounded by a thin mineralized layer of tile-like structures called tesserae. This cartilaginous skeleton is far less studied than bony skeletons, and although the tesserae of one stingray species (Urotrygonidae: *Urobatis halleri*) have been recently described, there is still little information about the variation of tesserae across species and its relation to growth and mechanics. The current study investigates the morphology of juvenile tesserae of different cartilages of a skate (*Raja undulata*) using a variety of histological stains (von Kossa, Mason's Trichrome and modified Azan Trichrome) and compares results with published data for *U. halleri* to determine if differences across species. *Raja undulata* tessellated cartilage showed similitudes to that of *U. halleri* in terms of morphology and position of chondrocytes and tesserae structure, exhibiting all major ultrastructural features recently described in *U. halleri*. However, a wide diversity of developmental stages and morphologies in both tesserae and cells were observed, even within individual cartilages. These results demonstrate that whereas the basic structure of Rajidae tesserae echoes that of other batoid tesserae, some differences exist in structure and developmental timing, which suggest species- or taxon-specific characters and may be the root of differences in adult tesserae geometry. Therefore, this study provides groundwork for future studies relating the observed characters to developmental processes, tissue mechanics and phylogeny.



Main Meeting, FG Developmental Biology
Oral Presentation

Cellular changes during diapause in *Daphnia* resting embryos

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Diapause is a form of dormancy, predetermined by the genotype allowing animals to survive harsh environmental conditions. During diapause, development, growth and metabolic activity is depressed until distinctive environmental cues signal favorable conditions. However, metabolic depression is challenging for cellular viability, and the mechanisms allowing cells to sustain such long periods of suspended animation remain elusive. We investigated this in the freshwater crustacean *Daphnia*, that breeds embryos destined to go into diapause when environmental conditions deteriorate. Using immunocytochemistry, we compared the mitotic activity, cellular activity, and cytoskeletal parameters in cells of diapausing and non-diapausing embryos at different developmental stages. We validated our results using quantitative PCR of respective target genes, 18S rRNA gene, actin and DNA methyltransferase. Whereas mitotic activity comes to a halt during diapause, cellular activity does not fully arrest on the transcriptional and translational level. This indicates that cells are not fully inactive during diapause but have the capacity to continuously translate proteins on a low level. Morphologically, we observe an atrophy of cytoskeletal filaments (both microtubules and actin-filaments), rendering the dormant cells compact and condensed. We anticipate that this saves resources but also enables a quick re-synthesis of the cytoskeleton upon resurrection. We here provide first insights into the cellular changes in *Daphnia* embryos during diapause.



Main Meeting, FG Evolutionary Biology
Oral Presentation

Predation effects on fitness and gene expression: genotype-phenotype mapping in *Daphnia*

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Fitness is determined by complex interactions between genotype and environment and might differ substantially among individuals of the same species. While genome-wide sequencing has become easier, a common challenge in identifying the genotypic basis of fitness variation in empirical studies is obtaining fitness measurements in replicated conditions. The ecological model organism *Daphnia* is well suited for this aim, since its clonal reproduction mode allows for a repeated testing of given genotypes in different environments. To identify the molecular basis of response to predation, we exposed 24 different clonal lines from 4 different populations to fish kairomones in a highly replicated setup and measured life history traits; the same traits were measured in the absence of stress. All these clonal lines were genotyped through RNAseq, providing genome-wide SNP data. A genome wide association approach revealed a few genes correlating with fitness in stressful and stress free conditions. A GxE analysis allowed inferring a limited set of genes where the observed fitness variation results from the interplay of both drivers. Furthermore, transcripts differentially expressed under predation were identified with an RNAseq experiment on two clonal lines with contrasting life histories. A co expression network approach allowed identifying modules highly correlated with treatment and fitness-associated traits. With this combination of approaches, we were able to narrow down to key genes correlated with fitness in *D. galeata* in contrasting environments, through changes at either the regulatory or the sequence level.



Main Meeting, FG Behavioural Biology
Oral Presentation

To scare or not to scare – effects of pile-driving and mitigation strategies on porpoises

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Pile-driving for offshore windfarms causes underwater noise likely to affect marine mammals over the next decades. The magnitude of impact depends largely on how efficient the effects can be mitigated and on how porpoises react to pile-driving noise. Mitigation strategies encompass different approaches ranging from alternative, less noisy construction strategies, over mitigation at the source, to scaring animals away before potential exposure. It is not clear at the moment which strategy is most promising in actually preventing detrimental effects on porpoises. We conducted a large scale acoustic monitoring with 21 acoustic data loggers during construction of the wind farm Dantysk (North Sea) to evaluate bubble curtains and seal scarers as mitigation. Results show that bubble curtains reduced the impact radius and duration in comparison to previous studies from 20km/15-24h to 12km/5h. The seal scarer caused similar displacement as pile-driving using bubble curtains (12km). While bubble curtains reduced both the zone of potential hearing loss and zone of displacement, seal scarers caused similar displacement distances as pile-driving in large scale displacement order to prevent hearing loss. When comparing the efficiency of bubble curtains to mitigate the impact it becomes clear that we have to take the hearing abilities of porpoises into account. When weighting a pile-driving signal with the inverse audiogram of a porpoise the estimated exposure period to cause temporary hearing loss increases by a factor of 231 relative to the assessment based on unweighted levels. This highlights that species specific exposure limits are needed to assess the possible impacts.



Symposium: Phenotypic Plasticity - RESPONSES of Animals to
Environmental Change
Oral Presentation

Reversible plasticity in mammalian energy-saving strategies a mechanism to cope with rapid climate change?

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A fundamental question of current ecological research is to illuminate the drivers and limits of species responses to human-induced rapid environmental change. Reversible phenotypic plasticity of labile traits provides a fast and flexible mechanism to respond to rapid changes. In this talk, I will review the potential and limitations of individual variation and plasticity of energy-saving heterothermy in mammals to cope with climatic change. Combining field recordings of body temperature, respirometry to measure energy consumption, experimental manipulation of temperature (laboratory) and food availability (field and laboratory), we studied reversible phenotypic plasticity in energy-saving heterothermy in two small mammal species facing very different predicted climatic changes. The grey mouse lemur (*Microcebus murinus*), a small primate of Madagascar is predicted to experience an increased frequency of catastrophic weather events. The eastern chipmunk (*Tamias striatus*), a squirrel of the temperate seasonal forest, will experience a gradual rise in ambient temperature. In both species we demonstrated among-individual differences in reaction norms of body temperature to environmental conditions, which had fitness consequences, suggesting heritable differences in phenotypic plasticity among individuals. Moreover, based on controlled experimental manipulations of food availability, we demonstrated the potential of flexible adjustments of energy-saving heterothermy to rapid changes of environmental conditions. Thus, high flexibility in energy-saving heterothermy as well as the potential for natural selection to act on this physiological flexibility might provide slowly evolving taxa, such as mammals, a mechanism of resilience to rapid climatic change.



Main Meeting, FG Physiology
Oral Presentation

Neuroendocrine control of environmental stress responses

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Insects are exposed to a continuous multiple stressors across a range of environments. Desiccation tolerance and survival is dependent on water and ion homeostasis by fluid transporting epithelia including the Malpighian tubules. Fluid transport by insect Malpighian tubules is modulated by diuretic neuropeptides (Coast and Garside, Ann. NY Acad. Sci. 2005;1040:1-8; Yeoh et. al., Insect Biochem Mol Biol. 2017 Jul;86:9-19). These have also recently been shown to affect desiccation and starvation tolerance in the insect genetic model *Drosophila melanogaster* (Cannell et. al., Peptides. 2016; Terhzaz, et al., PNAS, 2015;112(9):2882-7) and in pest insects (Terhzaz, et al., Pest Manag Sci. 2018 Apr;74(4):800-810). However, in addition to this, a novel role for Malpighian tubules in cold tolerance has been recently demonstrated, which occurs via homeostatic control of water and ion balance and is modulated by the capa neuropeptide (Terhzaz, et al., PNAS, 2015;112(9):2882-7; MacMillan, et. al., Sci Rep 2015;5:18607). Altogether, this current evidence suggests that at least three diuretic neuropeptides (capa, DH44, kinin) perform functions in environmental stress tolerance via the Malpighian tubules. Thus, Malpighian tubules, and diuretic neuropeptides, have much wider implications for physiology and behaviour beyond osmoregulation.



Main Meeting, FG Systematics, Biogeography and Diversity

Poster: Syst 1

The hidden species diversity of Brazilian velvet worms (Onychophora: Peripatidae) in scientific collections

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The Neotropical region houses a diverse albeit unexplored fauna of peripatid velvet worms (Onychophora) — terrestrial invertebrates relevant for understanding biogeography and animal evolution. These organisms have previously been reported from numerous areas in nearly all territories of the western hemisphere south of Central Mexico, yet only 85 Neotropical species of Onychophora have formally been named. In Brazil, for example, just 16 onychophoran species have been described, although previous studies suggest a new species occurring every 20–30 km in forested areas of this large country. Two problems may account for this situation: (1) Neotropical onychophorans are difficult to find, and (2) the conserved morphology among species hampers their identification based on few specimens. Consequently, undescribed specimens have accumulated over the years in scientific collections. Herein, we demonstrate how a sufficient amount of information can be obtained from single onychophoran specimens using an integrative approach. For our study, we considered specimens from Brazil deposited in four scientific collections. Specimens were strategically partitioned in order to provide enough material for scanning electron microscopy, molecular analyses, and to keep collection vouchers. Based on the analyses of morphological and molecular data, we identified 49 taxa in these collections: 41 new taxa and 8 known species. Although molecular techniques proved ineffective for specimens in aldehyde-based fixatives, their unambiguous identification was still possible using a morphological screening approach. Our findings increase the known onychophoran diversity in Brazil by over 350% and demonstrate that an integrative approach opens new doors for exploring the hidden diversity of Onychophora.



Main Meeting, FG Morphology
Oral Presentation

Bricks and anchors: strategies for load bearing and muscle attachment in the cartilage skeletons of sharks and rays

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Unlike most vertebrates, sharks and rays have skeletons made of ‘tessellated cartilage’, a predominantly unmineralized cartilage, wrapped in a rind of tiny, mineralized tiles called tesserae. Tessellated cartilage performs similar mechanical roles to bone; however, how muscles attach to this cartilage skeleton has remained unclear, largely due to the challenges of characterizing the complex 3d interactions of the multiple tissue types. We investigate the relationship between muscular forces, skeletal morphology, and tessellation in microCT scans of paired skeletal elements from an age series of stingray. We use iodine-stained samples to resolve musculature and a custom segmentation algorithm to quantify tessellation patterns and morphometrics. We show that during growth, blocklike tesserae are the first to appear in areas of high positive curvature where high loads are expected, followed by flatter tesserae in regions of low curvature. Tesserae increase in size as animals age, but new tesserae appear only in flatter regions of the skeleton, suggesting that high-load areas are constrained to be less mutable. In adults, the largest tesserae are found along pronounced ridges, which often border zones of muscle attachment. Muscles insert via broad bundles of Sharpey's fibers, anchored into concave regions characterized by poorly developed tesserae. These findings and the demonstration that tesserae align along axes of loading argue that the morphology and relationship of tesserae can be used to infer loading environments in tessellated cartilage, helping also to explain the high performance of sharks and rays, despite the apparent limitations of a cartilage skeleton.



Main Meeting, FG Morphology

Poster: Morph 15

Comparative analysis of the innervation pattern in the male copulatory organ of spiders (Araneae)

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In spiders, the male copulatory organ is developed as a modified part of their pedipalps, the so-called palpal organ. For decades, it was thought that this copulatory organ lacks neural tissue, which led to the assumption that it was insensitive. It was not until 2015, that neural tissue was found in the palpal organ of the Tasmanian cave spider *Hickmania troglodytes*, resulting in a paradigm shift regarding the role of male copulatory organs during copulation. This new finding was supported in 2017, when neurons and a sensory organ were found in the male copulatory organ of *Philodromus cespitum*. Since these studies only focused on distantly related spider species, the need for a comparative study, addressing the evolution of the innervation of the palpal organ across the spider tree of life became obvious. In the present study, we analyzed the histology of male palpal organs in key spider taxa by covering all infraorders. We particularly target the potential appearance of palpal neural tissue in the ground pattern of spiders and how it evolved throughout the spider tree of life.



Symposium: Phenotypic Plasticity - RESPONSES of Animals to
Environmental Change
Oral Presentation

Master of invasion - Is phenotypic plasticity the key of success in the invasive fruit fly *Drosophila suzukii*?

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In a world where everything is in motion change is omnipresent. In nature some process, as genetic adaptation, allow organisms to respond to environmental changes. However, the evolution of the genome which may enable adaptation due to random mutation, drift or selection is a long process. The case of invasive species is particularly interesting to study due to their short-term adaptations. Invasive individuals must have the ability to survive, reproduce and disperse in a new environment. In a life time scale, phenotypic plasticity is expected to play a major role in determining invasion pattern by allowing organisms to cope with environmental changes. Phenotypic plasticity is the ability of an organism to express different phenotypes from a given genotype in response to the environment. Furthermore, invasive species are assumed to be more plastic than non-invasive species and populations from the settlement area are expected to have evolved to a higher ability of plasticity than populations from the origin area. Here, we explored the phenotypic plasticity of the invasive fruit fly *Drosophila suzukii*, which recently invaded two continents (USA and Europe) simultaneously offering the possibility to use natural replicates for our experiments. We compared the reaction norms of different populations from both continents for different life history traits with regard to the developmental temperature. Our data reveal significant differences in developmental time, fecundity, wing size and pigmentation demonstrating high phenotypic plasticity in natural populations of *D. suzukii*. These findings indicate that plasticity plays a key role in the range expansion of this species.



Main Meeting, FG Neurobiology*

Poster: NB 18

State-dependent sensory activity through modulation of back-propagating action potentials

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The wide variety of behavioral responses animals show when presented with the same stimulus suggests that nervous systems processes sensory stimuli in a context- and state-dependent fashion. Accordingly, animals must encode, propagate, and integrate sensory information from many sources in its nervous system to respond appropriately to their environment. Interactions between different senses that may allow for state-dependent responses occur on many levels of neuronal processing, and are often due to modulatory influences present in specific sensory conditions. This neuromodulation can increase axon excitability and induce extra 'ectopic' action potentials, which can in turn, travel backward into encoding regions modifying sensitivity as sensory information enters into the nervous system. We hypothesize that neuromodulation of back-propagating action potentials is a mechanism by which one sensory pathway dynamically influences the sensitivity of another sensory pathway. Our data from the stomatogastric nervous system of the crab, *Cancer borealis*, suggests that this is the case. We show that the frequency of ectopic action potentials in a proprioceptive neuron is dynamically modulated by chemosensory neurons descending from the central nervous system. The back-propagating ectopic action potentials then lead to significant changes in proprioceptive encoding. Specifically, sensory bursts were delayed, and the number of sensory action potentials was reduced with higher ectopic frequencies. Computational modelling of the encoding region predicts that slow hyperpolarizing currents, such as those mediated by Calcium-activated Potassium channels, facilitate the changes in proprioceptive sensitivity. We are currently testing this prediction in the proprioceptive neuron using molecular and electrophysiological techniques.

*Contribution also presented in: Symposium: 5th Meeting of the Arthropod Neuroscience Network (Poster: ANN 2)



Main Meeting, FG Developmental Biology
Poster: Dev 6

Characterization of putative stem cell marker genes in *Nematostella vectensis*

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Stem cell research in cnidarians has, until now, been focused on the genus *Hydra*, as they possess an intricate population of so called interstitial or i-cells, which function as dedicated stem cells. However, i-cells have so far only been found in Hydrozoa and may therefore not represent the ancestral condition. The anthozoan *Nematostella vectensis* is, like hydrozoans, highly regenerative and shows no signs of senescence, suggesting a stem cell and tissue homeostasis system. As a possible means to identify putative stem cells in *Nematostella*, we cloned numerous homologs of genes that have a conserved role in stem cells in vertebrates and *Hydra* and conducted an *in situ* hybridization screen. In selected cases, we generated transgenic lines for *in vivo* lineage tracing. Through this approach, we were able to identify a population of putative stem cells residing in the pharyngeal ectoderm and endodermal tissue of *Nematostella*. Future prospects of this project include the generation of more transgenic lines as well as the characterization of marked cell populations through the generation of a cell type-specific transcriptome. Results generated from these experiments will help us understand how stemness is established, regulated and maintained in Cnidaria, as well as allow insight into the evolutionary history of this integral cell type.



Main Meeting, FG Systematics, Biogeography and Diversity
Poster: Syst 6

The power of single- and multigene molecular species delimitation in a recent grasshopper radiation

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With almost 200 species divided into 3 subgenera, the genus *Sphingonotus* Fieber, 1852 represents a highly diverse taxon with almost cosmopolitan distribution. High morphological and ecological conservatism, as well as relatively high levels of endemism have led to much taxonomic errors and systematic confusions. Hence, objective ways of species delimitation are needed. Molecular methods provide an opportunity to objectively delimit genetic units, which may or may not correspond to morphological species. In order to estimate the power of molecular species delimitation, we separately used single and multi-gene alignments of morphologically clearly assigned species and employed several species delimitation tools to the two datasets. In contrast to other larger scale barcoding studies it was not possible to separate all species using information of the COI gene fragment. This may be due to incomplete lineage sorting, pseudogenes or infrequent hybridization. The multi-gene dataset provided a better resolution and resolved the majority of species. Our study confirms previous hypotheses that classic single gene DNA barcoding is insufficient in diverse young radiations.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral Presentation

Phylogenomics of the longitarsal Colossendeidae resolves the evolution of a diverse and globally distributed sea spider group

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Sea spiders (Pycnogonida) are a group of marine benthic arthropods that is particularly diverse in the Southern Ocean. The “longitarsal” group of the sea spider family Colossendeidae is especially abundant in this region. However, this group also includes some representatives from other oceans, which raises the question where the origin of the group took place. Therefore, we here investigated the phylogeny of the group with a hybrid enrichment approach that yielded a dataset of 1607 genes and over one million basepairs. We obtained a well-resolved phylogeny of the group, which is mostly consistent with morphological data. The data support an Antarctic origin of the longitarsal Colossendeidae and multiple dispersal events to other regions, which occurred at different timescales. Such a scenario is consistent with other evidence for the Southern Ocean being a source for the deep-sea fauna. Our data also confirm that the genus *Colossendeis* is paraphyletic, as the multi-legged forms *Decolopoda* and *Dodecolopoda* group within it. Several genes show significant evidence for positive selection, and some of these show gene phylogenies incompatible with the species tree, suggesting that advantageous alleles may spread between species by hybridization (adaptive introgression). We further assessed the role of these genes in adaptation to Antarctic vs. non-Antarctic environments.



Main Meeting, FG Neurobiology

Poster: NB 21

**Neurohormones from a novel neurohaemal organ in
Daphnia: Adipokinetic hormone/red pigment concentrating
hormone-related peptide and corazonin**

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Antibodies against known *Daphnia pulex* adipokinetic hormone (DappuAKH) and the conserved arthropod peptide Arg7-corazonin (Arg7-CRZ), were used to provide chromatographic and immunochemical evidence for identical peptides in the closely related species *Daphnia magna*. Together with decapod crustacean red pigment-concentrating hormone, another AKH-/CRZ-related peptide (ACP), and vertebrate gonadotropin-releasing hormones (GnRHs) these peptides constitute the GnRH-superfamily. We demonstrate for the first time in crustaceans identified neuronal systems immunoreactive to DappuAKH and Arg7-CRZ in the brain and a novel neurohaemal organ of *D. magna*. The largest DappuAKH-containing neurons are neurosecretory neurons project to an area around the circumoesophageal connectives and to the ventral-lateral foregut walls. These neurohaemal areas are reminiscent of classical decapod neurohaemal organs such as the postcommissural organs. The positions and projection patterns of merely two distinct Arg7-CRZ-immunoreactive brain neurons are similar to those of insects. Whilst these finding bear few functional implications for water flea physiology at present, the conserved primary structures of the peptides and their neuronal distribution point to a common evolutionary history of both peptides and their neurons in arthropods.



Main Meeting, FG Evolutionary Biology
Oral Presentation

How mothers deal with unpredictable environments: The European common frog, *Rana temporaria*

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The evolution of life-history strategies should increase reproductive success and fitness of individuals. Alternative life history strategies like the offspring number – size trade-off, bet hedging or phenotypic plasticity are advantageous, if species develop in unpredictable environments and face a high risk of reproductive failure. Offspring of the European common frog (*Rana temporaria*) exhibit a high degree of variability in metamorphic traits and environmental factors alone cannot explain this phenotypic plasticity. Here, we tested whether the maternal genotype influences developmental time, body size and body condition of progeny in a forest pond in Germany. We collected fertilized eggs from the 57 *R. temporaria* clutches deposited in that pond. We used multilocus microsatellite analyses to assign metamorphosed offspring to mothers and to determine the number of fathers per matriline. We tested whether multiple paternity increases the variability of metamorphic traits in a single matriline. For full sib offspring we tested if variability differs between and within matrilines to test for bet-hedging strategies and/or phenotypic plasticity. Multiple paternity increased the variability in developmental time within a matriline, but not size or body condition. The variability for size and body condition was higher within matrilines than between them, which indicates that these traits are more influenced by maternal provisioning. The developmental time varied considerably between matrilines indicating a stronger environmental influence and phenotypic plasticity of tadpoles. By mixing different life history strategies in unpredictable environments, mothers can increase variability of progeny and therefore, their individual fitness.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral Presentation

Drivers of diversification in Mantophasmatodea (Insecta)

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Mantophasmatodea was described as an insect order new to science in 2002. High levels of colour polymorphism, species-specific vibrational communication, restriction to selected biomes, and limited dispersal abilities make this flightless group a novel and exciting order in which to study speciation and adaptive divergence. The most speciose family (Austrophasmatidae) occurs only in the Succulent Karoo and Fynbos biomes of South Africa. Within Austrophasmatidae, the morphologically cryptic sister-taxa *Karoophasma biedouwense* and *K. botterkloofense* were studied in detail to infer the drivers of population differentiation and speciation. A multidisciplinary approach was taken incorporating a fine-scale population genetic study (17 microsatellite loci), vibrational recordings, morphological measurements, and colour polymorphism data from 339 individuals collected from 30 sites, spanning the known distributions of both species. We combined this data with habitat information for each site. Our results indicate that some population-level differences (e.g. morphology) are not driven by evolutionary forces but are due to factors such as food availability. However, our genetic data show that both species are highly geographically structured, indicating that there is limited inter-population genetic exchange, even over very short distances. Our data suggest that diversification was likely driven by vicariance caused by climatic changes in southern Africa which also gave rise to many of the biodiverse and distinct vegetation types in the Cape Floristic Region with which Mantophasmatodea are heavily associated. Due to the restricted dispersal abilities of this group, isolated lineages are likely to have evolved in allopatry and achieved complete speciation in a short time frame.



Main Meeting, FG Physiology
Oral Presentation

Insect renal function - new insights from multi-omic approaches

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Most living species are insects, and their successful diversification depends at least in part on the ability to osmoregulate successfully across a broad range of ecological niches. Insect Malpighian tubules were first described in the 17th Century, and renal physiology has been studied intensively for 70 years, step-changes in our understanding have been brought about by the advent of genomics, transcriptomics, proteomics and metabolomics. These technologies are natural partners with (though do not obligatorily require) model organisms and transgenic technologies. This talk will review the impact of multi-omic technologies on our understanding of renal function and control in *Drosophila melanogaster* and other insects. References: Leader, D.P., et al. (2017) FlyAtlas 2: a new version of the *Drosophila melanogaster* expression atlas with RNA-Seq, miRNA-Seq and sex-specific data. *Nucleic Acids Research* 46, D809-D815; Yeoh, J.G.C., et al. (2017) DIneR: Database for Insect Neuropeptide Research. *Insect Biochemistry and Molecular Biology* 86, 9-19; Halberg, K.A., et al. (2016) The cell adhesion molecule Fasciclin2 regulates brush border length and organization in *Drosophila* renal tubules. *Nature Communications* 7; Halberg, K.A., et al. (2015) Tracing the evolutionary origins of insect renal function. *Nature Communications* 6, 6800.



Main Meeting, FG Ecology

Poster: Ecol 7

Ecology and interaction of bumblebees and their phoretic mites – a case study in Middle and Northern Germany

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The parasitic mite *Varroa destructor* with its potential to spread viruses is considered one of the main reasons for honeybee decline. Bee viruses are found in many wild bees, yet, their virulence and transmission is not well understood. The *Varroa* mite does not parasitize on wild bees and hence other vectors must be in place. Phoretic mites, common on many insects, and bees, especially on bumblebees, may have the potential to spread diseases among species of wild bees. Yet, only few studies have so far investigated the interaction between bumblebees (*Bombus*, Latreille 1802) and their phoretic mites. In our study, we analyzed about 250 bumblebees sampled in spring 2015 and 2018 at two sites each in Halle and Hamburg, respectively, and compared the species composition of bumblebees and the individual mite load between species over time. We used DNA barcoding to delimit mite species. Finally, we investigated body size as intertegular space and dry and wet weight to check for negative effects of mites to their host. Mite load is high at the beginning of the season and quickly decreases when queens finished nest establishment. The mite diversity on single bumblebees is high, but no association of specific mites to bumblebee species was detected, a finding opening the opportunity for cross species transmission of diseases via this vector.



Symposium: 5th Meeting of the Arthropod Neuroscience Network
Oral Presentation

Topographic organization of pectine neuropils in scorpions

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Chelicerates do not possess dedicated antennae but have evolved their second sets of appendages into the eponymous cheliceres. They rather have evolved dedicated chemosensors in different body segments. In scorpions, pectines are specialized comb-like structures, located on the ninth body segment, used for examining the substrate for chemo- and mechanosensory signals. The comb teeth, or pegs, are truncated beveled structures facing the substrate for probing, and are studded with numerous sensory receptors. Afferents from the pectines project into a distinct neuropil of the central nervous system, located behind the fourth walking leg neuropils. Detailed neuroanatomical data concerning sensory projections into the nervous system are still missing, although crucial for functional and evolutionary considerations. In this study, afferents of single pegs in *Mesobuthus eupeus* were analyzed by backfilling, combined with immunohistological labeling of neuropil regions. The latter revealed the lobular organization of the posterior pectine neuropil, and a second homogeneously structured anterior neuropil. Sensory projections from a peg enter the posterior pectine neuropil on the ventral side and innervate distinct portions of the neuropil: Afferents of distal pegs project to lateral areas, and afferents of proximal pegs projected to medial areas of the neuropil. After leaving the posterior pectine neuropil through a medially located tract, the axon bundles terminate in an anterior neuropil, with no distinct somatotopic organization. This topographic organization of the primary pectine neuropil suggests high spatial resolution of chemical gradients and mechanical stimuli on the substrate.



Main Meeting, FG Evolutionary Biology
Oral Presentation

Venom evolution in robber flies

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Venoms are evolutionary key adaptations but the understanding of toxin evolution is dominated by the analyses of a few lineages like Snakes, Spiders, Scorpions and Cone Snails. In the recent years more and more long-time neglected groups were added to a diverse list of species using a venom for predation, defence or inner species competition. Predatory robber flies (Diptera, Asilidae) have been suspected to be venomous due to their ability to overpower well-defended prey. With over 7000 species, a comparable small genome size (200-600mb) and some highly specialized groups (California-beekiller) the asilidae are an interesting model group added to the picture of venom evolution. This study provides a detailed characterization of the venom system of robber flies through the application of comparative transcriptomics, proteomics and functional morphology. Our results reveal asilid venoms to be dominated by peptides and non-enzymatic proteins. Contrary to what might be expected for a liquid-feeding predator, the venoms of robber flies appear to be rich in novel peptides, rather than enzymes with a putative pre-digestive role. One group of identified peptides closely resemble cysteine inhibitor knot peptides (ICK), of which neurotoxic variants occur in cone snails, assassin bugs, scorpions and spiders. Toxicity assays of these ICK-like peptides against honeybees revealed a role as a neurotoxin involved in the immobilization of prey. The novelty of the robber fly toxins suggests that the venom system evolved independently from hematophagous dipterans and other venomous insects.



Main Meeting, FG Behavioural Biology
Oral Presentation

Clever birds – The relationship between productivity and learning in layer hens

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The intense selection of laying hens for high egg productivity is assumed to cause undesirable side effects, including changes in behavior, due to trade-offs in energy expenditure. Such trade-offs may also affect cognitive abilities. Therefore, we hypothesized highly-productive laying hens to show altered learning performance in comparison to moderate productive hens. We tested the learning ability of four chicken lines that differed in laying performance (200 versus 300 eggs/y) and phylogenetic origin (brown/white layer; respectively, within performance). In total, 64 hens were tested in semi-automated Skinner boxes in a three-phase learning paradigm (initial-learning, reversal-learning, extinction). To measure the learning performance within each phase, we compared the number of active decisions needed to fulfill a defined learning criteria using linear models. Differences between the lines in reaching the criterion on each phase of the tasks were analyzed by using a survival analysis. A greater proportion of high productive hens achieved the learning criteria on each phase compared to less productive hens. Furthermore, high productive hens accomplished the learning criteria faster in the initial phase and in extinction compared to the less selected lines. Our results indicate that selection for productivity traits has led to changes in learning: high productive hens possess a better learning strategy in a feeding-rewarding context. This superior performance may be a potential response to any constraints and may enable the hens to efficiently acquire energy resources. Underlying mechanisms for this may be related to differences in neuronal structure, to foraging strategies or changes in personality traits.



Symposium: 5th Meeting of the Arthropod Neuroscience Network
Oral Presentation

Sensory control of locomotion in stick insects

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The Indian stick insect *Carausius morosus* is an important study organism in animal motor control and adaptive behaviour. In this talk, we will provide a brief overview over a set of recent studies on questions concerning adaptive, sensory-controlled coordination of a multi-limbed body. This will include experimental studies on distributed proprioception (load in particular), touch and vision. Methodologically, we will combine whole-body motion capture of unrestrained walking insects with ground-reaction force measurements and EMG recordings, but also extracellular nerve recordings and a hardware study in biorobotics. With regard to proprioception, we will elaborate on recent findings about a potential load-based mechanism of leg coordination, and discuss how this mechanism relates to adaptation of muscle force as the animals walk on different on inclines. Also, we will discuss the relative significance neural and mechanical information exchange among ipsilateral leg pairs. With regard to touch, we will show the potential use of vibration measurements at the antennal base for tactile localisation of objects. Moreover, we will report on the effects of different modalities on the sensory adaptation in a descending interneuron the conveys antennal information. With regard to spatial coordination of limbs in climbing, we discuss the relative significance of near-range tactile cues as opposed to far-range visual cues.



Main Meeting, FG Behavioural Biology
Oral Presentation

Biotremology in Heelwalkers: I got rhythm!

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Recognition of conspecific mates is crucial for successful reproduction. One communication mode employed by arthropods is the transfer of information via substrate-borne vibrations (biotremology). We investigated the vibratory communication signals in Heelwalkers (Mantophasmatodea), which locate their mates via percussive signals. We used males and females of *Karoophasma biedouwense* (Western Cape, South Africa), to explore if male quality is conveyed to the females via their signals. Additionally, the effect of temperature was investigated by recording males at 15 - 30°C. To assess how the variability of informative cues within male signals affects female choice, we used playback experiments. Male advertisement signals were stable irrespective of feeding status, but varied with male condition: better-conditioned males exhibited more pulses per pulse train (PT). Temperature has a significant effect on signals in *K. biedouwense* males, as pulse repetition times, PT durations and PT repetition times decreased with increasing temperature ($Q_{10} < 0.7$). Females, in contrast, responded to a variety of artificial male signals, far beyond the range of the natural PT-duration/pause – patterns. However, calls having too short pauses or PT durations were rejected, as well as unnaturally long or short pulse repetition times. We show that male signals vary with individual physical and environmental conditions. Females exhibited a broad acceptance of the overall temporal patterns but rejected pulse repetition times outside the species-specific average. The combination of all signal parameters as well as temperature coupling thus appear to contain the species recognition coding reinforcing species boundaries and potentially facilitating assortative mating in Mantophasmatodea.



Main Meeting, FG Evolutionary Biology

Poster: EvoBio 2

The effect of spermathecal secretions on sperm storage in *Drosophila melanogaster*

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Females of virtually any internally fertilising species store viable sperm, lasting from days to years, in their reproductive tract or in specialised organs. *Drosophila melanogaster* females store sperm for at least 14 days after mating. They possess two types of storage organs. The paired spermathecae serve for long-term sperm storage, while the seminal receptacle is used for short-term sperm storage. The spermathecae are surrounded by cells with secretory function, whose products as a whole are required for proper sperm storage in spermathecae and seminal receptacle. However, little is known about individual secretory products but several components of the spermathecal secretions have been suggested to support sperm viability, including aquaporins, antioxidants, antimicrobials and metabolic enzymes. We use the GAL4/UAS system to knock down the function of secretory cells around the spermatheca and test for the effect of individual spermathecal secretions on female sperm storage. We compare the location of sperm in the sperm storage organs as well as egg and offspring number in females with and without spermathecal secretory cells. We also examine females that have their spermathecal secretory cells enhanced and completely disrupted. We further assess the impact of single secretions, for instance several antioxidants, on female sperm storage.



Symposium: 5th Meeting of the Arthropod Neuroscience Network
Oral Presentation

A multimodal orientation compass in dung beetles

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Some dung beetles have developed a unique orientation behavior to avoid competition for food at the dung pat. They cut off a piece of dung, form it into a ball and roll it away along a straight path. To maintain their direction, these animals rely on multiple celestial cues, such as the sun and polarized light, for orientation. In addition, wind is often present in the beetles' habitat and could play a crucial role as reference when skylight cues are not available. This raises the question of how dung beetles define the relevance of different cues and how celestial and putatively wind information are integrated in the beetle's compass. To formulate an understanding of the beetles' compass, we tested their orientation behavior and analyzed the brain activity. Our experiments show that dung beetles rely on the sun rather than polarized skylight as main cue. Surprisingly, when skylight information becomes more ambiguous at high sun elevations, the beetles switch to a wind compass to maintain the same heading. The relevance of these cues seems to be defined prior to rolling, when a beetle dances on top of a ball and takes at least a celestial snapshot. Neurons of a brain region, the central complex, encode skylight information, and respond to wind stimuli. These neurons are therefore perfectly suited to integrate wind information into the beetle's sky compass. The reliance on multiple cues generates a robust compass that allows the animal to maintain a course at any moment in time.



Main Meeting, FG Ecology

Poster: Ecol 5

Predator-driven biotic resistance: dogwhelk preferences for prey and nonconsumptive limitation of prey recruitment constrain introduced barnacles on the Pacific coast of Hokkaido, Japan

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Introduced species are a major threat to the biodiversity of marine coastlines worldwide. Thus, understanding factors that constrain introduced species is a central goal of invasion biology. Consumption by native predators can limit introduced prey given that predators prefer such prey. Furthermore, predator nonconsumptive effects (NCEs), mediated through predator-released cues perceived by prey, can limit prey recruitment, a key demographic process for population establishment. However, information on predator NCEs is missing for recruitment in introduced prey. We addressed this knowledge gap on the Pacific coast of Hokkaido, Japan using native predatory dogwhelks (*Nucella lima*), native barnacles (*Chthamalus dalli*) and introduced barnacles (*Balanus glandula*). Seeking evidence for predator-driven biotic resistance against introduced prey, we experimentally examined dogwhelk preferences for barnacles in the lab, and dogwhelk NCEs on barnacle recruitment in the field. We found that dogwhelks preferred *B. glandula* over *C. dalli*, presumably as *B. glandula* prey is more profitable, as suggested by previous findings in congeneric dogwhelks. Moreover, we found that dogwhelk cues limited recruit density in both barnacles, likely as barnacle larvae moved away from such cues to reduce future predation risk. Finally, as recruitment occurred earlier in *C. dalli* than *B. glandula*, we found that the nonconsumptive limitation of *C. dalli* recruit density increased the area available for *B. glandula* recruits. This indirect effect, however, did not favour *B. glandula* recruitment, because dogwhelk cues also limited *B. glandula* recruit density. We conclude that *N. lima* preferences and NCEs contribute to predator-driven biotic resistance against the introduced *B. glandula*.



Main Meeting, FG Evolutionary Biology
Oral Presentation

Longevity and transposon defense, the case of termite reproductives

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Aging occurs in most organisms and appears to trade off with fecundity. In some organisms, such as queens of social insects, this trade-off is apparently absent, allowing individuals both a long life and a high reproductive rate. Within colonies, longevity differences of several magnitudes exist that can be found elsewhere only between different species. We studied aging in the wild in a highly social insect, the mound building termite *Macrotermes bellicosus*. Here, queens and kings can live for up to 20 years and the former concurrently lay ~20.000 eggs per day while workers live only few weeks. We show that gene-expression patterns differed little between young and old reproductives, implying negligible aging (1). By contrast, old and young major workers had thousands of genes differentially expressed, including hundreds of transposable elements (TEs) that were upregulated in old major workers. TEs can cause aging. Strikingly, genes from the PIWI-interacting RNA (piRNA) pathway, which are generally known to silence TEs in the germline of multicellular animals, were downregulated only in old major workers but not in reproductives. Continued up-regulation of the piRNA defense commonly found in the germline of animals can contribute to explain the long life of termite reproductives, implying somatic cooption of germline defense during social evolution. This presents a germline/soma analogy as envisioned by the superorganism concept: the reproductives and workers of a colony reflect the germline and soma of multicellular animals, respectively. (1) Elsner D, Meusemann K, Korb J (2018) PNAS:201804046.



Main Meeting, FG Morphology*

Poster: Morph 29

Immunohistochemical investigations of the brain of the water bear *Echiniscus* sp. (Heterotardigrada)

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Tardigrades (water bears) are microscopically small invertebrates that live in terrestrial habitats like mosses and lichens and are also represented in marine and limnic habitats. Water bears are part of the Ecdysozoa, but the exact classification is not yet settled. Tardigrades could be the sister group of Nematoda, Onychophora, Arthropoda or Onychophora + Arthropoda. Comparative studies involving the nervous system could help clarify the systematic relationships. However, studies of the last years have not offered a common pattern of the tardigrade brain. Currently, there are several contradictory theories about the construction of the brain, therefore many questions remain open. Does the brain consist of one or several segments? How are the brain lobes arranged? Does the brain of tardigrades contain a subesophageal or subpharyngeal ganglion? To address these questions, we performed immunohistochemical labelings of the nervous system of the heterotardigrade *Echiniscus* sp. using antibodies against acetylated and tyrosinated α -tubulin as well as synapsin. With these data we created a 3D model for a better visualization and understanding of the brain. The results argue against the existence of a subesophageal or subpharyngeal ganglion. Furthermore, we were able to detect three ventral commissures in the tardigrade head, each associated with a cluster of cell bodies. Our findings expand our understanding of the evolution of the brain and associated head sensory organs in tardigrades and lay the foundation for future comparative studies with other panarthropods.

*Contribution also presented in: *Symposium: 5th Meeting of the Arthropod Neuroscience Network (Poster: ANN 21)*



Main Meeting, FG Systematics, Biogeography and Diversity
Oral Presentation

More than meets the eye: genetic and morphological divergence between populations of North and Baltic Sea marine macrozoobenthos

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The Baltic Sea is a unique habitat with its brackish water and young age (ca. 8000 years). However, the organisms inhabiting the Baltic Sea were long thought to be but depauperate extensions of their North Sea ancestors. Only recently have we begun to appreciate the genetic distinctiveness of Baltic Sea populations, which might hint at beginning speciation. Adapting to the unique environmental conditions of the Baltic Sea would further accelerate genetic divergence and speciation. While adaptation is not easily proven, morphological, and therefore potentially functional differentiation might hint at adaptive processes. To gain a more comprehensive view of Baltic Sea diversity, we compared mitochondrial DNA and morphology in several prominent marine invertebrates of the macrozoobenthos from North and Baltic Sea. We find that Baltic Sea populations are either morphologically or genetically distinct, but rarely both or neither. We thus confirm the notion that the Baltic Sea is a unique habitat with distinct populations, which might stand at the brink of speciation. Future research aims at understanding whether the divergence between North and Baltic Sea populations is a recent phenomenon triggered by the extensive impact of human activity over the past 200 years, using time series available in natural history museums.



Workshop: From Gene to Function: Using CRISPR/Cas9 in Zoology
Oral Presentation

Using CRISPR/Cas9 to mark genetic neural lineages in insects

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CRISPR/Cas9 genome editing allows for precise manufacturing of transgenic lines to suit specific research questions. Inserting a construct at a specific location rather than a random one considerably reduces the chance of unwanted side effects such as mutations. This is preceded by a precise design of transgenic lines. I will present efforts in our lab in making such lines in *Tribolium castaneum* as well as in *Drosophila melanogaster*. We have built lines to mark neural cells throughout development by using two approaches. On the one side, we have used homologous recombination to edit a gene locus to express a bicistronic mRNA. By using the self-cleaving 2A peptide the expression of a transcription factor is faithfully reflected by EGFP expression. On the other side, I will also present a way to generate enhancer traps within specific genes via non-homologous end joining, which represents a faster, albeit less precise approach compared to building bicistronic reporter lines. Finally, I will share advantages of each method as well as their pitfalls and I will also present some recommendations on how to design future experiments.



Main Meeting, FG Behavioural Biology*

Poster: Behav 11

The influence of feeding routines on animal welfare in laboratory mice

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In most laboratories mice are kept under *ad libitum* diet. However, recent studies revealed negative effects of this feeding routine. In contrast, a restricted diet that causes a decrease in body weight of 10 % or more has been shown to cause an enhanced life span, a reduced risk of diseases and a reduction of the decline of cognitive abilities with age. Therefore, the aim of this study was to compare different feeding routines and their effect on body weight, anxiety-like behavior and fecal corticosterone metabolite concentrations as indicators of the animals' welfare. In a first experiment we compared (a) *ad libitum* feeding with (b) feeding a specific amount of food once per day (24h schedule) and (c) free access to food except during 4 hours per day (4h schedule). In a second experiment, we compared (a) *ad libitum* feeding with (b) a 24h schedule and (c) using an automated device to deliver premeasured food pellets at 6 different time points throughout the day (SnackClock, [1]). A 24h schedule or a SnackClock reduced the weight of male C57BL/6J mice to 90 – 95 % of their free feeding weight. In contrast, the 4h schedule only caused a transient weight loss in males and no significant differences in females. The anxiety-like behavior and the corticosterone metabolite concentrations are still under investigation. Our results will show whether the tested feeding routines are feasible alternatives to *ad libitum* feeding to improve animal welfare. [1] Adapted from: <https://hackaday.io/project/106587-snackclock>

* Contribution also presented in: Workshop: Animal Welfare (Oral Presentation)



Workshop: From Gene to Function: Using CRISPR/Cas9 in Zoology
Oral Presentation

Lessons learnt from CRISPR/Cas9 on the sea anemone *Nematostella vectensis*

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Since its discovery, CRISPR/Cas9 has become one of the most used molecular tools. One of its benefits is that it can be used on a wide range of organisms including Cnidaria. Using CRISPR/Cas9 we have successfully knocked out number of genes and generated a transgenic line in the cnidarian model organism *Nematostella vectensis*. Throughout this process we have learned valuable lessons regarding target design and indel-efficiency verification. One of the problems we encountered was a low percentage of target cleavage, which we could partially attribute to sgRNA self-annealing. We have also observed that although an indel with frame shift was generated by CRISPR/Cas9 a functional protein was still produced. We are currently working on knock in strategies both for marking mutation and tagging proteins.



Main Meeting, FG Physiology
Oral Presentation

The molecular basis of essential fatty acid limitation in *Daphnia magna* - a transcriptomic approach

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It is widely accepted that in many food webs, the trophic transfer efficiency among primary producers and herbivores is determined by the nutritional value of primary producers. In pelagic freshwater and marine ecosystems, secondary production by herbivorous crustacean zooplankton is often limited by the seston's content of essential ω 3 polyunsaturated fatty acids (ω 3 PUFAs). However, little is known about the genetic network behind the positive relationship between phytoplankton ω 3 PUFA content and zooplankton growth and reproduction. In our experimental study, we analysed gene expression changes of the freshwater cladoceran *Daphnia magna* under different food regimes differing in their ω 3 PUFA composition. To disentangle ω 3 PUFA effects from other factors, we fed *D. magna* with different pure phytoplankton cultures (i.e., algal and cyanobacterial diets) with or without supplementing the essential ω 3 PUFA eicosapentaenoic acid (EPA). As hypothesized, we observed enhanced growth on diets supplemented with EPA. We applied an Illumina RNA-seq approach to *D. magna* from different diet treatments to find and monitor genes that are regulated dependent on EPA availability. Of 26,646 potential protein products (mapped to the *D. magna* genome), we identified transcriptomic signatures driven by the different food sources. Further analyses revealed specific candidate genes involved in EPA metabolism, irrespective of the basal food source. This allows a first functional annotation of previously uncharacterized genes involved in the EPA-specific response of *D. magna* and may finally provide a link to molecular processes connected to ω 3 PUFA metabolism and conversion and thus trophic transfer efficiency in pelagic food webs.



Main Meeting, FG Behavioural Biology

Poster: Behav 12

The meaning of scent marks and location on the foraging behaviour of stingless bees

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Several species of stingless bees use scent to mark food sources. Additionally colour and location are important factors for the recognition of food sources. Here we used an experimental setup to test the relative importance of scent marks and location for visits to feeders in two species of stingless bees, *Melipona subnitida* and *Plebeia* aff. *flavocincta*. First the bees were trained for 30min to a feeder that was used as the marked feeder in the subsequent test. In the test the bees had to choose between a scent-marked and an unmarked feeder within 5min that were positioned at 15m and 17m distance from the hive. The distance of the training feeder as well as that of the test feeders, 15m or 17 m resp., were varied. *M. subnitida* neither showed a preference for the marked feeder nor a preference for the feeder located at the training position, but preferred the feeder at closest proximity to the nest. *P. flavocincta* chose the marked feeder significantly more often even if it was not established at the training position or further away from the hive. We conclude that *P. flavocincta* depends more strongly on scent markings than *M. subnitida* possibly due to the large differences in body size of the two species. Smaller bees are known to have a reduced visual capacity and therefore might not orientate according to visual parameters of the target such as colour hue, saturation or brightness but use scent cues instead.



Main Meeting, FG Morphology
Oral Presentation

On the ultrastructure of the epithelium of Pendergrast´s Organ of Acanthosomatidae (Insecta, Heteroptera, Pentatomoidea)

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The Pendergrast´s Organ (PO) are paired setose areas on the female abdominal segments. Within the Acanthosomatidae PO can be present on the female abdominal segments V, VI and VII. Based on phylogenetic analyses, PO on the abdominal segments VI and VII belong to the stem-species pattern of Acanthosomatidae, while PO on the female abdominal segment VII supports the sistergroup relationship of Acanthosomatidae and Lestoniidae. The PO plays an important role during oviposition. Females touch the setose areas of the PO and eventually rotate the eggs with their hind tarsi before depositing them. There is strong evidence that the PO produce secretions which may protect the egg clutch. Phylogenetic analyses reveal that the lack of PO in acanthosomatid *Elasmucha* is a reduction. Females of *Elasmucha*-species guard their egg-clutch and nymphs. The ultrastructure of the epithelium of PO was investigated using SBFSEM. Between the apical cuticle and the basal lamina three different cell types can be recognized: bristle cells, interstitial cell and gland cells. The PO epithelium meets the criteria of a multilayered epithelium, since only the PO gland cells are in contact with the basal lamina. A 3D-reconstruction reveals the relative position of cell organelles and the cuticular reservoir within a single PO gland cell. Reservoir and ductule of the PO gland cell are formed by an invagination of the cuticle.



Main Meeting, FG Ecology
Oral Presentation

The role of environmental reservoirs in the persistence and transmission of pathogens: Lessons from *Pseudogymnoascus destructans*, the causative agent of White-Nose Disease

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Hibernation decreases metabolic rate and body temperature resulting in a severe reduction of the thermal barrier for protection against fungal infections. Among them, *Pseudogymnoascus (Geomyces) destructans (Pd)*, the causative agent of White-Nose Disease, only emerged in North America in 2006 where it has caused the death of millions of bats. As bats clear the infection after hibernation, it remains unclear how they get infected each year and whether transmission rate is exacerbated by inter-individual contacts. We isolated >800 isolates from bats during hibernation and from the environment before and after hibernation over four years. Isolates were genotyped at 18 microsatellite loci making it possible to follow fungal individuals as they infect bats in different parts of the hibernaculum and over time. The spatio-temporal distribution of individuals clearly shows a pattern of environmental infection with bat-to-bat infections only playing a minor role. The frequency of the different individuals on the hibernating bats was strongly correlated to individuals' frequency in the environment prior to hibernation. We also demonstrated the survival of spores from April to October on walls of hibernacula in the absence of bats. These results show that the environment acts as a reservoir allowing yearly re-infection of bats as they enter hibernacula, which has important implications for disease management. Once the fungus has been found at a site, it will not be eradicated by the absence of bats alone, but needs to be actively removed from the environment to prevent future re-infection.



Main Meeting, FG Morphology

Poster: Morph 13

3D reconstruction of the smallest known insect photoreceptors: the stemmata of the first instar larvae of *Stylops ovinae* (Insecta, Strepsiptera)

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First-instar larvae of the Strepsiptera are among the smallest multicellular animals known, with an average length of 230 μm . So far, very little is known about the cellular anatomy of the stemmata of these extremely miniaturized larvae. Ultrastructural data are completely lacking. To illuminate the anatomy, the ultrastructure of the stemmata of the first larval instar of *Stylops ovinae* (Stylopidae) was analyzed using ssTEM (serial-sectioning Transmission Electron Microscopy). The 3D reconstruction revealed an identical cellular composition of all three stemmata: a biconvex corneal lens positioned distally to four corneagenous cells and five subjacent retinula cells. Additional pigment cells are not present. The rhabdome of each stemma is fused. The three rhabdomes of the stemmata, with maximal dimensions of 1.84 x 1.17 x 1.01 μm and volumes of 0.97 to 1.16 μm^3 , are the smallest described insect photoreceptors. Functional morphological adaptations pertaining to miniaturization are (1) the proximal displacement of parts of the cell bodies of the retinula cells; (2) the reduction of cell nuclei in the corneagenous cells; and (3) the presence of the smallest nuclei reported in arthropods so far, with volumes reduced to 1.37 μm^3 in the retinula cells. Besides the 3D reconstruction of the stemmatal morphology, numerical and volumetric information of all constituent cell types and their mitochondria and pigment granule contents are presented.



Main Meeting, FG Ecology
Oral Presentation

The effect of ectoparasites on the nesting preference of a migrant and a resident passerine species: a choice experiment

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Bird nesting cavities offer an ideal environment for ectoparasites, which can negatively affect both the offspring and the parental fitness component. Ectoparasites can survive the winter in old nest material or even in empty cavities. Previous work on cavity-breeding bird species indicates that they prefer to breed in cavities with less or no ectoparasites. Depending on the local level of nest parasite infestation and the effects on the hosts' fitness the evolved preferences of species may differ. The preference for parasite-free nesting sites may furthermore differ between resident species which have the whole year to acquire and defend a nesting site and migrant species which still have to claim a spot after they arrive. Migrants may therefore not be too picky about their choice of nesting site and may actually prefer the presence of old nest material regardless of the level of ectoparasites in order to facilitate speedy nest building. Here we tested, with a choice experiment, whether the resident Great tit (*P. major*) and the migrant Pied flycatcher (*F. hypoleuca*) prefer to breed in nest cavities without ectoparasites. To this end, we set up 30 locations in a new nest box area in Lingen (Germany) just before the breeding season in 2018. Per location, we offered three nest boxes, two nest boxes with old sterilized nest material and one nest box with old non-sterilized nest material. We next monitored the choices made. Here we report on the outcome of our experiment.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral Presentation

A taxonomic re-evaluation of the genus *Archaeopteryx* – implications for the diversity and biogeography of Jurassic stem-line representatives of birds

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With the description of the 12th skeletal specimen of the iconic primeval bird *Archaeopteryx* from the earliest Tithonian Painten Formation of Schamhaupten (Bavaria) (Rauhut 2018, PeerJ 6:e4191) we provide the first comprehensive diagnosis of the genus. Due to high level of homoplasy in the group Paraves, *Archaeopteryx* cannot be diagnosed on the basis of any single apomorphic characters, but only by an apomorphic set of combined characters. Accordingly, most specimens can actually be referred to *Archaeopteryx*, although the lost Maxberg and the fragmentary 'chicken wing' specimen cannot be evaluated with certainty. Interestingly, all *Archaeopteryx* specimens show a high amount of variation in the dentition (in terms of tooth number, spacing, and morphology) with no two specimens showing the exact same pattern. This could indicate the presence of more than one species of *Archaeopteryx*, but as the significance of this variation is unclear, a taxonomic evaluation on the species level is not possible at the moment. By contrast, the Haarlem specimen shows distinct differences in the morphology of the manus and the pubis compared to *Archaeopteryx*. A phylogenetic analysis places the specimen apart from *Archaeopteryx* inside the Anchiornithidae, which were only known from China, so far. On this basis, the Haarlem specimen was named as new taxon, *Ostromia crassipes* (Foth, 2017, BMC Evolutionary Biology 17:236), indicating a greater diversity of bird-like theropods from the Upper Jurassic of southern Germany and a more complex biogeographical evolution of paravian theropods.



Symposium: Phenotypic Plasticity - RESPONSES of Animals to
Environmental Change
Oral Presentation

Red does not always outperform black: morph-specific behavioural variation in response to environmental changes

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Variable selection pressures on individuals underlie the occurrence of distinct phenotypes within species. Rapidly-changing environmental conditions due to climate change are therefore likely to alter selection pressures and hence the current balance between phenotypes. In birds, colour polymorphism has been related to alternative behavioural strategies, potentially underlying different responses to extreme environmental conditions between colour morphs. To examine this point, we examined here how red- and black-headed Gouldian finches (*Erythrura gouldiae*) responded to experimentally-induced heatwaves of different intensities. The behavioural response of birds of different morphs was expected to vary, which may ultimately exacerbate or reduce initial behavioural differences between colour morphs. Accordingly, we found that the exploration behaviour of birds was negatively affected by temperature conditions, with red-headed individuals responding more strongly to temperature variations than black-headed individuals. In contrast, the behavioural balance between colour morphs remained unaffected by thermal conditions for the other behavioural traits we measured (aggressiveness, docility, food consumption). These results show that the behavioural balance between morphs is not static, and that exploration differences between morphs are more sensitive to environmental conditions than other behavioural traits. How such behavioural adjustments within species affect the balance between colour morphs in natural populations facing extreme environmental conditions remains to be determined.



Main Meeting, FG Morphology
Poster: Morph 1

Tracking the development of deep sea mussels during colonization by their symbionts

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Deep-sea mussels of the genus *Bathymodiolus* dominate many hydrothermal vents and cold seeps. Their vast biomass in nutrient-poor, deep-sea environments is possible through mutualistic symbioses with chemosynthetic bacteria that provide the mussels with nutrition. Previous studies on morphological adaptations to this unique feeding strategy reported enlargements of the gills that harbor the symbiotic bacteria, and a reduction of the digestive system in adult individuals. However, little is known about morphological adaptations in earlier life stages of these mussels such as metamorphosis and their acquisition of symbionts from the environment. We focused on the development of pediveliger to juvenile stages of three *Bathymodiolus* species (*B. azoricus*, *B. puteoserpentis* and *B. childressi*) from hydrothermal vents and cold seeps. Using a correlative approach that combined light-, fluorescence- and electron microscopy with synchrotron radiation based X-ray micro tomography, we could follow the development from pediveliger larvae through metamorphosis to juvenile stages. In pediveliger larvae, gill filaments began to develop and all tissues were aposymbiotic. Symbiont colonization occurred towards the end of metamorphosis. The digestive system was fully developed without signs of reduction in any of these life stages. Lipid granules in pediveliger stages comprised up to 14% of the mussel biomass and were degraded during metamorphosis. This work provides the first detailed insights into the early development of deep-sea mussels of the genus *Bathymodiolus*. It serves as a basis for understanding symbiont influence on host morphology during the transition of their feeding strategy from an aposymbiotic, filter-feeding stage to a symbiotic lifestyle.



Main Meeting, FG Evolutionary Biology
Poster: EvoBio 3

Male mate choice and aggregation behavior in relation to highly divergent mtDNA haplotypes in *Altica lythri* (Col., Chrys.)

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The flea beetle *Altica lythri* exhibits a complex genetic structure of three different mtDNA haplotypes. These haplotypes correlate with infections of the beetles with three strains of *Wolbachia*, who among other commonly co-occurring reproduction distorters are potentially responsible for a female biased sex-ratio. In *A. lythri*, depending on a female's haplotype, her offspring ratio will show a strong excess of females, or even no males at all. While the exact mechanism is unknown, male-killing or gynogenesis are possible candidates. Due to limitations of the amount of sperm in male beetles, mating with a female with an unfavourable haplotype can result in a greatly reduced number of offspring. In the case of gynogenesis the male might even copulate numerous times without producing any offspring. To counteract this, males should have developed behavioural strategies to recognize disadvantageous females and avoid aggregations or single females of certain haplotypes. In contrast, females in populations with high frequencies of all female producing haplotypes should actively search out males or aggregations with a high percentage of males in them to increase their chances for successful copulations. To test for these behaviours we conducted y-maze choice experiments with focus animals being given the choice between differently composed beetle groups with regard to a) their sex-ratio and b) their haplotypical make-up. The results further our understanding of the influence of the genetic structure on the population dynamics of *A. lythri*.



Main Meeting, FG Neurobiology*

Poster: NB 27

The use of spectral cues for orientation in the monarch butterfly *Danaus plexippus*

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Each fall millions of monarch butterflies (*Danaus plexippus*) migrate over thousands of kilometers from North America southwards to their overwintering habitat in Central Mexico. To maintain their migratory direction over this enormous distance, these butterflies rely on celestial cues, such as the sun and polarized skylight, as orientation references [Mouritsen and Frost, PNAS (2002); Reppert et al., Curr Biol (2004); Stalleicken et al., JEB (2005)]. In addition, a non-uniform distribution of longer and shorter wavelengths of light generates a skylight spectral gradient that could potentially be used as a compass cue by butterflies. Here, we asked whether we can test non-migrating butterflies under laboratory conditions and if they can use spectral cues for orientation. The headings of butterflies were tested individually while the animals were tethered at the center of a flight simulator. We presented spectral cues (green and/or UV light spots) to the animals while they were able to freely change their bearing with respect to the light stimuli. Even though the tested butterflies were in a non-migrating stage, they used the lights (green or UV) to keep a constant heading. When we changed the position of the visual stimuli by 180°, the butterflies changed their flight direction accordingly, suggesting that they use the presented cues for course maintenance. Further investigations will reveal if the butterflies use spectral or intensity information to keep their constant heading. Taken together, our data show that non-migrating monarch butterflies maintain a stable direction under laboratory conditions with respect to different spectral cues.

* Contribution also presented in: Symposium: 5th Meeting of the Arthropod Neuroscience Network (Poster: ANN 3)



Main Meeting, FG Morphology

Poster: Morph 30

The development of protocerebral sensory organs in *Amphibalanus improvisus* (Cirripedia, Crustacea)

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Morphological details of the development of the nervous system in crustaceans are very important for understanding the evolution of this very disparate arthropod group. But apart from the well-studied Malacostraca, knowledge of the development of the protocerebral sensory organs in the other groups of crustaceans is rather poor. We investigated the developing brain of *Amphibalanus improvisus* using immunohistochemical labeling against alpha-tubulin and various neurohormones, in combination with confocal laser scanning analysis and 3D reconstruction. Our results show that the morphology of the protocerebrum undergoes considerable change during development. The protocerebral sense organs considered in this study are the compound eyes and the frontal filament organs. We show that the nerves of both organs develop on parallel courses and maintain these during development. Furthermore, during the so-called second metamorphosis degradation of both nerves proceeds simultaneously. Since Cirripedia is grouped together with Copepoda and Malacostraca to form the Multicrustacea, a comparison of the development of the protocerebral sensory structures among these taxa is of particular importance. We provide an insight into the structural organization and development of the visual neuropils in cirripeds and compare them with those of malacostracans. Furthermore, the innervation of the compound eyes is compared to the nerve of the "Gickelhorn organ", a photoreceptor in copepods.



Workshop: From Gene to Function: Using CRISPR/Cas9 in Zoology
Oral Presentation

Regulation of developmental-age specific bacterial colonization by TLR receptors in *Nematostella vectensis*

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The establishment of host-bacterial colonization during development is a fundamental process influencing the fitness of many organisms, but the factors controlling community membership and influencing the establishment of the microbial ecosystem during development are poorly understood. *Nematostella vectensis* is an emerging model organism for Eco-Evo-Devo research and offers manifold possibilities for research of host-microbe interactions. *Nematostella* possesses a microbiota that is specific for its three developmental life stages: Planula larva, juvenile polyp and adult polyp. In recolonization experiments, we recolonized gnotobiotic adult polyps with age-specific microbiota of all three life stages, respectively. Following the dynamic reconstruction of the microbial community over the period of one month, we showed *Nematostella's* ability of shifting the early and juvenile microbiota composition into an adult one. Using a candidate approach, we hypothesize that bacterial recognition by Pattern Recognition Receptors (PRRs), especially Toll-Interleukin-1-Receptor (TIR)-domain containing receptors including the classical Toll-Like Receptor (TLR), play an essential role in the establishment of the age-specific microbiota. Using CRISPR/Cas9 genome editing, we are currently generating knock-out mutants for five TIR-domain receptors in *Nematostella* to evaluate their contribution to developmental-age specific bacterial colonization. Our results show that bacterial recognition in *Nematostella vectensis* varies during development, which may result in the establishment of developmental age-specific bacterial colonization.



Main Meeting, FG Evolutionary Biology*
Oral Presentation

Social evolution in the harvester ant genus *Pogonomyrmex*

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Queen number is a key component of ant societies and has repercussions for many aspects of an ant's life history and evolutionary trajectory. It becomes more and more apparent as we study species in more detail and include more populations per species that queen number is a very plastic trait that varies between generations, populations and species. The New World harvester ant genus *Pogonomyrmex* shows a great variation in terms of its social organization/queen number at all three levels. I will present socio- and population genetic/genomic as well as ecological data on several species and populations and describe the underlying ecological and evolutionary mechanisms that can explain the observed social polymorphism in the genus.

* *Contribution also presented in: Symposium: Phenotypic Plasticity - RESPONSES of Animals to Environmental Change (Oral Presentation)*



Main Meeting, FG Physiology
Oral Presentation

“Green insecticides” based on insect neuropeptides: concept and first results

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Insect neuropeptide hormones fulfil many tasks, such as changing behaviour or physiological actions. “Green insecticides” are substances that do not harm the environment and act discriminatively against pest insects (lethal) and beneficial insects (ineffective). The concept to use neuropeptides as “green insecticides” is based on the binding of the neuropeptide (the ligand) to its cognate G-protein coupled receptor. Once this interaction is understood, for example by using structure-activity studies, *in vitro* receptor assays and receptor modelling, peptide mimetics can be developed to find bio-stable agonistic analogues. The present paper reports on studies using the metabolic adipokinetic hormone peptide family as example. This hormone is crucial for providing energy for extensive muscle activity, thus all forms of locomotion. It is present in all insects but various isoforms (bio-analogues) exist. This may be a focal point to probe for specific binding to the endogenous receptor. Funding: EU Horizon 2020 (nNEUROSTRESSPEP); NRF (RSA)



Symposium: 5th Meeting of the Arthropod Neuroscience Network
Poster: ANN 4

Peptides of the adipokinetic hormone family in leaf beetles (Chrysomelidae)

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The family of Chrysomelidae comprises one of the most species-rich families of the Coleoptera with more than 37 000 species in over 2500 genera. The family harbours species that are very destructive on cultivated and ornamental plants such as potatoes (*Leptinotarsa decemlineata*), asparagus (*Crioceris asparagi*), Cape gooseberries (*Lema trilineata*) and lilies (*Lilioceris lillii*). The drive to use insect neuropeptides as “green insecticides” is under serious investigation. The metabolic adipokinetic hormone (AKH) family is one candidate in this international research effort. Here we studied the complement of AKHs in a number of members of the Chrysomelidae as a first step to later understand ligand/receptor interactions. We dissected the gland containing the AKHs (the corpora cardiaca), made a methanolic extract and used liquid chromatography and mass spectrometry to detect AKH peptides. All the investigated species of the subfamily Criocerinae (*C. asparagi*, *L. lillii*, *L. trilineata*) contain an octapeptide AKH, code-named Peram-CAH-I (pGlu-Val-Asn-Phe-Ser-Pro-Asn-Trp amide). Almost all members of the subfamily Chrysomelinae (*L. decemlineata*, *Chrysolina coeruleans*, *C. herbacea*, *C. kuesteri*, *C. fastuosa*, *Chrysomela populi*) have two octapeptide AKHs with the combination of Peram-CAH-I plus Peram-CAH-II (pGlu-Leu-Thr-Phe-Thr-Pro-Asn-Trp amide) or plus Emppe-AKH (pGlu-Val-Asn-Phe-Thr-Pro-Asn-Trp amide); only *C. populi* has the octapeptide combination Emppe-AKH plus Pyrap-AKH (pGlu-Leu-Asn-Phe-Thr-Pro-Asn-Trp amide). The structural similarity between the four peptides is obvious and a molecular evolution from Peram-CAH-I to Emppe-AKH (S5 to T5) and from Peram-CAH-II to Pyrap-AKH (T3 to N3) via point mutation is very likely. Funding: NRF (RSA), UCT Research Council



Main Meeting, FG Behavioural Biology
Oral Presentation

Signalling adjustment and its limitations to challenging environmental conditions in meerkats

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While many studies provide support for signal adjustment to anthropogenic impacts, studies on the effect of extreme, naturally occurring environmental conditions on species signalling behaviour and the limitations of flexible adjustment to such extreme conditions, are lacking. A certain level of signal adjustment would in particular be expected in species that occupy areas where frequent, but unpredictable, extreme environmental conditions occur, such as in some cooperative breeders. Droughts, which result in reduced food availability, lead to higher competition for the same food source and/or to an increase in group spread – thus making group coordination more challenging. Here we provide evidence from the long-term study on the cooperatively breeding meerkats in the Kalahari and a detailed comparison between a drought and adjacent non-drought year that the coordination among group members breaks down under extreme environmental conditions, resulting in an increased risk of group fission. We find an increase in call rate under harsh environmental conditions and suggest that group members may try to adjust calling to the extreme conditions to better maintain group cohesion during the drought, yet with limited success. Finally, we suggest the evolution of signalling systems to be adapted to the most common conditions rather than to infrequent extreme conditions, despite their potentially high fitness impact on a species.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral Presentation

First phylogenetic analysis of the centipede genus *Lithobius* Leach, 1814 (Arthropoda, Myriapoda) based on morphological and molecular data

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The Palearctic genus *Lithobius* Leach, 1814 includes more than 500 described taxa. A previous study suggested *Lithobius* as a non-monophyletic taxon (Koch & Edgecombe 2008) yet rigorous phylogenetic analyses to answer questions on the evolutionary history of this genus are still lacking. This study represents the first attempt to understand the internal phylogeny of the genus *Lithobius* and its relationships to other genera of the family Lithobiidae, based on morphological and molecular data. The species sampling focused on European *Lithobius* species collected in Austria, Spain, UK, Finland, Romania and Hungary. For the morphological part, we examined the mouthparts of 37 lithobiid taxa and obtained information from their peristomatic structures (Ganske et al. 2018), the mandibles and the first maxillae, using scanning electron microscopy. We extended the morphological character dataset of Koch and Edgecombe (2008) with describing six new characters with systematic value for the genus. In parallel, we evaluate three-dimensional data of the mandibulo-tentorial complex and the reproductive system, obtained with micro-computed tomography to search for apomorphies and plesiomorphies in Lithobiidae. For the genetic characterisation, sequences of the mitochondrial loci COI and 16S rRNA, and nuclear loci 18S and 28S rRNA have been acquired from 46 *Lithobius* species and a few other lithobiid genera. The combination of both approaches in a phylogenetic context is expected to address some evolutionary questions and shed light on the phylogeny of this challenging taxon. References: Koch M, Edgecombe GD (2008) J Morphol 269, 153; Ganske A-S, Edgecombe GD, Akkari N (2018) ZooKeys 741, 49.



Main Meeting, FG Behavioural Biology

Poster: Behav 7

Visual discrimination in the grey bamboo shark (*Chiloscyllium griseum*)

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The ability to recognize and distinguish between visual stimuli is fundamental for everyday survival of many species. While diverse aspects of cognition, including complex visual discrimination tasks, have been successfully assessed in fish including sharks, it remains unknown if they can learn a matching-to-sample concept using geometrical shapes and acquire the ability to distinguish between "same" and "different". For this purpose, a total of eight juvenile grey bamboo sharks (*Chiloscyllium griseum*) were trained in a simultaneous matching-to-sample (MTS) and two two-choice discrimination tasks using geometrical, two-dimensional visual stimuli (e.g. hearts, squares, circles etc.). All sharks showed quick associative learning but were unable to perform successfully in the simultaneous MTS procedure within a period of 70 sessions. Performance consistently ranged around the 50% mark and even allowing for secondary choices to be made (after choosing the center symbol which was always incorrect) did not improve results considerably. However, in the same-different task, which is still ongoing at the moment, it appears as if sharks learn to discriminate between two similar vs. two different symbols. These results suggest that grey bamboo sharks are not able to understand and implement the matching-to-sample concept, at least not within the provided time period and under present conditions. All sharks performed well in the general visual discrimination task and are expected to successfully complete the same-different task, thereby supporting previous results obtained for this species.



Main Meeting, FG Evolutionary Biology
Oral Presentation

Environmental coupling of heritability and selection is rare and of minor evolutionary significance in wild populations

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Predicting the rate of adaptation to environmental change in wild populations is important for understanding evolutionary change. However, predictions may be unreliable if the two key variables affecting the rate of evolutionary change, heritability and selection, are both affected by the same environmental variable. To determine how general such an environmentally induced coupling of heritability and selection is, and how this may influence the rate of adaptation, we made use of Open Access data of pedigreed, wild populations, as a unique opportunity to answer this important question at an unprecedented scale. Using 16 populations from 10 vertebrate species, which provided data on 50 traits (body mass, morphology, physiology, behaviour and life history), we found evidence for an environmentally induced relationship between heritability and selection in only 6 cases, with weak evidence that this resulted in an increase or decrease in expected selection response. We conclude that such a coupling of heritability and selection is unlikely to strongly affect evolutionary change even though both heritability and selection are commonly postulated to be environment dependent.



Main Meeting, FG Ecology
Oral Presentation

The effect of continuous and alternating starvation on flour beetles and their offspring

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Animals in nature are daily exposed to numerous stressors in different magnitudes. Stress in general and starvation in particular have different and often contradicting effects on various traits. Starvation studies usually focus on one starvation treatment (vs. a control) and its effect on one or two response variables only. We used the red flour beetle to study the effects of (a) a starvation gradient of 0-4 days, and (b) alternating starvation over 3 days, on multiple response variables: movement activity, food patch discovery, latency to emerge from shelter, body mass, water content and offspring number, mass and survival. As expected, continuous starvation had negative influence on body mass and water content. Beetles also became less active, explorative and bold, which stands in contradiction to some previous work. Although both number of offspring and their mass at mid-development diminished with starvation, starved females negatively affected the number of offspring, while starved males affected their mass. This suggests a non-adaptive parental effect, from the offspring perspective, due to parental starvation. Recuperation episodes generally negated starvation effects, with three exceptions: male body mass, water content and movement activity. We also found an inconsistent link between several response variables and starvation duration between the sexes. Females, which are generally larger than males lost mass at a quicker rate, and were also more starvation resistant. This was evident in their ability to take better advantage of recuperation episodes. Our results indicates that starvation had a differential effect on different response variables according to sex.



Main Meeting Keynote Lectures
Oral Presentation

Origins of diversity on islands: The nexus of ecology and evolution in community assembly

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A grand challenge in understanding the origins of biodiversity is to understand the relative influence of ecological processes that shape abundance and interaction networks subsequent to successful establishment, from evolutionary processes that lead to population divergence and speciation. One system that provides an opportunity to grasp this nexus of ecological and evolutionary processes is that of remote island archipelagoes, in particular when the component islands are arranged chronologically, as in "hotspot" islands. Multiple discrete volcanoes provide a temporal sequence of community assembly, with elevational gradients affording contrasting ecological barriers (temperature, rainfall). Here, I summarize research from the Hawaiian archipelago that seeks to understand how communities of arthropods have assembled across these gradients of space and time. Large-scale metabarcoding efforts provide data on species abundance, diversity, and interactions. Coupling these data with ecological metrics (interaction networks, species abundance) across the chronosequence provides insights into the evolutionary dynamics of the entire community. Within this framework, genomic data from target lineages reveal patterns of early population divergence. I highlight recent insights on patterns of assembly that show: (1) adaptive diversification is highly repeatable in certain lineages, not in others; (2) the early stages of adaptive radiation are characterized by extinction/ recolonization dynamics as opposed to simple population divergence; (3) differences between lineages in their patterns of species accumulation over time (under representation or overshoot relative to an island's carrying capacity) is tied to the mechanism of adaptive differentiation. And, (4) beta diversity increases with time, but the rate and pattern differ between lineages.



Main Meeting, FG Morphology

Poster: Morph 6

Muscle fiber type composition and muscle spindle density in the masticatory muscles of wolves and dogs

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Dogs show a remarkable diversity in cranial size and shape compared to wolves. However, it remains unclear whether the domestication of *Canis lupus* and the artificial selection of *Canis lupus* forma *familiaris* into more than 300 recognized dog breeds also had a bearing on the masticatory musculature and its muscle internal architecture. We investigated the Mm. temporalis et masseter of eight wolves and eight wolf-like dogs of different adult age stages (young adults: 2-5 years, old adults: >10 years) using histological techniques. We hypothesized that wolves compared to dogs had (1) a higher proportion of the slow contracting and enduring type I fibers compared to the fast contracting and fast fatiguing IIM fibers, and (2) a higher amount of muscle spindles which are proprioceptive receptors to detect length changes of the muscle. We found that the proportion of type I muscle fibers was higher in wolves than in dogs, although a linear mixed model revealed that this difference was apparently driven by an age bias in our samples. In contrast, dogs exhibited a higher muscle spindle density than wolves, irrespective of age differences. Yet, both groups showed a higher frequency of slow fibers and muscle spindles in the deeper muscle portions compared to superficial ones. This suggests a conserved structural pattern in the masticatory musculature of both wolves and dogs, in which the superficial muscle portions serve as mobilizers and stabilizers, while the deep muscle portions serve as stabilizers during jaw adduction.



Main Meeting, FG Morphology
Oral Presentation

Anything but void – the hemolymph lacunar system of *Penaeus vannamei*

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Ever since early anatomists started investigating arthropod morphology, the circulatory system has drawn major attention. In recent years, modern 3D imaging techniques and features have again increased morphological descriptions of this in some groups remarkably complex organ system and its features have served as source of phylogenetic relevant characters e.g. in Malacostraca. This led to a major shift in our understanding of the vascular part, i.e. the heart and associated arteries. However, when leaving the arteries, the hemolymph is channeled through a highly complex system of lacunae and sinuses which are still not readily understood. Therefore, detailed three-dimensional investigations are necessary to not only understand the structural but also the ontological nature of this elusive system. To this end, we investigated the circulatory system of the white leg shrimp *Penaeus vannamei* using micro computed tomography complemented with histological sections and confocal laser scanning microscopy followed by virtual 3D reconstruction. Our results comprise detailed visualization of the vascular system and – for the first time – also the three-dimensional structure of the lacunae and sinuses. Based on the lacunar morphology, we are now able to understand the functions of major lacunar subsystems in the broad context of hemolymph circulation in decapod crustaceans.



Main Meeting Keynote Lectures
Oral Presentation

Karl-Ritter-von-Frisch Medaille 2018: Functional morphology of animal attachment devices

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For attachment during locomotion, smooth and setose (hairy) adhesive pads located on different leg parts (claws, pretarsus, tarsomeres, tibia etc.) have been evolved several times independently in animal evolution. Some of these attachment structures have been studied already in Hooke's *Micrographia* (1665), but their functional mechanisms based on the interplay between the ultrastructure, material properties and physical interactions remained unresolved until recently. The reason for this is that such functional morphology research requires approaches of several disciplines: zoology, structural biology, biomechanics, physics, and materials science. In addition to the use of a wide variety of microscopy techniques, we established a set of experimental techniques that allows obtaining information about adhesive and frictional properties as well as local and global mechanical properties of materials of attachment devices, in order to understand physical mechanisms behind these biological structures. In my presentation, I will discuss the attachment structures, their surfaces and materials as well as their physical properties and show how they together contribute to the function. Conceptually, it is a trial to make a kind of "dissection" of the functional system at different levels of its morphological organization linked to specific properties. In order to show different functional principles, we experimentally tested many different locomotory attachment devices and tried to outline general rules of the interrelationship between their structure and function. Since these broad comparative studies include a wide variety of organisms, some questions about the evolution of these systems could be resolved. The results obtained from applying this approach are useful for high-tech areas, such as micro- and nanotechnology as well as for bionics (biomimetics) of novel surface-active and composite materials.



Main Meeting, FG Morphology

Poster: Morph 26

Functional morphology of spermathecae in leaf beetles (Coleoptera: Chrysomelidae)

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Cryptic female choice is one of major mechanisms of intersexual postmating selection. To understand how cryptic female choice works, many empirical data have been accumulated. However, the effects of interspecific female morphological variations on sperm dynamics are not well known yet, despite of morphological diversity of female genitalia found recently. Many animals have sperm storage organs, called spermatheca, in which sperm from different males are stored. Hereby we studied functional morphology of the spermatheca from six representative leaf beetle species using micro-computed tomography, scanning electron microscopy and confocal laser scanning microscopy. We found high diversity not only in external shapes of the spermatheca among species, but also in the internal structures. For example, the spermatheca of *Agelastica alni* is of a C-shaped simple type, and has a volcano-like projection as the internal structure of the spermatheca. Irrespective of the diversity in spermathecal shapes of the studied species, all females have a common pump-like structure, which carries directly attached muscles. In a certain area of the pump-like structure, where is presumably deformed during pumping, resilin dominated areas were detected. Based on these morphological data, we hypothesize how the spermatheca works and discuss how the morphological variations affect sperm dynamics.



Main Meeting, FG Ecology

Poster: Ecol 9

Detecting molecular mechanisms of predator-induced plasticity in *Daphnia* with (fluorescent) *in situ* hybridisation

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Phenotypic plasticity describes the ability of an organism with a given genotype to respond to changing environmental conditions by altering its phenotype. The freshwater crustacean *Daphnia* is a popular model organism for phenotypic plasticity and especially well-known for its predator-induced defences. With the publication of different *Daphnia* genomes, the use of molecular techniques has become feasible and many ongoing projects are detailing predator induced differential gene expression. A set of candidate genes with known function is now available but also many genes with no detectable orthologues have been identified. In order to further understand the molecular mechanisms underlying the formation of predator-induced defences, it is pivotal to localize differentially expressed genes in a tissue specific manner. We aim to detect differentially expressed mRNA using *in situ* hybridization. Even though this method is standard only few protocols have been working successfully in *Daphnia* and up to now only in embryos. In order to understand the molecular mechanisms of predator induced phenotypic plasticity, we have established a protocol for (fluorescent) *in situ* hybridisation in dissected *Daphnia* tissues and adult whole-mounts. With this we now want to detect selected target genes in the critical stages of defence expression. This will help us to further understand the molecular mechanisms of predator induced phenotypic plasticity.



Main Meeting, FG Morphology
Oral Presentation

Two joints are not enough – functional morphology of the protopodal part of thoracopods in malacostracans

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A dicondylar thorax-coxa joint permitting promotion/remotion followed by a dicondylar coxa-basis joint performing abduction/adduction is presumably the plesiomorphic pattern in the thoracopods of Eumalacostraca. Peracarida differ from this pattern and Mysidacea (Mysida and Lophogastrida) stand out in particular as both their thorax-coxa and coxa-basis articulations permit abduction/adduction, while an additional (third) intrabasal joint permits promotion/remotion. This intrabasal joint is formed by a membranous gap between an anteriorly located proximal triangle and the rest of the basis. Interestingly, an intrabasal joint of this nature is also present in Euphausiacea, and, with structural differences, in Anaspidacea, which in contrast exhibit the plesiomorphic articulation pattern between thorax-coxa and coxa-basis. The protopodal musculature also enforces the exopod, which fulfils various biological roles, including swimming, respiration and feeding. Around 20 functionally differentiated muscles are part of the protopodal muscular system. A μ CT-based comparison of the complex protopodal musculature is conducted, enhancing our 3-dimensional and functional understanding of these intrabasal joint constructions as well as of the exopods in the different groups. The possible homology of the intrabasal joint is discussed. While the additional joint is believed to have evolved in favor of the peracaridan marsupium, Euphausiacea and Anaspidacea do not have a marsupium, so other biological roles need to be assumed in these two taxa. The function and biological role of exopods changed from uniplanar movements and swimming/respiration in Anaspidacea and Lophogastrida to rotational movements and the additional role of feeding in Euphausiacea and Mysida.



Main Meeting, FG Behavioural Biology
Oral Presentation

The role of a geomagnetic compass for early learning behavior in desert ants

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Cataglyphis desert ants are famous navigators using a celestial compass (Müller et al. (1988) Proc. Natl. Acad. Sci., 85, 5287) and a step counter (Wittlinger et al. (2006) Science, 312, 1965) during far-ranging foraging runs. When leaving the nest for the first time, novices face the crucial challenge to calibrate their visual compass systems and learn panoramic landmarks. To achieve this, the ants perform stereotyped learning walks close to the nest entrance prior to first foraging. During learning walks, they perform multiple stops to gaze back towards the nest entrance, a tiny hole in the ground (Fleischmann et al. (2017) J. Exp. Biol., 219, 3137). As the nest entrance is invisible from the ants' positions, nest-centered gazes can only be adjusted by reading out the path integrator. Despite its prominent role for navigation during foraging trips, the celestial compass is not involved in this look-back-to-the-nest behavior (Grob et al. (2017) Front. Behav. Neurosci., 11, 1). The most promising remaining compass cue available during this early learning phase is the geomagnetic field, since it represents an earthbound reference and does not have to be calibrated or learned. Using systematic alterations of the horizontal component of the geomagnetic field at the nest entrance in the ants' natural habitat, we changed the direction of nest-centered views during learning walks in a predictable manner. This is the first demonstration that, in insects, a geomagnetic compass cue is both necessary and sufficient for accomplishing a specific navigational task (Supported by DFG SFB 1047/B6).



Main Meeting, FG Morphology

Poster: Morph 7

A new muscle cell morphology reveals serial homology of leg muscles in tardigrades (water bears)

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The taxon Tardigrada (water bears) consists of water-dwelling microinvertebrates with a 5-segmented body: a head and 4 leg-bearing segments. The tardigrade anatomy has been well characterized since their discovery more than two centuries ago, but the availability of new markers and techniques indicates that new insights can be gained even into organs and organ systems that were previously thought to be well understood. One such example is the tardigrade muscular system, which consists of single-celled muscles that cross the body longitudinally, transversally, or dorsoventrally, while ring and diagonal musculature is absent. More recently, studies have mapped the musculature of various tardigrade species based on fluorescent labeling of f-actin, a major component of muscle fibers. In this study, we reinvestigated the musculature of the model tardigrade *Hypsibius exemplaris* using an additional marker for myosin, another major component of muscles. Our results show that not only does each muscle consist of a single cell, but some muscle cells also possess multiple individual contractile strands that appear as separate, independent muscles when labeled only for f-actin. This discovery of single cells with multiple contractile branches enabled us to remap and serially homologize the individual leg muscles. In doing so, we propose that the musculature of the posterior-most legs is less derived than previously thought, especially if their backwards-facing orientation is taken into account. These results call for a reinvestigation of the musculature of other tardigrade species using additional markers like myosin and pave the way for a new functional interpretation of tardigrade locomotion.



Main Meeting, FG Developmental Biology

Poster: Dev 12

How to eat with your skin – radical body-plan changes in an animal-microbe symbiosis

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Although it is now widely recognized that beneficial microorganisms are critical for the healthy development of animals, we know remarkably little about how the microbiome affects phenotypic changes during early animal development. *Olavius algarvensis* is one of ~100 known species of gutless oligochaetes, marine interstitial annelids that have completely reduced their intestinal tracts, and rely on chemosynthetic bacteria for their nutrition. These bacteria are harbored just below the cuticle, and 'eaten' by the worm's epidermal cells through phagolysosomal digestion. In this study, we examined the embryonic development of *O. algarvensis* and the role of its symbionts in this process, using serial-section histology with light, confocal and transmission electron microscopy combined with metatranscriptomics of different developmental stages. Like all other oligochaetes, *O. algarvensis* developed directly into juvenile worms in the cocoon. The symbionts were transmitted vertically from the parent to the cocoon, where they occurred extracellularly in the fluid surrounding the embryo. Early development, including gastrulation, closely resembled that of non-symbiotic oligochaetes. At later stages, however, the formation of mouth and anus through invagination of the buccal and anal cavities, as well as the midgut through epithelialization of endodermal cells were suppressed. Instead, the symbionts colonized the host by attaching to the surface of the ectodermal cells. Subsequent secretion of the cuticle resulted in their integration into the host's body-wall. We are currently analysing gene expression during these key developmental events to better understand how these hosts and their symbionts interact to form the radically changed body-plan of the adult oligochaete.



Main Meeting, FG Developmental Biology

Poster: Dev 13

Stem cell expression and skeletal muscle development of lesser-spotted dogfish larvae (*Scyliorhinus canicula*)

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Muscle development and growth has attracted the attention of researchers for decades. Information about skeletal muscle formation in fish was generally gained from fast growing commercial species like the Atlantic salmon (*Salmo salar*) and carp (*Cyprinus carpio*) or the model fish *Danio rerio*. However to understand the muscle development in total, it is important to study also more basal taxa, like Chondrichthyes. So far, information on body muscle structure of adult sharks is scarce and studies on muscle formation including myogenesis are missing. Therefore, this study will give first insights on muscle development in lesser-spotted dogfish larvae (*Scyliorhinus canicula*; Linnaeus 1758). We compared the trunk skeletal muscle anatomy in 870- and 2900-degree-day-old lesser-spotted dogfish larvae via immunohistochemistry and Western blot analysis as well as haematoxylin/eosin staining. Our results revealed poorly differentiated muscle formation in the trunk segments of the younger larvae and fully developed skeletal muscle with a division of red and white muscle tissue in the older larvae. The PAX7 stem cell marker, which is present in all developmental stages of teleost fish, was only expressed in the younger dogfish (Grunow, et al. (2016). Stem cell expression and development of trunk musculature of lesser-spotted dogfish (*Scyliorhinus canicula*) reveal differences between sharks and teleosts. Acta Zoologica DOI: 10.1111/azo.12167). The results show the necessity of examining the skeletal muscle development in sharks to understand the evolutionary changes from basal cartilaginous fishes to evolutionary younger teleosts.



Main Meeting, FG Morphology
Poster: Morph 18

The bearer of bad news: comparative morphology of metasomata in scorpions

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Scorpions are among the most popular research objects within Arachnida and there is an impressive body of knowledge about their biology, distribution, morphology etc. The venom sting, in particular, has gained a lot of attention due to its fatal effects. Therefore, it is especially remarkable, that up to now there is basically no comparative morphological study on the metasoma, the body part, which enables the venomous injection. The metasoma can be characterized as variation on a theme, not only between species but also between sexes: it always consists of five body segments and a venom sting. Nevertheless its form ranges from long and thin, short and rather reduces to thick and very dominant. Due to its high morphological variability, it also plays a key role in taxonomy. In this study, we therefore aim to investigate species representing major scorpion clades and covering most of the morphological variation. Using high resolution micro-computed tomography and 3D-reconstruction we present first visualizations of metasomal external skeletal elements in combination with their musculature. Results will be discussed along recent hypotheses on phylogeny and the metasomata segments will be compared in terms of their serial homology. Based on these findings, further questions may be clarified, for example: is there a connection between the carina and the muscle attachment sites in the metasoma? Or are there hints of a hydraulic system in scorpions?



Main Meeting, FG Behavioural Biology
Oral Presentation

Sex-specific pace-of-life syndromes in cavies (*Cavia aperea*)?

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Sexes may often experience different selection pressures leading to sex-specific allocation between reproduction and self-maintenance. Traits such as behaviour or physiology, are expected to adaptively covary with life history, forming so-called pace-of-life syndromes (POLS). Sexes commonly differ in pace-of-life, as a result of their different reproductive roles and environment. Here, we tested whether male and female wild cavies express sex-specific POLS and if endocrinological correlates underlie differences in syndromes. To test whether male and female cavies differ in POLS we measured growth rates and adult stress-coping, risk-taking, and social behaviour. To test whether endocrine correlates may explain sex-specific variation, we additionally measured plasma cortisol, testosterone and oestrogen in adult animals. As predicted, we found sex-specific POLS which correlated with sex-specific patterns in steroid levels. These results are in line with recent theory suggesting that sex-specific POLS are highly prevalent across taxa with potential consequences for the evolution of POLS. To understand how behavioural variation is integrated with life history and physiology, and to achieve a more holistic framework, future studies should explicitly incorporate potential sex differences in POLS.



Main Meeting, FG Neurobiology*

Poster: NB 1

Adaptive control of locomotion: How do stick insects master the transition from level to slope walking?

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Goal-directed, unrestrained motor behaviour in a variable and unpredictable environment requires animals to adjust their limb movements appropriately. In mammals, neuromuscular strategies with functionally distinct transition strides between level and slope walking have been found (Gottschall & Nichols, 2011, *Phil.Trans.R.Soc.L.B.*, 366(1570), 1565-1579). So far, comparable strategies for coping with changes in walkway slope have not been described for insects. In fact, slope-dependent changes have been studied mainly in steady state situations either at given slopes, during upside-down walking, or in climbing a stair of given height. With the present study, we evaluate the behavioural adjustments of unrestrained walking stick insects (*Carausius morosus*) in response to a step change in slope of the walkway ($\pm 45^\circ$). Graham (1983, *J.Exp.Biol.*, 104(1), 129-137.) suggested that stance phases can be divided into an early support and a later propulsive part, in line with the protractor coxae muscles showing braking activity during early stance (Graham & Wendler, 1981, *Physiol.Entomol.*, 6(2), 161-174). Here, we analyse the hind leg protraction/retraction system of the stick insect, using simultaneous recordings of whole-body kinematics and muscle activity in freely walking animals. Our results suggest an early load-dependent activation of both muscles with delayed retractor activity in case of only little load, corroborating the idea of a biphasic power stroke. In contrast, adjustments of leg kinematics were very small among steady state situations. The most prominent differences occurred only during the transitional steps between level and slope walking. Further studies may address the contribution of other muscles (e.g., depressor trochanteris) and legs.

* Contribution also presented in: *Symposium: 5th Meeting of the Arthropod Neuroscience Network (Oral Presentation)*



Main Meeting, FG Evolutionary Biology
Oral Presentation

Interaction of male age and mitonuclear epistasis effects on male reproduction in *Drosophila melanogaster*

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The factors affecting the maintenance of variation of male reproductive success represent a central question in evolution. The variation can be affected by both genetic and environmental factors. We constructed mitonuclear introgression lines of *Drosophila melanogaster* from three geographically different populations and examined males at two ages. This design allowed us to separate the independent effects of mitochondrial and nuclear genomes and male age. Male age and the nuclear genome explained a large proportion of variation in sperm function and male fertility. The mitochondrial genome also had a sizeable effect, expressed primarily through epistatic interaction with the nuclear genome. However, disruption of population-specific coevolved mitonuclear genotypes did not lead to general reductions in performance, as might be predicted under a scenario mitonuclear coadaptation. Most importantly, our findings suggest male fitness is determined by epistatic intergenomic interactions, which are more pronounced in younger males. These results provide us with a deeper understanding of the contribution of mitonuclear epistasis to male reproduction.



Main Meeting, FG Neurobiology
Oral Presentation

Epo-induced neuroprotection is mediated by orthologues of the orphan cytokine receptor CRLF3

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The cytokine Erythropoietin (Epo) is a major regulator of erythropoiesis but plays additional roles in cell protection in various tissues including the nervous system. While circulating Epo binds to the homodimeric classical Epo receptor (EpoR) on erythroid progenitors to promote erythropoiesis, additional receptors that bind hormonal and/or locally released Epo for tissue protection seem to be expressed by various cell types. The nature of these “alternative” Epo receptors is currently under discussion. In this study we investigated whether the orphan cytokine receptor-like factor 3 (CRLF3) is involved in Epo-mediated neuroprotection. We identified orthologues of human CRLF3 in the beetle *Tribolium castaneum* and the locust *Locusta migratoria* and demonstrated their necessity for Epo-induced protection of their brain neurons in vitro. Knock down of their expression by soaking RNAi abolished the neuroprotective effect of Epo and non-erythropoietic Epo variants under hypoxic condition. In order to further investigate the importance of CRLF3 in Epo signalling, we study *Drosophila* cells that do not naturally express a CRLF3 orthologue and are endogenously not sensitive to Epo. We transfected these *Drosophila* cells with the beetle Tc-crlf3 in order to check whether the transfected cells gain Epo sensitivity and to generate a powerful experimental system to investigate the structure and function of Tc-CRLF3 in more detail. Finally we broadened the research to mammalian cell lines investigating the importance of CRLF3 in neuroprotection and its expression in response to harmful stimuli. Our studies aim to support the development of Epo derivatives that specifically activate neuroprotective mechanisms.



Main Meeting, FG Behavioural Biology

Poster: Behav 8

Acoustic discrimination in the grey bamboo shark (*Chiloscyllium griseum*)

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Sharks use sound to locate prey, predators and mates. Most research on sound detection in elasmobranchs has focused on determining hearing thresholds and attractiveness to sound sources. So far, only one study investigated acoustic discrimination abilities in Portjackson sharks using jazz vs classical music. Here we trained eight adult bamboo sharks (*Chiloscyllium griseum*) in a more simple acoustic discrimination task, in which they had to distinguish between two frequencies (80 Hz, 30Hz) emitted from a single loudspeaker in a pseudorandom order. Each frequency was associated with a separate feeding location, each positioned within the same distance from both the starting compartment and the loud speaker. In the first experiment, the position of the feeding location was signaled by turning on a green light in conjunction with the respective sound frequency. All sharks successfully solved the task within 21-24 sessions. Several transfer tests indicated that sharks used visual and acoustic cues to find the feeding location; however, when placed into conflict, light provided a much stronger cue than sound. In addition, the transfer tests revealed a preference for the 80 Hz sound and the associated feeding location. In a second experiment, the light cue was omitted. Results showed that within ten sessions, six out of eight sharks successfully associated the two frequencies with their respective feeding location. Determination of detection thresholds, responses to gradual changes in frequencies and discrimination abilities of more complex sound sequences are currently underway.



Main Meeting, FG Behavioural Biology

Poster: Behav 9

Detection and discrimination of travel direction of vortex rings by harbour seals (*Phoca vitulina*)

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Harbour seals can detect and analyse water movements using their vibrissal system. One type of water movement are vortex rings, i. e. stable structures of water circulation through and around a ring-like structure. Vortex rings are produced by certain swimming movements of fish. They can last in the water up to minutes after their generation (e. g. Niesterek and Hanke (2013), *J. Comp. Physiol. A* 199, 139), traveling through the water on stable paths. They thus bear the potential to inform the seal about the presence of a prey fish. Here we investigated the ability of stationary harbour seals to discriminate vortex rings of different travel directions (Krüger et al. (2018) *J. Exp. Biol.* 221: DOI:10.1242/jeb.170753). A harbour seal was trained to position its snout on a target under water in a reproducible position. Two identical vortex ring generators were positioned in front of the animal at adjustable angles to the left and to the right. One vortex ring generator, which was selected pseudorandomly from trial to trial, sent a vortex ring travelling towards defined portions of the seal's vibrissal array. The seal had to choose the correct vortex ring generator by selecting a response target on the left or the right side. Angles between the vortex ring generators were adjusted to identify a limit for the difference in vortex ring travel direction that the seals could still discriminate, the minimum hydrodynamically perceivable angle (MHPA). We found that angles at least down to 5.7° from the midline can be discriminated.



Main Meeting Keynote Lectures
Oral Presentation

Smelling to survive - Insect olfactory neuroecology

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Insects are heavily dependent on olfactory input for more or less every fitness-related activity; finding a mate, locating food, identifying a suitable oviposition site or avoiding an enemy. This strong reliance on the sense of smell has provided pronounced evolutionary selection pressures for the system to be sensitive, specific and fast. Here, I will provide a number of examples of how the insect olfactory system solves the tasks outlined above. In the vinegar fly olfactory input is processed in different ways, often dependent on the ecological significance of the signals detected. More general information from the environment is processed in a cross-fibre-based system, where many different types of olfactory sensory neurons are activated and their input is compared in the central nervous system. Specific types of information are, however, often processed in separate, so-called "ecologically labelled lines." When such a line is activated, naturally or artificially, the behavioural response of the fly can be predicted with high certainty. My laboratory has revealed such labelled lines for food, sexual mates, oviposition sites and for odours emitted by detrimental microorganisms. In sphingid moths we are presently identifying similar features but so far concentrate more on the behavioural relevance of certain odours and their detection. By combining wind tunnel studies with optical imaging in the brain of the moth we have established specific stimuli eliciting feeding behaviour and others eliciting oviposition. In conclusion, I will bring the data from flies and moths together to provide our present ideas regarding olfactory function in insects from an evolutionary and ecological perspective. Always with a strong behavioural component.



Symposium: 5th Meeting of the Arthropod Neuroscience Network
Oral Presentation

Developmentally arrested precursors of pontine neurons establish an embryonic blueprint of the *Drosophila* central complex

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Serial electron microscopic analysis shows that the *Drosophila* brain at hatching possesses a large fraction of developmentally arrested neurons with a small soma, heterochromatin-rich nucleus, and unbranched axon lacking synapses. We digitally reconstructed all 812 “small undifferentiated” (SU) neurons and assigned them to the known brain lineages. 54 SU neurons belonging to the DM1-4 lineages, which generate all columnar neurons of the central complex, form an embryonic nucleus of the fan-shaped body (FB). These “FB pioneers” develop into a specific class of bi-columnar elements, the pontine neurons. Even though later born, unicolunar DM1-4 neurons fasciculate with the FB pioneers, selective ablation of these cells did not result in gross abnormalities of the trajectories of unicolunar neurons, indicating that axonal pathfinding of the two systems is controlled independently. Our comprehensive spatial and developmental analysis of the SU neuron adds to our understanding of the establishment of neuronal circuitry.



Main Meeting, FG Developmental Biology
Oral Presentation

Beyond terminology: what does 'larva' and 'metamorphosis' really mean?

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In all fields of science, specific terminologies are used for facilitating a precise communication. Yet, often several different categories are in fact summarised under the same term. Such an ambiguous terminology can potentially cause severe misunderstandings in communication and has demonstrably done so in the past. I here aim at discussing two tightly interlinked terms from comparative developmental biology, namely the two terms 'metamorphosis' and 'larva'. I will demonstrate that both terms can only be used in a strict comparative framework, and no absolute, but only relative criteria can be applied for outlining both of them. Furthermore, I will demonstrate that criteria that can be used to identify cases of 'metamorphosis' and 'larva' depend on numerous different underlying evolutionary processes. Therefore, both terms on their own are in fact highly misleading, as mentioned above, summarising several different categories under the same expression. I use mainly, but not exclusively, arthropods as an example. Here both terms have been used very differently in various lineages, more loosely in some, but very strictly in others. In lineages in which very strict approaches have been applied, additional terms have been introduced for cases almost, but not entirely fulfilling the criteria for the two terms. This has tremendously complicated any comparison on a wider scale. The comparison between different lineages of arthropods is strongly hindered by a century-old tradition of complicating terminologies. I in general advocate to be more precise but simple in scientific communication, aiming at outlining proper criteria and identifying underlying processes.



Main Meeting, FG Ecology
Oral Presentation

Admixture and fast speciation in species complexes of phytophagous Hymenoptera and Orthoptera: a MuseOMICS approach

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Clusters of molecular OTUs, e.g., mitochondrial haplotypes or DNA barcodes, are considered to correspond closely to biological species. This generally holds true, but exceptions exist. In particular, phytophagous Hymenoptera and acridid Orthoptera exhibit sharing of haplotypes across species complexes, even comprising different genera, and/or barcode divergence within species: The phenomenon was detected in >20% of species studied in the former (N=822) and 41% in the latter group (N=70). 'Symphyta' and Acrididae are holo- vs. hemimetabolan, extremely species-rich vs. comparatively species-poor, and have small vs. very large genomes. Potential reasons for haplotype sharing among species are hybridization, incomplete lineage sorting, nuclear mitochondrial pseudogenes (numts), and the influence of *Wolbachia* bacteria. We studied a selection of species of the two groups from Central Europe and applied RAD sequencing to generate genomic data sets with the aim of detecting possible admixture. Specifically, we used the hyRAD approach for low-quality DNA samples, as many species were only available in the form of historical museum material. To study numts in Orthoptera, we first isolated mitochondria from tissue to extract the barcode ortholog and then ran an amplicon sequencing to study the diversity of numts.



Main Meeting, FG Systematics, Biogeography and Diversity
Poster: Syst 10

Museum collections – a time machine to the past

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The scientific importance of collections of natural history museums is fundamental since they are the basis of each taxonomically systematic as well as applied environment-related research. They represent archives of life that provide answers to many scientific questions such as how biodiversity changes in certain environments, either through evolutionary processes in geologically long or short periods, or through man-made transformation of habitats. One could say that museum collections are time machines, which gives the researcher a glimpse into the past. One example of how important collections can be concerning changes in biodiversity is the case of *Ostrea edulis* Linnaeus 1758. The populations of the European flat oyster decreased dramatically in the beginning of the 20th century and eventually became extinct in the Northern Sea, except for a small population in the Limfjord, Denmark (Yonge (1966) Oysters, London, Collins; Barry (1981) Irish Fisheries Investigation Series B 24, 1–12; Korringa (1952) The Quarterly Review of Biology 27, 266–308). The reasons for this species to become extinct are still debated, which is why we used the collections of several museums (NORe museums, the Natural History Museum London and the Naturalis Biodiversity Centre Leiden) to map the change in distribution and diversity over the past 200 years.



Symposium: Phenotypic Plasticity - RESPONSES of Animals to
Environmental Change
Oral Presentation

Nutritional quality modulates phenotypic plasticity

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Trait based functional and community ecology is en vogue. Most studies, however, ignore phenotypical diversity by characterizing entire species considering only trait means rather than their variability. Phenotypical variability may arise from genotypical differences or from ecological factors (e.g., nutritionally imbalanced diet), and these causes can usually not be separated in natural populations. We used a parthenogenetic model system (the oribatid mite *Archezogozetes longisetosus* Aoki) to exclude genotypical differences and quantify exclusively ecologically induced trait variation. We investigated patterns of dietary (10 different food treatments) induced trait variation by measuring the response of nine different traits (from life history, morphology and exocrine gland chemistry). Nutritional quality (measured as carbon-to-nitrogen ratio) influenced all trait means and their variation. Some traits were more prone to variation than others. Imbalanced food led to lower trait mean values, but also to a higher variation of traits. The variation of trait means seems to be a predictor for food quality, while the variation of trait variation (across many traits of animals fed on one resource) may be an indicator for trade-offs an animal has to deal with while feeding on a particular diet.



Main Meeting, FG Behavioural Biology

Poster: Behav 13

From correlation to causation - testing the effect of intra-sexual competition on gift strategy in nursery web spiders

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Even though nuptial gifts are not particularly rare among arthropods, for spiders this behavioural trait is unique to very few species, including the nursery web spider *Pisaura mirabilis* (Clerck, 1757). Males facilitate mating by offering silk wrapped gifts to females. These can either be genuine, consisting of prey to be eaten by the female during copulation, or cheaper worthless donations, such as exoskeletons of previously consumed insects or even plant parts. Males with worthless gifts can “cheat” females into mating, but suffer from shorter copulations and therefore reduced sperm transfer. Since females of this species are highly polyandrous, the risk of sperm competition has been suggested as a factor influencing the males’ gift strategy, with males reducing gift investment when facing high competition risks. Furthermore, previous field studies have shown a correlation between the intensity of intra-sexual competition and the frequency of worthless gifts produced by males in a German population. To test this hypothesis we have developed a semi-field approach by setting up experimental populations in field enclosures and manipulating the operational sex-ratio (OSR). We assessed the quality of the gifts (genuine or worthless) produced by males exposed to either male-biased or female-biased OSR. We expect males to cheat more frequently when experiencing a male biased OSR with high competition risk compared to a female biased population. We will present here the results of this study along with an evaluation of a novel approach for conducting behavioural experiments in nursery web spiders.



Main Meeting, FG Evolutionary Biology
Oral Presentation

Royal matchmaking: ants carry young queens to alien nests to promote outbreeding

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The mating biology of social insects is often a rather unexciting event, with little evidence for strong inter- or intrasexual selection. Male and female sexuals meet in ephemeral mating aggregations, where there is little time for defending a harem or choosing the best of several mating partners. The ant genus *Cardiocondyla* provides a surprising exception to this rule. In many tropical species, wingless males engage locally in fatal fighting for access to female sexuals in their natal nests. Most colonies of these species contain multiple mother queens and occasionally adopt unrelated queens, which allows outbreeding. In contrast, colonies of temperate species obligatorily contain only a single mother queen, and inbreeding coefficients suggest that 70-80% of all matings are among siblings (e.g., Lenoir JC et al. (2007), *Mol Ecol* 16, 345). But what explains the remaining 20-30% of outbreeding? We observed that workers of *Cardiocondyla elegans* carry related female sexuals from their own nest over distances of more than 10 m and deposit them in the nest entrance of alien colonies, where they mate with unrelated males. Interestingly, workers appear to choose particular colonies as recipients for their sexual sisters, and a preliminary microsatellite analysis suggests that they carry the young queens predominantly to nests to which they are less closely related than to an average colony in the population. Supported by DFG (He 1623/42).



Symposium: 5th Meeting of the Arthropod Neuroscience Network
Oral Presentation

The central complex and the neural basis of insect navigation

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The ability to move between places is one of the defining features of animals. Irrespective of diverse navigation strategies, at each moment in time, an animal has to decide whether to turn right, left, or whether to move straight. For these elementary decisions, the animal's brain has to compare the current heading with the intended heading and initiate steering if both disagree. In insects, the central complex (CX) in the brain is involved in encoding current heading and in steering control. Based on its role in path integration, we recently suggested that the goal direction is also encoded in the CX. Path integration is a computation that continuously updates an animal's internal position estimate relative to a point of origin, enabling straight-line homing after a convoluted foraging trip. Efficient path integration requires combining a compass as directional reference with an odometer for distance measuring. Bees use polarized skylight for estimating directions and translational optic flow for estimating distances. Neurons responding to both visual stimuli converge on CX cells that are suited to form a distributed memory of the foraging journey. Computational modelling revealed that this memory can be transformed into steering commands by comparing it to the current heading encoded by CX head-direction cells. This computation is enabled by the conserved, intricate connectivity patterns within the CX, generating the neural circuitry for elementary navigation decisions. We propose that this concept can be expanded to encompass all navigation strategies and might constitute the ancestral function of this highly conserved brain region.



Main Meeting, FG Morphology
Oral Presentation

Chewing à la newt: Intraoral food processing in a salamandrid newt and the evolution of intraoral cyclic behavior

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Vertebrate feeding systems have evolved remarkably diverse specializations that allow exploitation of a great variety of food sources. Besides the initial food acquisition, intraoral processing, i.e. mechanically reducing food within the mouth, or chewing, has played a major role in evolutionary adaptive procedures to successfully exploit food sources in a given trophic environment. Processing mechanisms are known for all major vertebrate clades, from fishes to mammals, but form and function of the processing apparatus to crush, grind, or puncture food items can differ substantially between and within major groups. However, rhythmic and coordinated cyclic movements of skull, jaws and hyobranchial elements appear to be a common trait. While processing mechanisms in amniotes (sauropsides and mammals) and fish-like vertebrates have been subject of intense research, processing mechanisms in lissamphibians remain relatively unstudied, resulting in the common perception that lissamphibians simply do not chew and instead swallow prey whole. Here, we present the first results from behavioral observations, high-speed x-ray videos and anatomical analyses of an undescribed intraoral processing mechanism employed by *Triturus carnifex*. The salamandrid newt *T. carnifex* displays a conspicuous behavior following prey-capture, involving rhythmic head bobbing, coordinated with cyclic gape and hyolingual movements. Our x-ray recordings reveal that, rather than chewing prey between upper and lower jaw elements as typically seen in other tetrapods, *T. carnifex* processes prey by rasping it against its palatal dentition. We compare the processing mechanism of *T. carnifex* with those known for fishes and amniotes and discuss it in an evolutionary context.



Symposium: MorphoEvoDevo - A happy threesome? – Keynote Lecture
Oral Presentation

Toward a healthy synthesis: Morphology, Phylogenetics, Evolution and Development

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Science progresses with advancements in technology and the refinement of theories. These changes can lead to shifts in the roles of subdisciplines that form an interdisciplinary approach. Especially in cases in which disciplines reunite or integrate to novel alliances (e.g. EvoDevo), old misconceptions intrinsic to one of the subdisciplines can inhibit their fusion or can even cause harm to the whole interdisciplinary approach. Therefore it is necessary to assess the disciplines and their potential roles in relation to each other. Theories and approaches have to be evaluated on the background of the state-of-the art and misconceptions have to be overcome. I will discuss in my talk the roles of morphology, evolution and development as individual disciplines and point out some of their misconceptions e.g. anthropogenic bias, using current examples. I will try to provide a perspective about their synthesis that unites their strengths and helps to enhance potential synergistic effects.



Main Meeting, FG Neurobiology*

Poster: NB 9

Calcium imaging in tethered behaving honeybees

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Honeybees are known for their remarkable sensory-guided behavior like using adaptive navigation based on terrestrial landmarks, sky-compass cues, and optic flow information. These abilities have been demonstrated mainly in behavioral experiments. The pathway implicated in navigation in other insects —leading to the central complex — has been traced and identified anatomically in bees (Zeller et al. 2015, Held et al. 2016). Calcium imaging has been used in completely fixed bees and showed a spatial segregated response in the upper unit of the anterior optic tubercle to monochromatic light stimulation (Mota et al. 2013). In addition, multi-site local field potential recordings have been performed in the optic lobes of tethered bees that walked on an air-supported ball in an LED arena (Paulk et al. 2014). Another visual pathway connects the optic lobes to the mushroom body calyces. Intracellular recordings in bees showed that those neurons are color and motion sensitive (Paulk and Gronenberg 2008, Gronenberg 1986). We seek to combine the strengths of these approaches and establish stable, targeted two-photon calcium imaging in the brain of tethered honeybees, walking on an air-supported ball in an LED arena. To this end, we label populations of neurons using bulk loading of calcium sensors. We are specifically targeting the anterior optic tubercles as well as the basal ring and collar of the mushroom bodies. We will discuss our ongoing efforts to record the physiological responses of neurons in these regions during different tasks like single or multiple stripe fixation and optic flow presentation.

* Contribution also presented in: Symposium: 5th Meeting of the Arthropod Neuroscience Network (Poster: ANN 5)



Main Meeting, FG Morphology

Poster: Morph 11

The morphology of hyopalatinal arches and its meaning for inter- and intrarelations in Alepocephaliformes

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The Alepocephaliformes are an order of deep-sea fish living in around 200-6000m depth of the oceans. They are mostly dark colored and reaching up to 150cm. Three families are known with 137 species. All members lack a swim bladder and an adipose fin. For years this order was placed in changing relations with other teleost fish by using morphological features until genetic studies grouped them as part of the Otocephala. Thus they are closely related to Clupeiformes and Ostariophysi. Morphological features supporting this thesis are virtually lacking yet. Furthermore, the exact relationship of the families to each other hasn't been resolved properly. In this study hyopalatinal arches of members of the Alepocephalidae and the Platytroctidae were examined. For this purpose, their bones and cartilage had been stained before they were dissected. The idea was to find possible morphological features to test the phylogenetic position proposed by genetic studies. The suspensorium was chosen, because of its many bones and features, which are often characteristic for a particular fish group. The survey showed, that there are in fact features of the two families, which seem to be specific for each. Also, it was possible to find possible apomorphies between the Alepocephaliformes and their possible sister-groups. More similarities were found with the Clupeiformes, but it is necessary to collect more data from more species – especially members of the rare Bathylaconidae, as well as more morphological features must be examined in high detail, e.g. the gill arches.



Main Meeting, FG Neurobiology*

Poster: NB 5

Toward a biomimetic Johnston's organ for touch localization

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Tactile exploration of the near-range environment appears ubiquitous in insects. For instance, walking stick insects continuously move their pair of antennae to find footholds for their front legs. Each antenna bears different types of mechanoreceptors, each potentially contributing to touch localization. Among them, Johnston's organ, a chordotonal organ in the pedicel, probably encode contact-induced vibrations. Extracting tactile information from vibrations is a tempting approach for insectoid robots as it requires less wiring than pressure sensor arrays and, in contrast to static force sensing strategies, does not necessitate lasting contact phases. Theory shows that the first vibration modes, i.e. the lowest natural frequencies, are sufficient to estimate the radial distance of hits along a flexible beam. However, in practice, measuring low-frequency components requires proportionally long signal episodes. Not only the resulting latency would impede timely applications, like locomotion control, but also the damped vibrations may vanish too quickly. Hence, it could be beneficial to exploit higher frequency bands. Since beam theory predicts accurately only the few first vibration modes, we experimentally tested whether and which high-frequency bands could be used to estimate the contact distance along a plastic tube rotated by a servomotor. For a range of contact distances, vibrations were sampled with high rate and sensitivity, using a piezoelectric pickup for acoustic guitar, taped to the base of the antenna. Systematically varied bands of the corresponding power spectra were evaluated by support vector regression. We demonstrate that accurate distance estimates can be obtained from various frequency bands, including high-frequency ones.

* Contribution also presented in: *Symposium: 5th Meeting of the Arthropod Neuroscience Network (Poster: ANN 6)*



Main Meeting, FG Systematics, Biogeography and Diversity
Oral Presentation

A morphometric approach to the diversity of fossil and extant larvae of neuropteran insects

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Larvae of many arthropods have quite different morphological features and, coupled to this, different lifestyles if compared with their adult forms. This holds especially true for holometabolous insects. Naturally this is also the case for the holometabolous ingroup Neuroptera. Neuropteran larvae have a predatory lifestyle and possess an evident morphological specialization in their extremely elongated mandibles. In fact, the mandibles form complexes with parts of the maxillae, combining them to a pair of piercing-sucking stylets. In most representatives these are used for injecting venom into the prey and later on for sucking the body fluids. Larval diversity is quite astonishing, including for example: 1) aquatic, almost worm-like, flexible active hunters in nevrothiids; 2) sand-buried ambush predators, partly with sand funnel pits as in ant lions (*Myrmeleontidae*), with sometimes fierce, enlarged stylets; 3) parasite-like forms (later larval stages of *Mantispidae*). There is also a rich fossil record of such larval forms, mostly from different types of amber. Yet, fossil larvae are challenging to be included into evolutionary reconstructions as in most cases identifying the species a fossil holometabolous larva belongs to remains an educated guess. We therefore use a morphology-oriented approach by applying morphometrics. Ten dimensions were measured in extant and fossil neuropteran larvae. Differences in morphology can be recognised and can be correlated to specific time slices (mostly 100 mya, 50 mya, and today) allowing us to reconstruct changes of larval morphology through time.



Workshop: From Gene to Function: Using CRISPR/Cas9 in Zoology
Oral Presentation

CRISPR/Cas9 genome editing applications in zebrafish

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Within the workshop, I will summarize and discuss the current applications of CRISPR/Cas9 mediated genome editing used in zebrafish. These will include our own experience as well as published applications, ranking from simple knockout strategies and tissue specific transcription modifications to knock in approaches. I will also discuss common pitfalls of the procedures and the outcomes.



Main Meeting, FG Ecology*

Poster: Ecol 10

Responses to ending up in different environments: Effects of salinity on growth, metabolism, and behaviour in overwintering invasive gobies

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Round gobies (*Neogobius melanostomus*) successfully invaded and established populations both in freshwater and brackish habitats in rivers and estuaries throughout Western Europe as well as the Great Lakes region in North America. We address the question of phenotypic plasticity, local adaptation and ecological divergence incurred by salinity differences and its direct and indirect effects on morphology, metabolism, behaviour and gonadal investment after being exposed to controlled overwintering conditions at native or foreign salinity conditions. Our results reveal different reaction norms in response to temperature changes, striking morphological differences between populations, consistent individual behavioural types, and a strong effect of salinity exposure - regardless of population origin (Baltic Sea vs River Rhine). Conversely, even under common garden conditions, populations differ with respect to behaviour, gonadal investment, and energy allocation. We discuss our results with an emphasis on the important links between individual behaviour, its population background, and the ecological context.

* Contribution also presented in: *Symposium: Phenotypic Plasticity - RESPONSES of Animals to Environmental Change (Oral Presentation)*



Symposium: Adaptations to Hematophagy in Blood-feeding Parasites
Oral Presentation

Adaptations to hematophagy in blood-feeding parasites

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'Blut ist ein ganz besonderer Saft' (Johann Wolfgang von Goethe: 'Faust I'). 'Blood is a very special juice', especially if you want to drink it from a living donor. To do that you have to approach a host, cut open or penetrate its skin and drink without being detected. You have to make sure that the blood does not clot during feeding or during storage in your intestinal tract. You should avoid to induce inflammation or immune reactions in your host (since you may want to use it more often). You have to make sure that the blood in your intestine is maintained in a native state over extended periods and is not degraded by endogenous or bacterial enzymes. Most hematophagic animals have acquired special structural, physiological and molecular adaptations to this very special way of feeding. Special mouthparts allow penetration or slicing open the host skin, salivary gland cells generate secretions that are effectively transferred to the wound. They contain anesthetizing, anti-coagulatory, anti-inflammatory substances, inhibitors of complement activation, protease inhibitors, fibrinolytic factors and anti-microbial substances. The intestinal tract is specifically designed to take up loads of blood (the probability of finding a suitable blood donor is low) that is digested in small portions over extended periods. The storage compartments often harbor symbiotic bacteria that keep blood degrading microorganisms from spoiling the stored material. This symposium brings together scientists from different areas of expertise and working on entirely different groups of blood-feeding animals (ticks, bugs, leeches, sand flies, mosquitos).



Main Meeting: Public Evening Lecture
Oral Presentation

Der stille Überlebenskampf zwischen Pflanzen und pflanzenfressenden Insekten: Eine chemisch-ökologische Perspektive

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Ein Großteil uns bekannter mehrzelliger Arten sind Insekten und mehr als die Hälfte davon sind Veganer. Obwohl eine solche Fülle z.T. hochspezialisierter Insekten die Pflanzen angreift, ist unsere Erde dort, wo es ausreichend Licht und Wasser gibt, grün bedeckt. Pflanzen und Insekten sichern ihr Überleben durch ein ausgeklügeltes Wechselspiel, das vielfach auf chemischen Signalen beruht. Pflanzen erkennen Insektenbefall nicht erst dann, wenn sie angefressen werden, sondern können bereits auf Insekteneier reagieren. Sie erkennen die Eier oft am klebrigen Sekret, mit dessen Hilfe Insekten ihre Eier an Blätter heften. In Reaktion auf die Eiablagen können Pflanzen Maßnahmen mobilisieren, die zum Absterben der Eier führen. So induzieren z.B. Eiablagen eine Veränderung von Blattdüften, wodurch parasitische Wespen angelockt werden. Die durch eiablage-induzierte Blattdüfte angelockten Parasiten töten die Eier ab. Aber Pflanzen können nicht nur "duftende" Hilferufe an Eiparasiten aussenden, sondern Insekteneier auch als "Warnung" vor aufkommendem Larvalfraß erkennen. Eierbelegte Pflanzen verteidigen sich effektiver gegen die schlüpfenden Larven als Pflanzen, auf denen keine Eier abgelegt worden sind. Durch Eiablagen "gewarnte" Pflanzen zeigen andere Transkriptom- und Metabolomreaktionen auf schlüpfende Larven als eifreie Pflanzen. Somit kann also ein winziges, unauffälliges Insektenentwicklungsstadium, das Ei, den Verlauf von Insektenbefall an einer Pflanze signifikant beeinflussen. Hilker & Fatouros (2015) *Annu. Rev. Entomol.* 60: 493-515; Hilker & Fatouros (2016) *Curr. Opin. Plant Biol.* 32: 9-16



Main Meeting: Public Evening Lecture
Oral Presentation

The silent struggle for survival between plants and herbivorous insects: A chemo-ecological perspective

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The majority of known multicellular species are insects, and more than half of them are vegans. Although plants are attacked by a plethora of insect species, our earth is covered by vegetation wherever sufficient light and water is available. Plants and insects secure their survival by sophisticated interactions which often are mediated by chemical cues. Plants do not only notice insect infestation when damaged by feeding, but they also respond to insect eggs. They may detect the eggs by sticky secretions used by insects to attach the eggs onto leaves. In response to eggs, a plant mobilizes defenses targeting the eggs. For example, insect eggs can induce a change of leaf odor, thus attracting parasitic wasps which kill the eggs. However, plants do not only call parasitoids for help by emission of egg-induced leaf odor, they also can take insect eggs as "warning" of impending larval herbivory. Egg-deposited plants defend themselves more effectively against hatching larvae than plants which never have experienced egg depositions. Plants "warned" by insect eggs show different transcriptomic and metabolomic responses to larvae than egg-free plants. Hence, a tiny, inconspicuous insect developmental stage, the egg, may significantly affect the outcome of infestation of plants by insects. Hilker & Fatouros (2015) *Annu. Rev. Entomol.* 60: 493-515; Hilker & Fatouros (2016) *Curr. Opin. Plant Biol.* 32: 9-16



Main Meeting, FG Neurobiology*

Poster: NB 26

Neurotransmitters in the scorpion central nervous system

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Regarding the morphology of the central nervous system (CNS) and the distribution of neurotransmitters, Chelicerata in general and scorpions in particular received less attention in comparison to mandibulate representatives. Although some studies described certain neurotransmitters in scorpion CNS, these investigations were often focused on certain structures, e.g. the pectine neuropils. A holistic approach to determine distribution and morphology throughout the entire CNS is still missing. However, the identification of individually identifiable neurons has been shown to be an important character complex to study phylogenetic relationships. Therefore, immunohistochemistry was performed on the CNS of *Mesobuthus martensii*, *M. eupeus* and *Euscorpius italicus*. Antibodies against serotonin, histamine, FMRF-amide, allatostatin and glutamic acid decarboxylase, the synthesizing enzyme of GABA, were used. Anti-serotonin staining supports previous studies, where clusters of immunoreactive cells are found pairwise along the midline of the suboesophageal ganglion. Results of histamine labeling indicate a closer relationship to Araneae than to Xiphosura as there are three histaminergic cells per brain hemisphere. These cells are located anterior and superior of the arcuate body, and their projections arborize throughout the entire synganglion. First results of FMRF-amid staining indicate a pairwise pattern. There seem to be two cells per hemisphere in each leg ganglion. Also, two clusters of cells are situated in front of the protocerebrum as well as in the anterior and posterior part of the suboesophageal ganglion. The distribution of immunoreactive neurons and their projections will be presented in detail and comparisons to other arthropods as well as phylogenetic conclusions will be discussed.

*Contribution also presented in: *Symposium: 5th Meeting of the Arthropod Neuroscience Network*
(Poster: ANN 16)



Main Meeting, FG Physiology
Oral Presentation

Metabolic adjustments during starvation in *Daphnia pulex*

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Like many plankton organisms, *Daphnia pulex* face variable food supply in their aquatic habitat. To maintain physiological performance during periods of starvation, adjustments of the metabolism are needed. The dynamics of metabolites and the transcriptional regulation of metabolic enzymes during food deprivation were analysed. Animals were motile for 12 days during nutritional limitation using carbohydrate, lipid and protein stores. In the first 40 h of starvation glycogen concentration declined and gluconeogenesis from metabolites of protein and lipid degradation kept up free glucose concentration and even increased it temporarily. Lipid stores declined transiently. A maximum of α -ketoglutarate was observed after 24 h. Additionally, the role of HIF-1 (hypoxia-inducible-factor-1) for starvation-induced gene regulation was studied. Enhanced α -ketoglutarate concentrations then correlated with a subsequent decrease of nuclear HIF-1 levels. Analysis of the expression of HIF-1 target genes during food deprivation was carried out for enzymes involved in carbohydrate and lipid metabolism. All transcripts showed a maximum between 17 and 20 h after the transfer to algae-free medium, but only hexokinase and long chain acyl-CoA synthetase mRNA concentrations were raised after 64 h. RNA-Seq analysis of animals after starvation revealed a significant upregulation of genes of defense-mechanisms and carbohydrate transport/metabolism after 16 h, whereas extracellular structures, energy production/conversion and coenzyme transport/metabolism were significantly down-regulated.



Main Meeting, FG Systematics, Biogeography and Diversity
Poster: Syst 3

Phylogeography of the Tasmanian mountain shrimps (*Anaspides*; Malacostraca) - Multiple immigrations into subterranean habitats and biodiversity

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Anaspidacea is an enigmatic taxon within Malacostraca with uncertain phylogenetic affinities. They are considered to be “living fossils”, due to fossil records, reaching back 400000 Million years, and many primary characters. The best known genus *Anaspides* is endemic to Tasmania and shows a remarkable geographical and vertical distribution. Seven species are recognized to date, occurring in freshwater habitats such as tarns, small streams, lakes, and also in caves. We studied the genetic differentiation within the morphologically recognized species, as well as the immigration and adaptation in subterranean habitats. Significantly, however, the molecular data suggest several more species than so far described. Special focus is laid on the multiple instances of immigration of *Anaspides* into the subterranean habitat. Immigration is known to have happened at least three times independently across Tasmania (Mole Creek, Mt. Field, Ida Bay/Hastings), but our data suggest that this number could actually be higher. Remarkably, surface and cave forms sometimes share the same COI-haplotypes. In addition to this mitochondrial marker we also sequenced partial 28S rRNA. Entry into subterranean habitats appears to have occurred in the Pleistocene rather than Tertiary and may represent opportunistic expansion into new habitats created by the action of glacial meltwaters on existing karst formations. Morphological differences between surface and cave forms affect body pigmentation, the shape and spination of the telson, the length of sensoric appendages and the number of ommatidia. Remarkably, is that different lineages show the same adaptations, especially the evolution of a cave-type telson.



Main Meeting, FG Morphology
Poster: Morph 22

Sensing the environment – an atlas of the malacostracan sensory appendages

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The Malacostraca, which is one of the largest crustacean groups with over more than 20,000 living species, includes many familiar and almost all economically relevant representatives such as crayfish, crabs, lobsters, shrimps, prawns, and spiny lobsters. Crustaceans feature two pairs of mainly sensory head appendages, the antennule and antenna (first and second antennae). While most malacostracans inhabit marine environments (from pelagic, over benthic to burrowing forms all over the world), some species can be found in freshwater and even terrestrial habitats. Malacostraca evolved a considerable morphological diversity along with their wide distribution. While a number of recent studies have reviewed the evolution of the crustacean central nervous system and of the sensory processing areas associated with the antennules and antennae, the morphological diversity of these head appendages, their size disparity and especially the diversity of their sensillar equipment are rather understudied. Therefore, this study sets out to explore the morphological diversity of the antennules and antennae in representatives of 18 groups of Malacostraca. For this purpose, we use composite macrophotography, fluorescence and light microscopy, and in addition scanning electron microscopy as well as X-ray microscopy (μ CT) to catalogue the antennules and antennae of about 40 species from different collections. We pay special attention to the localization and arrangement as well as size aspects of sensilla. Ultimately, we want to understand evolutionary aspects of these highly specialized sensory organs and possible correlations to the sensory landscape which the animals face in their specific habitats.



Main Meeting, FG Ecology

Poster: Ecol 1

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

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



Main Meeting, FG Physiology
Oral Presentation

Light-gated channelrhodopsin-2 alters calcium signaling for power control in the indirect flight muscle of *Drosophila*

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Calcium is a major cellular component that controls contraction dynamics in muscle cells. Although the indirect asynchronous flight muscle (AFM) in insects is stretch-activated by cyclic lengthening, recent data show that *Drosophila* finely matches calcium concentration to the instantaneous muscle power needed for flight. We hypothesize that calcium in AFM controls a calcium-dependent troponin complex to balance stretch- and calcium-induced muscle contraction. To study calcium control in AFM, we employed the Gal4/UAS system and genetically modified muscle calcium control in *Drosophila* by genetic insertion of the light-gated, m-cherry tagged calcium channel channelrhodopsin (Chr-2) expressed under the AFM-specific Act88F promoter. Fluorescence microscopy on m-cherry suggests that Chr-2 is successfully expressed in AFM compared to controls. To test channel function, we generated two fly lines: one line with the expression of the calcium indicator GCaMP6 and one line with double expression of Chr-2 and GCaMP6. Since Chr-2 and GCaMP6 are sensitive to the same excitation wavelength, we compared relative fluorescent signaling between the two lines. Working hypothesis is that in resting GCaMP6 flies, AFM fluorescent signals are weaker than in the double mutant Chr-2/GCaMP6 because of light-gated influx of calcium from the extracellular space. Chr-2 lines were subsequently tested in a virtual reality flight simulator during laser-activation in order to estimate the impact of calcium surplus on muscle mechanical power output and wing motion control. Preliminary flight data show significant changes in wing motion during laser light activation.



Main Meeting, FG Ecology
Oral Presentation

Effects of nutrient stoichiometry on the top-down control of stream periphyton: compensatory feeding in the freshwater gastropod *Ancylus fluviatilis*

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Primary producer biomass is determined by both nutrient availability (bottom-up control) and grazing activity by herbivores (top-down control). Fluctuations in primary producer stoichiometry may cause grazers to optimise their food intake through behavioural strategies, which may in turn affect the control of primary producer biomass. Such linkages between nutrient availability and grazing control are as yet poorly understood. In this study, we tested whether the stream-dwelling freshwater gastropod *Ancylus fluviatilis* would increase its food consumption rate with decreasing food quality, a behaviour known as compensatory feeding. We performed a full factorial microcosm experiment in which two levels of algal phosphorus content (low versus high) were crossed with grazer presence/absence in circular running water flumes. The food consumption rate of *A. fluviatilis* was significantly higher in the low phosphorus compared to the high phosphorus treatment, supporting the compensatory feeding hypothesis. As a result, in the presence of grazers, algal biomass was significantly lower under low phosphorus availability, while it was not affected by nutrient enrichment in the grazer-free flumes. Furthermore, phosphorus level and grazing interacted in determining periphyton spatial heterogeneity, which was significantly higher in the grazed phosphorus-poor than in the high phosphorus treatment. Our findings suggest that nutrient enrichment may lead to a weaker top-down control of algal biomass in stream ecosystems and to a reduced spatial heterogeneity of periphyton.



Main Meeting Keynote Lectures
Oral Presentation

**Deutsche Forschungsgemeinschaft - Meet DFG @ DZG
2018: How to set up your career and get funding for your
research ideas - DFG funding programmes and application
procedures**

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This talk will give an overview of the different funding programmes of the DFG (Individual grants and coordinated research programmes) and explain the most important criteria for successful proposals. We present Dos and Don'ts in setting up a proposal and discuss recent developments in terms of funding programs and evaluation criteria. Professor Thorsten Burmester as a member of the Fachkollegium of the DFG will be present to share his experiences as a reviewer.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral Presentation

Taxonomy and distribution of southeast Asian chelonians

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The Indo-Burma region represents a global biodiversity hotspot that harbours the highest diversity of freshwater turtles and tortoises in the world. The outstanding diversity across Southeast Asia was shaped by the area's complex tectonic and climatic history. Continental collisions and sea level changes repeatedly connected and disconnected landmasses and alternating glacial and interglacial periods forced populations to retract and expand. A combination of species distribution modelling techniques with phylogenetic analyses helps to unravel the phylogeographic history of extant taxa. To assess whether widespread lowland chelonian taxa represent species complexes that correspond to zoogeographic barriers I examined the phylogeographic structure of aquatic turtles of the genus *Malayemys* and of the terrestrial species *Indotestudo elongata*. Differentiation within *Malayemys* was determined using mitochondrial DNA, microsatellite loci, morphological analyses and the paleo-projection of a Species Distribution Model, while morphometric and colouration-related characters and mitochondrial DNA were used to determine variation in *I. elongata*. These analyses revealed *Malayemys* to consist of three genetically distinct groups, exhibiting distinct nuclear gene pools and morphology. Consequently, the study led to the recognition of three species one of which hitherto unknown. In contrast, genetic and morphological variation was only moderate in *I. elongata* and apparently not associated with zoogeographic features that have induced divergence in other lowland reptiles. This lack of divergence is likely attributed to a long history of human mediated dispersal of a once small and localised ancestral population.



Main Meeting, FG Morphology
Poster: Morph 27

Evolutionary implications of dentitional metamorphosis in caecilian amphibians: a revisit

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The dentition of fetuses and juveniles differs from that of adults in morphology, position and even in function among caecilian amphibians. Caecilians are fossorial pantropical amphibians renowned for their remarkable diversity of reproductive modes and life histories. Functionally fetal or vernal teeth are used to scrape off oviducal epithelium and to stimulate the secretions of nutrients or used to peel off the mother's skin post-partum or post hatching. The dentition of several caecilian species was studied on 3D-reconstructions gathered from microCT scanning. In our comparative morphological analysis we tried to cover representatives of all currently recognized caecilian families: Our study includes the genera *Epicrionops* (Rhinatreumatidae), *Ichthyophis* (Ichthyophiidae), *Boulengerula* (Herpeliidae), *Geotrypetes* and *Schistometopum* (Dermophiidae), *Caecilia* (Caeciliidae) and *Typhlonectes* (Typhlonectidae). Intraspecifically we compared different ontogenetic stages i.e., larvae, juvenile, subadult and adult. Significant differences, if present, were especially found on the dentals of a given species, e.g., young *Caecilia pachynema* had higher numbers and morphological different teeth on the dentale, compared to fully independent ontogenetic stages. Teeth on the upper jaw also varied in number and morphology. However, no such differences were found in herpeliids *Boulengerula fischeri* and *B. taitanus* but also in phylogenetically basal *Epicrionops bicolor*. There are interspecific differences in tooth number among Ichthyophiids between larval and terrestrial stages. Larval *Ichthyophis supachai* had splenial teeth, but *Ichthyophis* cf. *kohtaoensis* lacked those. An updated knowledge on the dentitional metamorphosis in caecilians can help to draw conclusions about a specific ecology and life history but also supports the understanding of amphibian evolution.



Main Meeting, FG Neurobiology

Poster: NB 20

Neuronal plasticity of predator induced defences in *Daphnia*

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Phenotypic plasticity describes the ability of an organism with a given genotype to adapt to changing environmental conditions by developing context-dependent phenotypes. Predator-induced morphological defences represent a special form of phenotypic plasticity and have been well described in freshwater crustaceans of the genus *Daphnia*. The different species display a range of morphological defences against different predators rendering them less susceptible to predation. The predation risk is indicated by predator-specific chemicals, which are detected by *Daphnia* using chemoreceptors on the antennules. Subsequently, a series of biological reactions, including neuronal and endocrine signalling, is initiated. However, the precise neuronal pathways and the associated cellular sites involved in defence expression have not yet been identified. Here we aimed to describe predator-induced neuronal plasticity of the nervous system. We induced crest expression in *Daphnia longicephala* and found that morphologically defended animals show an increase in brain size. Using immunohistochemistry and confocal imaging we counted the number of cells in the nervous system and determined the number of presynaptic sites using a specific marker in control- and predator-exposed specimens. While the number of nerve cells remained unchanged, we observed an increased number of presynaptic sites in induced animals. Our results show neuronal plasticity in *Daphnia* and indicate that the underlying neuronal network is remodelled and adapted upon the perception of predator specific cues.



Symposium: 5th Meeting of the Arthropod Neuroscience Network
Oral Presentation

Evolution of sensory centres

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Because of the lack of fossil evidences, it is difficult to estimate the brain architecture of pre-Ediacaran animals before the divergence of deuterostome/protostome or deuterostomia/ecdysozoa. The brains of the organisms in the distal ends of those evolutionary clades, such as mammals and insects, or vertebrates and arthropods, show surprising similarity in their sensory systems. In the visual system, lower centres have retinotopic columnar architecture whereas higher centres are organized into multiple regions each of which handles specific aspects of visual information. In the olfactory system, odour-specific glomeruli convert the chemical information of odorant composition in the air to a physical map of distributed neuronal activity. Likewise, sweetness, bitterness and other gustatory information are represented in segregated areas of the gustatory centre. Centres that receive sound and gravity are linked, and different modalities of somatosensory signals are received in the layered centres in the nerve cord that are aligned in the corresponding order between mammals and insects. The similarity is too consistent to be regarded as a result of multiple coincidences. Rather, early Bilateria without hard skeleton may already have possessed a rather complex brain that receives signals from all the five major sensory modalities. In this regard it is interesting to note that, in spite of the architectural similarity of sensory centres, peripheral sensory cells may appear rather different both in terms of development and molecular machinery. Whereas all the sensory cells emerge from the epidermis and project axons to the central nervous system in insects, long dendrites arising from the neurones near the CNS project to the subcutaneous sensory cells in mammals. Receptors that perceive odorants and somatosensory stimuli are not directly comparable between the two clades. During neurogenesis, structures of sensory centres are often established before peripheral neurons innervate, and they retain their architecture even during metamorphosis when all the sensory neurons are reformed. Such independence might in part explain the discrepancy between architectural similarity of sensory centres and developmental/molecular difference in the sensory cells.



Main Meeting, FG Morphology
Oral Presentation

Reconstruction of the circulatory system of the velvet worm *Euperipatoides rowelli* (Onychophora: Peripatopsidae)

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The organization of the circulatory system in the last common ancestor of Panarthropoda (Onychophora + Tardigrada + Arthropoda) is poorly understood, as this system might have been lost in tardigrades and is understudied in onychophorans. We therefore performed detailed 3D reconstructions of the circulatory system of the onychophoran *Euperipatoides rowelli* using synchrotron radiation-based X-ray micro-computed tomography (SR- μ CT) and complete series of semithin sections. Corrosion casts, scanning electron microscopy, and histological and immunohistochemical data were used to obtain additional morphological information. Our study revealed that two types of segmentally repeated channels are responsible for directing hemolymph from the main cavity of the trunk into the pericardial sinus surrounding the ostiated heart: the hemal channels and the pericardial channels. Each body segment contains 15 ring-like hemal channels, which are associated with plicae (transverse skin folds or annuli), but only one pair of pericardial channels that are formed by the extensions of the pericardial lining at the level of the heart ostia. The heart opens anteriorly into the head sinus, the organization of which is more complex than previously thought, as we recognize two rather than one portions: the supratharyngeal sinus, and the supracerebral sinus, both of which have wide, paired ventral openings. Our findings suggest that the last common ancestor of Panarthropoda might have possessed an elaborate, segmentally organized circulatory system, which was modified in different arthropod lineages. Future studies should aim at identifying homologous elements in the circulatory systems between onychophorans and representatives of all major arthropod groups.



Main Meeting, FG Ecology*

Poster: Ecol 11

Enforced evolution via epigenetic pressure in drosophilids: Proof of principle via olfaction and oviposition

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One ecological strategy of organisms to adapt to harsh environmental conditions is epigenetic plasticity (Bossdorf et al., 2010). Besides rapid mutation, genetic engineering or transposon control, targeted epigenetic pressure is therefore considered to be one option of so-called Assisted or Enforced Evolution, where organisms are adapted to desired conditions artificially (f.e. Springer, 2013). Here we focus on intentionally inducing epigenetic changes in the model organism *Drosophila melanogaster* via nutrition in a transgenerational experiment. While its sister species *Drosophila sechellia* not only readily accepts the toxic hexanoic acid (HA) in its food, but also feels olfactorily attracted to it and deposits its eggs exclusively on the ripe *Morinda* fruit containing HA, *D. melanogaster* reacts highly aversive to the odor and taste of HA (Prieto-Godino et al., 2017). In this study, *D. melanogaster* is to be adapted to readily consume HA and also to perform oviposition on a nutrient medium containing it via exposing to constant environmental stress. The special purpose of this experiment is to find out whether epigenetic effects are plausible candidates for targeted adaptations in animals, starting with Drosophilids (Janjic, 2017), including to ascertain in which way the epigenetic changes appear: At what tempo? Continuous over time or discrete from one certain generation? etc. Thus, this experiment contributes to explaining some possible aspects of the past evolution and speciation of *D. sechellia* and further to evaluating future potentials of Enforced Evolution in applied ecology, be it because of economic, climate change, or even astroecological reasons.

* Contribution also presented in: *Symposium: Phenotypic Plasticity - RESPONSES of Animals to Environmental Change (Oral Presentation)*



Main Meeting, FG Morphology

Poster: Morph 2

Mechanical and structural characterization of stingray inspired tessellations using computational techniques.

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A distinctive morphology has defined the cartilage of elasmobranch fishes (sharks and rays) for more than 400 million years. Although similar to mammalian hyaline cartilage, the entire cartilage skeleton surface is covered with layer of minute polygonal, mineralized tiles called tesserae. Our group's recent studies have described variety of previously unrecognized anatomical and ultrastructural features of tesserae using three-dimensional materials and structural characterization techniques, which shows tesserae are not simple homogenous blocks, but rather exhibit pronounced local variation in cell and mineral density and several distinct structural features that suggest mechanical roles. Tesserae are believed to manage stress distribution in a way which minimizes damage to the cartilage, while also providing flexibility and stiffness. However, the links between the ultrastructure/mechanics/material properties of tesserae remain unknown, due to the difficulty of performing mechanical tests on their intricate, three-dimensional structural features. Computational techniques helped us (parametric modeling, finite element analysis) to model tesserae in 3D and parametrically vary the ultrastructural key morphological features to determine their effect on skeletal properties. We show that some structural features (e.g. spoke-lamina-number, cellular-center-radius) have little effect on tesserae stiffness, whereas there is a 6% increase with the increase in higher contact zone. These models support new hypotheses regarding growth, load management and ultrastructural interaction with tesserae mechanics. For example, the tesserae-center, one of the most cell-dense regions, experiences high stress and we hypothesize that cells here act as sensors, collecting information for growth. Additionally, the lamina prevents crack propagation by alternating high-low stress in the spoke.



Main Meeting, FG Neurobiology*

Poster: NB 2

Effects of thoracic connective lesions on inter-leg coordination in freely walking stick insects *Carausius morosus*

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Multi-legged locomotion requires appropriate coordination of all legs. Whereas behaviourally derived coordination rules can adequately describe many aspects of inter-leg coordination, the neural mechanisms underlying these rules are still not entirely clear. The fact that inter-leg coordination is strongly affected by cut thoracic connectives in tethered walking insects suggests that neural information exchange among legs is important (Dean, 1989, *J.Exp.Biol.* 145:103). As yet, load transfer among legs can contribute to inter-leg coordination without neural information exchange among legs (Dallmann et al., 2017, *Proc.R.Soc.Lond.B* 284:20171755). Since load transfer does not work in tethered walking animals, we tested whether connective lesions had equally strong effects if load transfer among legs was possible. To do so, we recorded all six protraction/retraction angles in animals that either had one thoracic connective cut unilaterally (pro-meso or meso-meta), or had undergone corresponding sham operations. Overall, our results were similar to those of Dean. In particular, the leg anterior to the lesion started its swing phase largely independent of the posterior leg's step-cycle. Pro-meso-lesioned animals walked more slowly, and all lesioned animals showed increased sideward translation than sham controls. Whereas Dean reported large-amplitude swing movements of the hind leg, freely walking animals tended to drag it along, with low-amplitude protraction/retraction movements remaining. Spatial coordination of lift-off and touch-down locations were more consistently and strongly impaired than reported by Dean. We conclude that load transfer among legs cannot rescue the impairments of inter-leg coordination after connective lesions, suggesting that neuronal information transfer is mandatory for ipsilateral inter-leg coordination.

* Contribution also presented in: *Symposium: 5th Meeting of the Arthropod Neuroscience Network* (Poster: ANN 17)



Main Meeting, FG Behavioural Biology

Poster: Behav 2

The neglected sense: Orientation by passive electrolocation in the weakly electric fish, *Gnathonemus petersii*

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Like all weakly electric fish *Gnathonemus petersii* generate electric organ discharges (EOD) to actively scan their environment for food and to communicate with conspecifics. In addition, *G. petersii* possess a passive electric sense with which they can detect external electric fields in their environment. In contrast to passive electrolocation in sharks and rays, little is known about the function of this sensory modality in weakly electric teleosts. In this study, we tested whether *G. petersii* can use its passive electric sense for orientation in a hole-board arena supplied with local static electric fields (DC) as navigational cues for finding hidden insect larvae. Fish responded with spontaneous search behaviour when an electric field was switched on. Within a few days, fish learned to quickly (< 10 s) find a hidden larvae indicated by an electric field stimulus. Transfer tests revealed that fish mostly relied on the information provided by the local electric fields. They often followed place shifted electric fields, and search latencies increased if the electric field was switched off. Overall, fish used a combination of an allocentric and egocentric strategy to find the food. These data show that *G. petersii* can use weak DC electric fields for orientation in their aquatic habitat. Future work will include estimation of behavioural thresholds and the conduction of additional transfer tests to identify all sensory cues and to reveal the exact navigational strategies used by the fish.



Main Meeting, FG Evolutionary Biology

Poster: EvoBio 4

Morphological adaptations to extreme maternal and allomaternal care in spiders

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Extended brood care in non-social species is assumed to have facilitated the evolution of helping and thus of sociality. The spider genus *Stegodyphus* comprises solitarily and cooperatively breeding species, and females perform extended brood care. Thus the genus is perfectly suited for investigating adaptations to cooperative brood care. In the highly inbred social species, brood care including regurgitation feeding and matrophagy, is not only performed by mothers but also by virgin females (allomothers). We investigated the morphological adaptations associated with this extreme brood care and its reversibility in mothers of the solitarily breeding spider *Stegodyphus lineatus* and compared it to mothers and allomothers of the cooperatively breeding *Stegodyphus dumicola*. We found that brood care in solitarily breeding mothers is associated with massive disintegration of their midgut tissue. Mothers in the social species face similar progressive tissue transformation, although less pronounced. Changes are reversible in both species when brood is lost. In contrast to virgins of the solitary species, allomothers in the social species are capable of providing for offspring and show similar internal changes compared to mothers. We found late vitellogenic eggs in virgins of the social, but not of the solitary species. This suggests that allomaternal care in cooperative *Stegodyphus* is linked to the ability of unmated females to mature eggs, which may trigger the full sequence of brood care activities. The physiological ability of virgin females to provision offspring is key for acquiring indirect benefits, and likely represents an adaptation to cooperative breeding.



Main Meeting, FG Morphology

Poster: Morph 5

Reproduction at depth - the reproductive morphology of hydrothermal vent crabs

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Little is known about the Bythograeidae – a brachyuran family that is endemic to hydrothermal vents. Up to date, six genera have been described with 14 species. Almost everything we know about this family is based on a single species of the genus *Bythograea*. Hydrothermal vent crabs are very similar to shallow-water brachyurans in their basic biology, but have also evolved characteristics specific for life at hydrothermal vents (Dittel (2008) Journal of Shellfish Research, Vol. 27, 63-77). To expand our knowledge about reproductive anatomy of these crabs, we investigated the female seminal receptacle and the male gonopods of the genus *Austinograea*. To do so we used a combination of different methods: histology, magnetic resonance imaging (MRI), micro computed tomography (μ CT) and scanning electron microscopy (SEM). The results show a seminal receptacle, which fundamental characteristics are homologous to shallow-water brachyurans. Especially conspicuous is the proportion of glandular epithelium within the seminal receptacle, which differs from other brachyuran species. The morphology of the gonopods is described in great detail. In conclusion, the reproductive system of *Austinograea* combines classic characteristics of other known Brachyura, yet distinct specific traits can be found in these organs too.



Main Meeting, FG Developmental Biology
Poster: Dev 9

Embryonic staging of an emerging onychophoran model species

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Onychophora (velvet worms) belong to the closest relatives of arthropods. Together with Arthropoda and Tardigrada, they form the Panarthropoda. The peripatopsid species *Euperipatoides rowelli* Reid, 1996 has been studied intensively in recent years and has emerged as a model for evolutionary and developmental biology. Numerous molecular studies concerning gene expression in *E. rowelli* have been published. Nevertheless, no comprehensive description of the embryogenesis is available for this species, which would be important for contextualizing the expression patterns during onychophoran development. A previously published embryonic staging based on scanning electron microscopy (SEM) comprises seven stages. However, these stages are too broadly defined, and the individual developmental events are not precisely described. To provide a more detailed staging, we examined embryos of *E. rowelli* throughout the embryonic development, focusing on segment formation and external morphology. To achieve this, we analyzed the expression patterns of engrailed and examined the external morphology of the same embryo using whole-mount in situ hybridization and SEM, respectively. In addition to a new staging system, these methods enabled us to follow the development of different structures such as the antennae, legs, eyes, and nephropores. The combined analysis of both the expression pattern and the external morphology of a single embryo allows for a more precise definition of the embryonic stages of *E. rowelli*. This study thereby provides a framework for further studies in developmental and evolutionary biology.



Main Meeting, FG Evolutionary Biology
Oral Presentation

An evolutionary approach to the molecular basis of circalunar clocks

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While in 2017 the Nobel price was awarded for unraveling the molecular basis of circadian clocks, the molecular underpinnings of circalunar clocks (i.e. biological clocks timing lunar phase) are still entirely unknown. In the marine midge *Clunio marinus* (Diptera: Chironomidae) we can tackle this problem with an evolutionary approach: Living in the intertidal zone, *Clunio* has timed its life cycle to the tides by circadian and circalunar clocks. As the tides differ dramatically along the coastline, *Clunio* populations show many local genetic adaptations in their clocks. By QTL mapping, genome screens and comparative molecular analysis, we can identify the adaptive genes and thereby pinpoint previously unknown clock molecules. With this approach we identified Ca²⁺/Calmodulin-dependent protein kinase II (CaMKII) as a modulator of circadian timing (Kaiser et al. (2016) Nature, 540, 69). In this study, we assembled a chromosome-scale *Clunio* reference genome, performed QTL mapping for timing differences and sequenced genomes from differently timed populations. We detected timing-associated genes within the QTLs based on the correlation of genetic divergence with timing differences. The data suggest that timing adaptation happened from standing genetic variation and involves regulatory changes. Subsequent molecular analysis substantiated that adaptation in circadian timing relies on modulating alternative splicing of CaMKII, entailing a mechanistic model of how DNA sequence changes translate into adaptive timing phenotypes. Currently, we apply this evolutionary approach to find the molecular basis of various circalunar timing phenotypes, including differential sensitivity to environmental time cues and the complete loss of circalunar timing in certain *Clunio* strains.



Main Meeting, FG Evolutionary Biology
Oral Presentation

How ontogeny and plasticity contribute to adaptation: Changes in the visual system of Nicaraguan Midas cichlids

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Identifying the molecular mechanisms driving adaptive divergence is a major goal in evolutionary biology. The role of plasticity in promoting phenotypic divergence has been studied in multiple systems. Yet, it remains largely unclear to what extent adaptive or non-adaptive plasticity facilitate evolutionary change. The Nicaraguan Midas cichlids fish repeated adaptive radiations (*Amphilophus citrinellus* cf.) provide a great opportunity to address such questions. About 2,000 generations ago, fish from a source population in a shallow and turbid great lake colonized multiple newly formed deep and clear crater lakes. The photic environments of these lakes differ substantially, and in response to this change, the visual system of the derived populations adapted by tuning visual sensitivities accordingly and by increasing developmental plasticity and changing ontogenetic trajectories. However, the underlying molecular mechanisms that caused these changes in visual sensitivity are still largely unknown. Analyzing retinal transcriptomes of populations from the two environments reared under different light regimen, as well as comparing ontogenetic trajectories within these light regimen allowed us to answer the following questions: Are the genetic networks underlying phenotypic plasticity, ontogenetic changes and population divergence in visual sensitivities the same? What role do plasticity and ontogeny play in adaptation to novel light environments?



Main Meeting, FG Morphology

Poster: Morph 17

The ultimate legs of *Lithobius forficatus* – a morphological analysis of transformed arthropodia

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The ultimate legs of centipedes are special. They are never or rarely used for locomotion, and a plethora of different behavioral adaptations are associated with the morphological transformation of these legs. Many centipede species possess significantly elongated, thickened, or pincer-like ultimate legs, and frequent sexual dimorphisms indicate a pivotal role in courtship and mating. In addition, glandular pores are much more often present on ultimate legs than on walking legs, signifying their relevance in secretion, chemical communication, or predator avoidance. We characterize the transformed ultimate legs in comparison to walking legs in *Lithobius forficatus* in terms of general morphology, typology and distribution of epidermal sensilla, and architecture of associated nervous system structures. Although the ultimate legs still largely resemble walking legs, all methods applied reveal that they feature a series of distinctions that sets them apart from a walking leg. Substantial differences were found in the configuration of specific podomeres, musculature equipment, increased abundance of epidermal glands, presence of a novel type of cuticular sensilla, as well as the augmentation of primary processing centers in the ventral nerve cord. Altogether, lithobiomorph ultimate legs are an intriguing example into transformational processes shaping arthropodia.



Main Meeting, FG Morphology
Oral Presentation

A look inside: Approaching the “mysterious” pupal development of holometabolan insects

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The post-embryonic development of holometabolan insects is traditionally differentiated into three phases: larval phase, pupal phase, adult phase. Of these three phases, the pupal phase has apparently gained least attention. Already basic considerations turn out to be challenging and causing discussions. For example, despite the seemingly exceptional status of the pupa, it can in principle be recognised from a functional point of view as another specialised transitory larval stage as also present in numerous different euarthropod lineages, such as many malacostracan crustaceans. More important, in the sister group to Holometabola also different ingroups evolved a pupa-like transitory stage. This becomes interesting when considering that, although all holometabolan insects have a pupal stage, these are so different that we can not reconstruct a ground pattern state of the pupa for Holometabola easily. Even its identity as a “resting stage”, which is often advocated, needs to be questioned. Also processes during pupal development seem largely not well understood. We present new data on pupa morphology of tenebrioniid beetles. Two different methods were used to investigate the pupae: 1) bleaching specimens with hydrogen peroxide to turn the cuticle transparent, and 2) histological sections. Bleached specimens provide access to changes of the outer morphology during pupal development, i.e. differentiation of articles, setae, wings and so on. Histological sections provide access to the development of inner structures such as muscles and internal organs. Observation on both systems indicate that pupal development is very gradual and does not differ significantly from developmental processes in other euarthropods.



Main Meeting, FG Morphology
Oral Presentation

Three-dimensional reconstruction of the brain and its neuropils in the onychophoran *Euperipatoides rowelli*

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Onychophorans (velvet worms), a group of terrestrial invertebrates, compose together with tardigrades (water bears) and arthropods (chelicerates, myriapods, crustaceans and hexapods) the taxon Panarthropoda. The close relationship of onychophorans to arthropods renders them an important group for understanding arthropod evolution. Arthropods, which are one of the best characterized animal groups in terms of distribution and diversity, are, due to their enormous success, fascinating for researchers, who aim to clarify the basis of their superior abundance. Lately, the nervous system has become a key trait for understanding the evolution of many animal groups. Despite a vast diversity across the arthropod groups, a similar organization of neuronal structures, such as the brain and the paired nerve cords, is present in all major groups. In order to get better insights into the evolution of the nervous system, an investigation of one of the arthropods' closest relatives, the onychophorans, becomes indispensable. To obtain detailed insights into the organization of the central nervous system in onychophorans as well as the connectivity of their neuropils, we analysed a series of histological sections of the onychophoran *Euperipatoides rowelli* (Peripatopsidae). In doing so, we designed, for the first time, a 3D model of the onychophoran brain and the anterior part of their nerve cords. Our findings not only yield a better understanding of the onychophoran brain composition itself but furthermore provide useful information for a comparison with the brains of arthropods.



Main Meeting, FG Systematics, Biogeography and Diversity
Poster: Syst 2

High degrees of cryptic microendemism in the scorpion genus *Buthus* as revealed by DNA barcoding

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Microallopatry and microendemism are often results of allopatry in strongly structured landscapes. The mountain ranges of northern Africa represent an area which provides the prerequisites for extensive speciation in a geographically limited area. Especially philopatric taxa and species with limited dispersal abilities tend to diverge in genetically structured lineages. This divergence, however, may not be reflected in the morphology if the selective conditions are relatively homogeneous and diversification was fast. Hence, extensive genetic diversity may be frequently overlooked. Here, we studied cryptic genetic diversity in the scorpion genus *Buthus* across the Atlas Mountains of Morocco, and neighboring regions in Europe and Northern Africa. We used DNA barcoding and statistical species delimitation methods to investigate cryptic diversity patterns. Depending on the method we detected between xxx and xxx molecular operational taxonomic units, which do not correspond to morphologically identified species. Commonly used morphological traits have evolved multiple times. Further, it appears that Europe has been colonized several times by the genus. Our analyses show that the current taxonomy of the genus is flawed and that commonly used morphological traits may not be suitable to distinguish local taxa. Likely this patterns hold up for a variety of other taxa with little mobility suggesting a high potential for undetected diversity in this hotspot region of biodiversity.



Workshop: Animal Welfare
Oral Presentation

Husbandry of two species of flying foxes in a laboratory animal setting

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Bats (Chiroptera) play an important and significant part within the global ecosystems. Current outbreaks in humans and new research results emphasise their role in the transmission of highly infectious zoonotic diseases such as Ebola, Nipah, Rabies or SARS. To prevent and decrease the risk of bat-related disease outbreaks in human populations and improve the conservation of bats and their native environment, research on the role of bats in the epidemiology and infectiology of pathogens has to be intensified. For this purpose, the Institute of Novel and Emerging Infectious Diseases (INEID) has established breeding groups of two species of African flying foxes (*Eidolon helvum* and *Rousettus aegyptiacus*) on the grounds of the laboratory animal holding facilities of the FLI Riems. The presentation will describe the husbandry as well as the veterinary care of both species at the FLI Riems. Since 2016, the breeding colony husbandry has been augmented to include husbandries for laboratory trials, including infectiological experiments with viral pathogens. Cell lines derived from specimens of the collection as well as international collaboration with fellow institutions for the sake of providing them with sample material have been established.



Main Meeting, FG Developmental Biology
Oral Presentation

Rethinking the role of the nervous system: Lessons from the freshwater polyp *Hydra*.

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The emergence of the first nervous systems in evolution allowed animals to perceive signals from the environment and to respond to them by moving in an active, organized manner. Accumulating evidence suggests that in addition to this conventional role, the nervous system may orchestrate other organismal functions, such as development, tissue homeostasis, and immune function. Our recent studies on the freshwater polyp *Hydra*, a non-bilaterian animal which is among the first metazoans that possess a nervous system, revealed a central role of the nervous system in host-microbiome crosstalk. Molecular profiling of the *Hydra* nervous system by single-cell transcriptomics revealed that the neurons express an unexpectedly rich repertoire of immune receptors and signaling pathways and secrete a variety of putative antimicrobial peptides. Further analysis of some neuropeptides by transgenesis demonstrated that they shape the microbiome on the body surface of *Hydra*. Behavioral assays uncovered that the symbiotic bacteria influence the activity of the *Hydra* nervous system by directly interfering with neuronal receptors. In bilaterian animals, the host-associated microbiota is also in a permanent dialog with the host enteric and central nervous systems. Together these findings point to a universal role of the nervous system in mediating host-microbe interactions throughout the Metazoa and suggest that it emerged to orchestrate multiple functions involved in maintaining the metaorganism integrity. The work is supported by the Deutsche Forschungsgemeinschaft (CRC 1182: „Origin and Function of Metaorganisms“) and a grant from Wallenberg Advanced Bioinformatics Infrastructure at SciLifeLab (Sweden).



Main Meeting, FG Developmental Biology

Poster: Dev 14

The role of chitin deposition during tracheal morphogenesis in *Drosophila*

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The fact that the development of the tracheal system in *Drosophila* is relatively well understood makes it one of the best models for more detailed questions on organogenesis. A general feature of the maturation of many organs and tissues is the deposition of an extracellular matrix (ECM) which provides biochemical and structural support, participates in cell adhesion, regulates cell-cell communication, and senses and transduces mechanical signals. Also the development of the tracheal system is highly dependent on the deposition of a chitinous so-called apical extracellular matrix (aECM) which provides structural support and regulates cell-cell communication during the process of morphogenesis and tube maturation. The exact temporal and spatial control of aECM secretion, and thus chitin deposition, is therefore crucial for the correct morphogenesis of the tracheal system. Recently it has been demonstrated that chitin deposition requires not only the activity of the chitin synthase Krotzkopf verkehrt (Kkv) but also the activity of two other genes, namely expansion (Exp) and rebuff (Reb). Interestingly, it was found that the concomitant misexpression of Kkv and Reb/Exp during the embryonic development not only leads to advanced and increased chitin deposition, but also to defects in tube size and cell rearrangements during tracheal morphogenesis. To characterize these defects and understand the contribution of chitin deposition to tracheal morphogenesis we used immunostainings in combination with cLSM and 3D-reconstruction to study the molecular interactions between Kkv and Exp/Reb in relation to various other markers (e.g. E-Cadherin and Crumbs) known to affect cell rearrangements and tube size regulation.



Main Meeting, FG Neurobiology
Poster: NB 28

Shape discrimination in the weakly electric fish *Gnathonemus petersii*: local or global cues?

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During active electrolocation weakly electric fish *Gnathonemus petersii* evaluate the distortions that nearby objects cause in the fish's self-produced electric signals. It was shown that fish can discriminate between objects differing in shape, size or material. However, often it remained unknown which sensory cues the fish had used for object recognition. Here we tested whether discrimination of isovolumetric objects differing in shape is based on global template matching or on local object features. Fish were trained in a two-alternative forced-choice procedure to discriminate between two aluminium objects (cube, sphere, pyramid), a rewarded S+ and a punished S-. After the fish's performances reached more than 75% correct discriminations, choice behaviour was evaluated in unrewarded/unpunished transfer tests with new contour-objects, consisting only of 3-D contours of the training objects made from copper wires. Subsequently, these contours were more and more reduced, until the fish did no longer discriminate between them. In addition, different fractions of the contour of the S+ and the S- were tested against each other. The fish could distinguish equally well between the contour objects as between the original training objects. The discrimination performance was still high when just particular minor fractions of the contour of the S- or the S+ were left. For a decision, fish evaluated both objects and did not rely only on features of the S+ or the S-. Our results imply that the fish did not perform global template matching but instead used local object features for shape discrimination.



Main Meeting, FG Systematics, Biogeography and Diversity
Poster: Syst 13

Development of polygonal scales in the genus *Atherina* (Teleostei, Atheriniformes)

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The majority of teleostean taxa bears scales. Independent of their principal scale type, i.e. cycloid or ctenoid, they are usually more or less rounded or slightly square structures. The scales of atheriniform fish, especially their type and shape, have been studied only in very few investigations so far. The available data describes the scales of only five species in three genera. The Atheriniformes, however, comprise about 350 species inhabiting freshwater, brackish and marine habitats. This gives reason to expect a high variability in their scale shape and scale ornamentations. For example, the scales of *Atherina* are cycloid with a hexagonal/octagonal shape, while the scales of *Odonthestes* are square and exhibit additional ornamentations. In an attempt to figure out the initial condition of atheriniform scales, we looked at the development of the scales of *Atherina presbyter*. Furthermore, we compared scales of three different species of the genus *Atherina*. The results gave clues on the general ontogeny of scales as well as the high diversity of scales within one family.



Main Meeting, FG Neurobiology
Poster: NB 17

Infrared object motion-processing in the rattlesnake hindbrain depends on rate- as well as spike time encoding mechanisms

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Pitvipers have a specialized sensory system to detect infrared (IR) radiation. Sensory information is transmitted from the pit membrane to the hindbrain nucleus of the lateral descending trigeminal tract (LTTD) and further relayed to the nucleus reticularis caloris (RC). Using in vitro whole brain preparations of rattlesnakes with functionally intact pit membranes, we characterized the response patterns of RC-neurons during IR object motion. Bi-directional horizontal motion stimuli were produced by an IR-emitter that crossed the pit membrane in either temporo-nasal (t-n) or naso-temporal (n-t) direction. Upon IR object motion, the recorded neurons exhibited a prominent directional tuning with respect to both the numbers of evoked spikes and the length of the interspike intervals (ISI). With respect to alterations in spike numbers, considerably more RC neurons increased the spike firing during IR object motion in t-n than in n-t direction. In contrast, the majority of neurons with significant changes in spike timing displayed shorter ISI and therefore exhibited higher instantaneous frequencies (i.e. signal gain) for n-t motion stimuli. Accordingly, RC neurons were more sensitive to object motion in t-n direction, while higher precision was obtained for objects that crossed the pit membrane in n-t direction. In an ecologically context, the high sensitivity for an entrance of an IR object (e.g. prey) into the field of view of a snake from the temporal side facilitates prey detection. After crossing the midline of the snake's field of view, the same object could be tracked with high precision to allow for an accurate strike.



Main Meeting, FG Physiology

Poster: Phy 10

Chitosan as a non-toxic transfection reagent for ENaC antisense oligonucleotide delivery in human airway epithelial cells

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Cystic fibrosis (CF) is the most common lethal genetic disorder in the Caucasian population. The disease is caused by mutations in the cystic fibrosis transmembrane conductance regulator (CFTR) gene encoding a cAMP-dependent chloride channel. Defective CFTR is associated with a Na⁺ hyperabsorption mediated by the epithelial sodium channel (ENaC). The dysregulation of these proteins leads to an imbalance of ion and water transport causing problems in multiple organs, especially in airways and lung. Recently, we established a non-viral delivery system for wtCFTR-mRNA based on chitosan (CS) to restore CFTR function. The aim of this work is to develop a similar system to deliver ENaC antisense oligonucleotides (ASO) to correct Na⁺ hyperabsorption. CS-ASO complexes were harnessed at varying charge ratios (+/-) and characterized for their physicochemical properties (e.g. size, zeta potential, stability). Most promising complexes (+/- 90, 85 mM NaCl) had an average size diameter of 150 nm, zeta potential of approximately +30 mV, were relatively stable in transfection medium over 24 h and were therefore chosen for transfection experiments. Primary human nasal epithelial cells grown on Transwell® permeable filters were incubated with CS-ASO complexes for 24 h (0.45 µg ASO/cm²). Afterwards, functional Ussing chamber measurements were conducted. Measurements showed decreased Na⁺ current mediated by ENaC confirming successful transfection with CS-ASO complexes. With the results presented herein we mark the start of the development of a double-tracked strategy to cure abnormal ion transports in CF.



Main Meeting, FG Behavioural Biology
Oral Presentation

Feeling sick modifies social interactions in wild house mice (*Mus musculus domesticus*)

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Social interactions are central to many organisms and influence behaviour and ultimately fitness. We present data from a long-term study on wild house mice in a Swiss barn to discuss the significance of social interactions of a rodent in its natural environment, exposed to parasites and diseases. Since pathogens can be transmitted by social context, we analysed their effect on mating and social interactions by manipulated disease status using an immune challenge (lipopolysaccharide injection, LPS). Tested under laboratory conditions, immune-challenged males presented with a receptive female could not maintain the production of sexually attractive signals. Females spent significantly less time near LPS-injected than near control males, suggesting that they used some of these cues when making mating decisions. LPS-injected males had reduced testosterone, which might be a unifying mechanism down regulating the sexual signals quantified. In a second experiment, we immune-challenged mice in a free-living population and monitored their social interactions by automatic RFID tracking. LPS treated mice showed reduced connectivity to their social groups. This happened as a function of own behaviour, rather than through conspecific avoidance. We incorporated these disease-induced changes of social connectivity among individuals into models of disease outbreaks over the empirically-derived networks. The models revealed that changes in host behaviour frequently resulted in the disease being contained to very few animals, as opposed to becoming widespread. Infection induced behavioural alterations thus affect an individual's social dynamics with consequences for its reproductive success as well as the spread and outbreak of diseases.



Symposium: Adaptations to Hematophagy in Blood-feeding Parasites
Oral Presentation

A tick salivary serpin IRS-8 is an anticoagulant playing role in tick feeding and pathogen transmission

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A tick *Ixodes ricinus* is an important disease vector in Central and Eastern Europe. As an adaptation to blood feeding, tick saliva contains a complex mixture of components to minimize defense response of their host. Saliva and its components have been shown to suppress host immune responses at the site of attachment that may disrupt tick feeding. Proteins in tick saliva inhibit blood coagulation, complement, leukocyte functions, proliferation of T lymphocytes and cytokine production. Serpins are the largest superfamily of protease inhibitors with diverse functions and unique mechanism of inhibition. Serpins have been studied in blood feeding arthropods mainly for their ability to modulate host immune and hemostatic functions. Despite a high number of identified serpin transcripts in ticks, only few of them were characterized functionally to date. Here we present a novel serpin from the saliva of *I. ricinus* tick named IRS-8 (*Ixodes ricinus* serpin-8). This serpin is predominantly expressed in salivary glands and midgut of adult ticks during late phase of 7-8 days long feeding. RNA interference of IRS-8 in ticks led to decreased ability to infect mice with *Borrelia spirochetes*, the pathogen causing Lyme disease. IRS-8 actively inhibited blood coagulation proteases by forming covalent complexes. Anti-coagulatory activities of IRS-8 were confirmed by PT and aPTT assays. We tested also its effect on platelet aggregation. Finally, we present crystal structure of IRS-8. Tick salivary serpin IRS-8 is a pluripotent biomolecule playing role in tick feeding and pathogen transmission.



Main Meeting, FG Behavioural Biology
Oral Presentation

How highly eusocial bees find flowers – A comparative study of the Australian sugarbag bee and the Western honeybee

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Bees play an important role as pollinators worldwide. While the Western honeybee (*Apis mellifera*) and the Buff-tailed bumblebee (*Bombus terrestris*) are thoroughly studied with regard to their sensory physiology and pollination capacity, little is known about stingless bees from tropical and subtropical regions. Here, comparative experiments with two highly eusocial bee species, the Western honeybee, *A. mellifera*, and the Australian sugarbag bee, *Tetragonula carbonaria*, have been conducted to compare their colour preferences. Stimuli made of pigment powders that allow manipulation of single colour parameters, in this case saturation and brightness of a blue colour hue, were used to study spontaneous colour preferences of free-flying honeybees and sugarbag bees. The results show that *A. mellifera* prefers more saturated colour stimuli, while brightness has no effect on colour choice. In *T. carbonaria* neither saturation nor brightness affected colour preference. These findings correspond to known colour preferences in *A. mellifera*, but raise the question whether *T. carbonaria* chose flowers according to any colour parameters or if their choice behaviour is driven by other factors.



Main Meeting, FG Evolutionary Biology

Poster: EvoBio 1

First proteomic analysis of the venom composition of pseudoscorpions and insights into the venom delivery system of the book scorpion *Chelifer cancroides*

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With venom glands in their chelal hands, pseudoscorpions possess a unique venom delivery system, which evolved independently from those of scorpions and spiders. Studies about the composition of their venom are complicated by the small size of these arthropods. Very recently, the venom composition of the pseudoscorpion *Synsphyronus apimelus* (Garypidae) was investigated by means of transcriptome analysis of chelal tissue. So far, however, a proteomic analysis of pseudoscorpion venom has never been performed. Nevertheless it is crucial to identify the genuine venom compounds, which are not necessarily detected by homology with known sequences from other arthropods. The present study demonstrates for the first time the application of electrical stimulation for repeated venom extractions using the pseudoscorpion *Chelifer cancroides* (Cheliferidae). Subsequent proteomic analyses of venom samples with different mass spectrometry approaches revealed highly reproducible results regarding venom components. By applying a combined transcriptomic and proteomic approach, several of the most abundant venom compounds could be identified. Interestingly, the respective precursors of *C. cancroides* do not show any homology with known precursors responsible for venom compounds in other arthropods. SEM images confirmed the presence of the lamina defensor at the base of both venom teeth. Indeed, we found indications that the lamina defensor might be involved in the process of releasing venom. Results of the present study can be used as starting point for a large-scale investigation of venom from pseudoscorpions. Moreover the biological activities of potential venom compounds of *C. cancroides* should be investigated with respect to potential pharmaceutical effects.



Main Meeting, FG Developmental Biology
Oral Presentation

Agouti-related peptide 2 drives convergent evolution of stripe patterns across cichlid fish radiations

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The color patterns of African cichlid fishes provide striking examples of convergence, the recurrent evolution of phenotypic similarities. For instance, across the more than 1,200 species of the East African Rift Lakes of Victoria, Malawi and Tanganyika, melanic horizontal stripes have evolved numerous times. Here, we discovered that the same locus accounts for this evolutionarily labile trait. Regulatory changes of agouti-related peptide-2 (*agrp2*) act as a molecular switch controlling the presence of horizontal stripes. In Lake Victoria cichlids, we identified a skin-specific ~1kb cis-regulatory element that modulates *agrp2* expression. However, underlying mutations are not conserved across cichlid radiations, indicating that different regulatory mechanisms affect *agrp2* expression and thereby stripe patterns in other cichlid species flocks. Using CRISPR-Cas9, we demonstrate that *agrp2* acts as a repressor of stripes and its knockout reconstitutes stripes in a non-striped cichlid, *Pundamilia nyererei*. Thus, we identify *agrp2* as a major regulator of color pattern convergence and diversification in cichlids.



Main Meeting, FG Behavioural Biology
Oral Presentation

Relationship between corticosterone and the personality of zebra finches

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Animal personality describes behavioural differences between individuals that are consistent across time and contexts. Especially the understanding of relationships between physiology and personality traits is of great interest. The connection between personality traits and hormones such as testosterone and cortisol resp. corticosterone has been demonstrated in a number of species. However the strength and direction of these relationships seem to depend on the species as well as on the measured behaviour. In order to understand the underlying mechanism in more detail a study linking different behaviours and hormonal concentrations of the same species is needed. In this study we investigate how zebra finches, artificially selected for different personalities, differ in their baseline plasma concentrations of corticosterone. We have developed a standardized test battery comprising three personality traits. We measured aggression towards a mirror, exploration in a novel environment and fearlessness in a tonic immobility test in a captive population of wild-type zebra finches (*Taeniopygia guttata*). We established bi-directional selection lines on each of these three traits. Repeated blood samples were taken from the fourth generation of these selection lines to analyse baseline corticosterone levels. First analyses show that corticosterone is repeatable in all lines with highest repeatability in our explorations lines, although exploration is no heritable trait in our zebra finches. Furthermore individuals selected for fearlessness show the smallest variance of corticosterone.



Main Meeting, FG Behavioural Biology
Oral Presentation

Nest height preferences of altricial and precocial birds in captivity

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For many laboratory studies, avian species are used and reproduced in captivity. These species are usually domesticated species, which to a certain extent are shaped by artificial selection. Domestication processes may have led to changes in physiology but also in behavior. In terms of animal welfare, it is important to provide the animals appropriate housing and breeding conditions. Finding the optimal place for breeding requires the birds to estimate many dimensions in nature, which are often more restricted under captive conditions. We here focused on an aspect that can easily adjusted to the requirements of the animals in captivity, i.e. the height of the breeding nest. We tested nest height preferences for breeding in captivity in a precocial bird species, the chicken, and an altricial bird species, the zebra finch. Furthermore, by using highly domesticated and more wild-type strains for both species we aimed to detect potential changes in nest height preference from artificial selection. We assumed the altricial birds to prefer elevated nest positions as this may provide shelter from predators, whereas we expected the precocial birds to favour ground nesting. In both species, our hypothesis was confirmed. Chickens preferred to breed at low levels, despite they can learn other heights, while zebra finches prefer to breed elevated. High domesticated strains and more wild-type strains within both species differed not from each other, suggesting that nest height preferences are highly conserved behavior traits. Considering these findings in captive populations may increase the welfare of birds.



Main Meeting, FG Behavioural Biology

Poster: Behav 14

Shell-use as a tool in the Pacific hermit crab *Coenobita compressus* H. Milne-Edwards, 1836

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Animals' cognitive abilities can be tested by allowing them to choose between alternative tools, only one of which offers the right solution to a problem. Hermit crabs are evolutionarily specialized to carry empty shells as portable homes, a behavior which qualifies as tool use. *C. compressus* prefers remodeled shells inherited from conspecifics. Hence, the shell morphology is essential for these animals and abandoning their home demands a critical cost-benefit analysis of the new shell for decision-making. Here, we designed a two-choice behavioral setup in which *C. compressus* had to decide between alternative shells to solve a novel problem of escaping confinement. Using X-ray microtomography combined with 3D-printing, we copied preferred shells and then added artificial alterations to the inner or outer shell architecture, designing only some shells to be a perfect match to the escape opening of the crab's enclosure. In our setup, crabs therefore had to choose an otherwise less preferred shell, since only this shell had the right external morphology for the crab to free itself from confinement. Surprisingly, across multiple experiments we found that crabs were willing to forgo their preferred shell and choose the less preferred shell that enabled them to escape. While these results suggest some level of problem-solving cognition, it remains unclear whether crabs solved this problem through trial-and-error or were aware of the deeper connection between escape and exterior shell morphology. We suggest this simple behavioral assay can serve as a foundation for more in-depth studies of invertebrate cognition, decision-making, and learning.



Main Meeting, FG Developmental Biology
Oral Presentation

A new insight into palatal ossification in the Neognathae

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The skull of vertebrates serves several functions and has undergone many adaptations in evolution. An interesting case is the development of a kinetic skull in neognathous birds that allows to move the beak independently of the neurocranium. In this evolutionary adaptation, a bone that stabilizes the skull of dinosaurs, the ectopterygoid, seems to have been lost in birds. Moreover, the hemipterygoid secondarily detaches from the pterygoid anteriorly to form an intrapterygoid joint. We reinvestigated this development, unresolved for a long time, and report that the pterygoid of adult barn owls develops from two ossification centers. Around developmental stage 35 (staging after Köppl et al. (2005) *Developmental Dynamics*, 233, 1248) first a bony spicule appears at the position of the pterygoid. Shortly afterwards a second ossification center can be identified anteriorly. The two ossification centers fuse rapidly to form a single bone, termed the pterygoid in the adult bird. Our new data, thus, suggest that the pterygoid in barn owls and possibly other bird species is not a single bone, but a bone that emerges by fusion of two bones. We offer two possible explanations: The anterior ossification center may be a remnant of the archosaurian ectopterygoid or alternatively an independent ossification center of the hemipterygoid.



Main Meeting, FG Evolutionary Biology
Oral Presentation

Diversity overload – niche partitioning resulting in various shell sizes and tooth morphologies in a radiation of gastropods in “ancient lake” Tanganyika

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Among the key questions addressed in evolutionary biology are those referring to the causation of speciation. Model systems for studying these processes can be found in so-called “ancient lakes” as they harbor spectacular examples of species flocks. Our research model is comprised of about 50 closely related paludomid gastropods inhabiting Lake Tanganyika and the surrounding river systems, with extreme diverse morphologies not only with regard to their shell but also with regard to their radulae. Against the background of a phylogeny combined with a molecular clock approach we analyzed the shell size following classical ecological niche models (Hutchinson’s rule). In addition, we evaluated the radula morphology and its mechanical properties by nanoindentation, a test measuring hardness and elasticity modulus. Our results reveal that these species reduce competition for needed resources by a) their body size, b) their radula morphologies and properties as adaptation on the particular substrate they feed on. In the context of a dated backbone phylogeny we found that most lineages are older than the lake and that after the rifting of the East African subcontinent several lineages of paludomid gastropods colonized the lake from the surrounding river systems independently. Due to these colonization events, some lineages show clear signs of adaptation to the new lacustrine environment, while others still have traits that can be interpreted as adaptations to riverine habitats.



Symposium: Phenotypic Plasticity - RESPONSES of Animals to
Environmental Change
Oral Presentation

The importance of plasticity for coping with environmental stress

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Environments are changing rapidly and to cope organisms have to adapt. Adaptation can take many shapes and occur at different speed depending on the type of response, the trait, the population, and the environment. Focusing on thermal stress and ectotherms I will provide examples from our work on the importance of plasticity for coping with variable and stressful environments. First I will discuss costs and benefits of plasticity induced to cope with stressful temperatures. This will be based on results from laboratory and field studies on ectotherms from temperate, tropical and arctic regions. One conclusion from these studies is that upper thermal tolerance seems to be plastically constrained in many species. Second I will discuss physiological coping mechanisms induced in response to environmental fluctuations and stressful conditions. These include observations from transcriptomic, proteomic and metabolomic studies on *Drosophila* and pinpoint that thermal fluctuations may affect the physiology through mechanisms partly independent of average temperature. Third I will present results from genomic studies aiming at pinpointing the evolutionary capacity and genetic architecture of plasticity. This is based on a study using the *Drosophila* Genetic Reference Panel to discuss genetic aspects of thermal reaction norms and environment specific genetic architecture of cold resistance. Last I will discuss how small population size and inbreeding impact on the flexibility of individuals and their ability to cope with stressful conditions. Here our results pinpoint that inbreeding by environment interactions are important for our understanding of the biodiversity crisis that we are currently facing.



Main Meeting, FG Physiology
Oral Presentation

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

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Whales are well adapted to a marine life and some species may conduct dives of remarkable depth and length. Usually, the mammalian brain is highly sensitive to any shortage of oxygen, and most mammals show severe depression of neuronal functions and neuronal damage within minutes of hypoxia. However, the brain of whales is not affected during long dives and remains functional during dives for up to 2 h without surfacing. Physiological adaptations in diving mammals have been extensively examined, while the molecular mechanisms underlying the unusual hypoxia tolerance of the whale brain are still largely unknown. For a better understanding of the molecular adaptations in the cetacean brain, we generated transcriptomes of the deep-diving pilot whale (*Globicephala melas*), the killer whale (*Orcinus orca*) and a terrestrial relative, the cattle (*Bos taurus*). We employed RNA-seq to analyze the abundances of transcripts in the brain of the pilot whale and the orca, as well as in the bowhead whale (*Balaena mysticetus*), the beluga whale (*Delphinapterus leucas*) and the minke whale (*Balaenoptera acutorostrata*) (transcriptomes are online available at NCBI) and compared them with transcriptomes from the brain of cattle. Gene ontology analyses revealed a high expression of genes related to translation in the whale brain, indicating a higher protein synthesis. Furthermore, enrichment analyses show a higher aerobic capacity and an increased stress response in the whale brain. These results suggest a specific evolutionary strategy in whales to sustain the demands for metabolic energy during cerebral hypoxia.



Symposium: Adaptations to Hematophagy in Blood-feeding Parasites
Oral Presentation

Tyrosine degradation - Achilles heel of blood feeding gluttony of *Ixodes ricinus*

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Transcripts encoding enzymes of tyrosine catabolism were found to be substantially up-regulated in the digestive tract of blood-feeding hemipteran *Rhodnius prolixus*. Disruption of this catabolic pathway leads to very high mortality rate, therefore presenting promising drug target for blood-feeding parasites eradication. Unlike in *R. prolixus*, gene encoding 4-hydroxyphenylpyruvate dioxygenase (hppd) in the tick *Ixodes ricinus* is mainly transcribed in extra-intestinal tissues. HpmRNA levels remain negligible in the gut of adult females during the blood feeding but steadily increase in the course of off-host blood meal digestion for up to two weeks. RNAi-mediated hpsilencing as well as administration of HPinhibitors via an artificial membrane feeding caused premature mortality of nymphal as well as adult stages of *I. ricinus* few days after full engorgement. Thus the death occurrence in hppd-deprived ticks is likely caused by impaired tyrosine catabolism although the agent(s) causing the toxic effect in ticks still remains unknown. We were not able to detect any death-causing crystals of accumulated tyrosine as described in *R. prolixus*, yet we observed markedly increased concentrations of tyrosine and the up-stream phenylalanine in the haemolymph of fully engorged females that were treated with the HPinhibitor. Given the low aqueous solubility of tyrosine (0,5 mg / ml) we cannot exclude the possibility of detrimental micro-crystal formation. Nonetheless, whether the high concentration of tyrosine, phenylalanine or other derived metabolite(s) or, on the other hand, a scarcity of downstream tyrosine degradation products are responsible for the observed pre-mature tick death remains to be investigated.



Symposium: Adaptations to Hematophagy in Blood-feeding Parasites
Oral Presentation

Anticoagulants and bacterial symbionts as means to study the evolution of blood feeding in leeches

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Understanding evolutionary transitions in behaviour, ecology and morphology, as well as the origin and distribution of biological diversity, is fundamental in biology. However, each of these presupposes a robust and reliable phylogenetic hypothesis to give direction and timing to evolutionary events and to reveal the underlying processes (mode) driving evolutionary divergence. Despite of their cosmopolitan nature, abundance, evolutionary significance and medical utility, no phylogenetic hypothesis exists for the subclass Hirudinea (leeches), which makes inferences regarding the evolution of the group unnecessarily strenuous. Beyond providing a general framework for the evolution across leeches, the phylogeny is an important component in addressing the evolution of bloodfeeding in these medically important animals by deciphering both the diversity, selection and evolutionary histories of the anticoagulation factors that are frequently used in modern medicine, as well as the function and phylogenetic histories of the bacterial symbionts that seem to play a vital role in leech growth and feeding strategies. Here, I discuss the phylogeny of leeches and provide hypotheses on the evolution of bloodfeeding through transcriptomic and genomic data relating to both anticoagulants and bacterial symbionts.



Main Meeting, FG Morphology
Poster: Morph 28

Mating changes genital morphology in the silk spider *Nephila clavipes*

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The strategy of repeated matings by a male with a single female is well documented in many animal groups from insects to birds and mammals. It occurs mainly in species in which males are not able to closely guard their mates. The selective advantage is generally considered to be securing paternity. By transferring sperm repeatedly, males increase their fertilization success at the time of ovulation or oviposition. In the Golden silk spider *Nephila clavipes*, however, this explanation does not hold since male copulatory organs are depleted of sperm already after a single copulation and males are not able to replenish sperm supplies. Nevertheless, males that reside in the web of a female, repeatedly court and mate with her. We hypothesized that repeated, non-sperm transferring matings might serve to manipulate the female's sperm storage site. We staged groups of females with cohabiting males. Females were fixed for morphological analyses after different cohabitation times and included virgin females as a control group. The sperm storage organs (spermathecae) were compared using semithin sections. We show that mating has a remarkable effect on the volume of the spermathecae of *N. clavipes*; it is twice as large after mating compared to virgin females. The resulting spermathecal volume did not depend on the length of time the male resided in the female web, which we used as a proxy for the number of copulations. However, since males transfer accessory substances during mating, it seems possible that these substances have additive, manipulative effects.



Main Meeting, FG Ecology

Poster: Ecol 4

***Daphnia pulex* populations: Influence of predators on population size and genotypic variability**

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Diversity is a major precondition for the adaptive reaction to environmental change. Biodiversity at all levels (genetic, species, interactions) is crucial for ecosystem function and longevity as biodiversity means redundancy which stabilizes ecosystems because extinct species/genotypes can be replaced. In addition, the presence of individual trait variation and/or phenotypic plasticity can stabilize population fluctuations and thereby prevent extinction. A very plastic and important genus in lake ecosystems is the microcrustacean *Daphnia*. Different clones of *Daphnia pulex* express various degrees of phenotypic plastic defenses: Some very sensitive clones express strong defenses already in the presence of only a few predators, while less sensitive clones express defenses only at very high levels of predation pressure. The costs and benefits of this variability at the individual and the population level are, so far, little understood. We conducted mesocosm experiments to investigate the impact of predation on artificial *Daphnia pulex* populations composed of clones with differing trait variabilities. These populations were exposed to the three-spined stickleback *Gasterosteus aculeatus* and the phantom midge larvae *Chaoborus obscuripes* as predators. We monitored the genetic variability using microsatellite-markers after four, eight and twelve weeks. We found that the same three clones dominated all treatments (with and without predators). These clones showed only weak anti-predator responses. We hypothesize that their high tolerance for predatory stress might give them an advantage in intraspecific competition.



Main Meeting, FG Evolutionary Biology

Poster: EvoBio 5

Multiple origin of flightlessness in Phaneropterinae (Orthoptera: Tettigonioidae) bushcrickets

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Possession of wings and fly-ability have developed in higher insects, but secondary reduction of wings is taxonomically widespread. Phaneropterinae consist of more than 2000 species worldwide. In contrast to tropical counterparts, the majority of the 300 European species have reduced their wings and became flightless. To clarify whether this secondary loss might be a result of several evolutionary events, we present a molecular phylogeny based on three nuclear gene sequences (18S, H3, ITS2). We studied 42 taxa of wingless species in conjunction with species from all European long-winged Phaneropterinae genera. The analysis resulted in four phylogenetic lineages: (i) flightless species of the western Mediterranean genus *Odontura* form the first group, (ii) a South-American flightless species from the Andes cluster outside, (iii) long-wing taxa from the tribes Acrometopini, Ducetiini, Phaneropterini and Tylopsidini well separated and divided by a deep branching pattern, (iv) Barbistini as the largest group contained all other European flightless species. We conclude that wing reduction has led on to radiation in Northwest Africa and Southwestern Europe (genus *Odontura*) and a massive radiation in South-eastern Europe and the Middle East (tribus Barbistini). Therefore, we are redefining the tribus Odonturini, well separated from the other flightless tribus Barbistini. The phylogenetic evidence suggests an independent origin of these two groups. The occurrence of flightless Phaneropterinae species on other continents might be the result of a general pattern of energy saving under unfavourable ecological conditions, as most species are found on colder mountains or in food restricted semi-deserts.



Main Meeting, FG Neurobiology*

Poster: NB 7

The visual system of Amblypygi

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The chelicerate tree is still unresolved. Hence, comparable morphological characters are desperately needed for a phylogenetic reconstruction. On this account, we analyse in this study the neuroanatomy of the visual system of Amblypygi and compare the results with visual systems of previously studied chelicerate taxa – i.e. those of Pycnogonida, Xiphosura, Scorpiones, Pseudoscorpiones, Opiliones, and Araneae. Several amblypygid species (*Heterophrynus elaphus*, *Phrynus pseudoparvulus*, and *Damon medius*) are studied with different techniques. The visual neuropils of the median and lateral eyes are identified with cobalt fills. The basic structure of the visual neuropils, as well as the protocerebrum generally, is described by means of osmium-ethyl gallate procedure and μ CT. Our results indicate close evolutionary relationships of Xiphosura, Scorpiones and Amblypygi, at least of their visual systems. In all three taxa, the retinula cells of the median and lateral eyes project to a first and a second visual neuropil in a like manner. Furthermore, R-cell fibres of the median eyes overlap with lateral eye R-cell fibres.

*Contribution also presented in: *Symposium: 5th Meeting of the Arthropod Neuroscience Network* (Poster: ANN 7)



Symposium: Adaptations to Hematophagy in Blood-feeding Parasites
Oral Presentation

Investigations of salivary gland cells and salivary proteins of the medicinal leech, *Hirudo verbana*

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Medicinal leeches (*Hirudo* sp.) are highly specialized blood-feeders. Leeches use up to 100 salivary proteins to acquire nutrients from body fluids of vertebrates. Only 15% of them have been identified thus far, and they include analgesic, anticoagulant, anti-inflammatory and antimicrobial proteins (Baskova et al. 2004, Biochem Mosc 69, 770; Hildebrandt and Lemke 2011, Naturwiss 98, 995). During feeding leeches secrete their salivary proteins into the host wound, but they may also affect the storage of ingested host blood in the crop of the leech. To identify leech salivary proteins that fulfill biochemical functions in the host-parasite interaction, linked sets of proteomic and transcriptomic data are needed. We determined that an adult leech has ~40,000 salivary gland cells containing ~1.2 mg protein. Because leeches secrete most of their salivary proteins during one round of feeding, we predicted that secretory proteins should be diminished or absent in salivary gland tissue of freshly fed animals. In fact, we found that 2D-gels loaded with salivary tissue extracts from freshly fed leeches contained 50% fewer spots than extracts prepared from unfed animals. To identify and characterize some of these putative salivary proteins, we screened the *Hirudo verbana* EST-library (NCBI). We expressed the recombinant forms of three antistasin-like proteins (ALPs) and a protein with a potato-inhibitor-family-I-motif (PI-protein). Unlike described antistasins, the ALPs inhibit neither blood coagulation factor Xa in human plasma nor trypsin. PI-proteins are defense-related proteins commonly found in plants. Because the leech PI-protein possesses no anti-coagulative properties, we predict anti-inflammatory or anti-microbial effects.



Main Meeting, FG Systematics, Biogeography and Diversity
Poster: Syst 11

Implications of the newly discovered species richness of the dwarf spider genus *Shaanxinus* Tanasevitch, 2006 (Araneae, Linyphiidae, Erigoninae) from Taiwan and Vietnam

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Dwarf spiders are of special interest due to their sexually dimorphic prosomal structures in males. Glandular secretions within these structures serve as nuptial gifts, and thus sexual selection may have contributed to their high species richness. However, species diversity of dwarf spiders in East Asia is understudied. By applying a branch-beating collecting method, we discovered 13 undescribed Taiwanese and one Vietnamese dwarf spider species of the Genus *Shaanxinus* Tanasevitch, 2006, which previously only included two described species from Mainland China. We reconstructed the dimension of glandular tissues associated with male prosoma modifications in *Shaanxinus*, as well as the detailed palpal structure using micro-computed tomography. Sequences of the genetic markers COI, 16S and 28S corroborated the monophyly of some species, as well as male-female matching. However, we found no barcode gap for species identification for these mitochondrial markers, due to parafyly/polyphyly of morphologically delimited species in the DNA trees. This led to the discovery of two cryptic, yet morphologically distinct species. In the case of morphologically indistinguishable but genetically distinct specimens, we discuss incomplete lineage sorting and introgression as possible causes of mtDNA parafyly/polyphyly. According to our findings of their geographical distribution and sexual traits, the species richness of *Shaanxinus* is possibly a result of both natural and sexual selection.



Main Meeting, FG Systematics, Biogeography and Diversity
Poster: Syst 8

Character variability of some Primnoidae (Cnidaria: Octocorallia) from cold-water reefs in the North Atlantic and bordering seas

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Among deep-water dwelling corals, Primnoidae are a prominent family within the octocorals. They commonly occur on outer continental shelves or slopes around the world, with 13 genera known from the Atlantic Ocean. Modern visualisation techniques like SEM pictures have improved documentation of their morphological characters - like sclerites - and their variability. Sclerites are used for identification in octocoral taxa. Six scientific cruises collected Primnoid samples during almost 20 years from the North Atlantic Ocean and bordering seas. In a faunistic study of the material six genera and ten species were identified and their characters investigated: *Acanthoprimnoa goesi*, *A. pectinata*, *Callogorgia verticillata*, *Candidella imbricata*, *Narella bellissima*, *N. versluysi*, *Plumarella aculeata*, *P. aurea*, *P. pellucida* and *Primnoa resedaeformis*. Shapes and surface sculptures of sclerites vary within the species but also within individual colonies, depending on the species. The most distinguishable disparity in surface sculpturing was found for *Callogorgia verticillata* from the Mediterranean and East Atlantic waters. The height of marginal and body wall scale spines, as well as the sclerite sculpturing differs among the examined samples of *Acanthoprimnoa goesi* samples. However, samples of *Candidella imbricata* from West and East Atlantic locations revealed no distinct differences in the sclerites' sculpturing, while sclerite shapes of *Primnoa resedaeformis* from North-East Atlantic locations appeared highly variable. While the current overall morphological differentiation of Primnoid species appears conclusive, the variability of sclerites within some species needs further research in term of more material and genetic patterns.



Main Meeting, FG Developmental Biology

Poster: Dev 15

The microstructure, proteomics and crystallization of the limpet teeth

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Limpets are marine mollusks using mineralized teeth, one of the hardest and strongest biomaterials, to feed on algae on intertidal rocks. However, most of studies only focuses on the ultrastructure and chemical composition of the teeth while the molecular information is largely unknown, limiting our understanding of this unique and fundamental biomineralization process. In this study, we investigated the teeth of limpet *Cellana toreuma* from three perspectives: 1) by using electron microscopy to observe the microstructure of the teeth; 2) by using proteomics and RNA-seq to investigate the proteins involved in the limpet teeth and 3) by *in vitro* crystallization experiment combined with Raman spectroscopy to investigate the effects of proteins and chitin framework on crystal formation. It is found that the limpets formed alternatively tricuspid teeth and unicuspid teeth. Small nanoneedles were densely packed at the tips or leading regions of the cusps. In contrast, big nanoneedles resembling chemical synthesized goethite were loosely packed in the trailing regions of the cusps. Proteins extracted from the whole teeth such as ferritin, peroxiredoxin, arginine kinase, GTPase-Rabs and clathrin were identified by proteomics. Goethite-binding experiment coupled with proteomics and RNA-seq highlighted six chitin-binding proteins (CtCBPs). Furthermore, these proteins or the framework chitin only induced packing of crystals without affecting their crystal polymorphs *in vitro*. This study provides insight into the unique biomineralization process in the limpet teeth at the molecular levels, which may guide biomimetic strategies aimed at designing hard materials at room temperature.



Main Meeting, FG Evolutionary Biology
Oral Presentation

The role of bacterial infection on ageing and lifespan in the worm (*Caenorhabditis elegans*) model system

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Ageing and lifespan are super-phenotypes influenced by most factors present in a laboratory setting, making results difficult to interpret. Yet, still today lifespan curves and 50% survival statistics are used in the majority of ageing studies to measure the effects of drugs, mutants and a myriad of other factors on ageing and lifespan. Such studies are produced en masse in model systems, particularly in yeast, worms, flies and mice. This practice is complicated by the fact that the causes of death remain undescribed for model organisms. While it may be normal practice to subdivide human deaths into different pathologies, this is not done in model systems. In this talk I will show results from necropsies in worms that have died of old age and describe their common pathologies. I will then describe a concept known as 'mortality deconvolution', where standard lifespan curves are broken down by these pathologies to gain a better understanding of the ageing process. Finally, building on these methods, I will talk about the confounding role that infection plays within standard ageing studies using an example of pharyngeal infection in *C. elegans*. More broadly I will conclude by discussing how the forefront of current ageing research rests on the linking of the ultimate (evolutionary) with the proximate (cellular) causes of ageing.



Symposium: Adaptations to Hematophagy in Blood-feeding Parasites
Oral Presentation

Hirudin-like factor 8 derived from the Asian leech, *Hirudinaria manillensis*

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The mechanisms inducing blood coagulation in the host have to be effectively inhibited by blood-feeding parasites like leeches. Thus, leeches secrete salivary proteins like hirudin into the skin wound of host animals to inhibit thrombin, the most important coagulation inducing protease in the body fluids of vertebrate hosts. Several isoforms of hirudin have been identified in medicinal leech species, e.g. in *Hirudo* sp., *Hirudinaria manillensis* or *Macrobdella decora*. We have discovered that leeches express several isoforms of a new class of proteins that structurally resemble hirudin, the so-called hirudin-like factors (Hlfs). Expression of such Hlfs could be experimentally verified in salivary gland cell containing tissue samples isolated from *Hirudo* sp. and *Hirudinaria* sp. Nothing is known about the function of these proteins. For this reason we started the functional characterization of such factors, initially using one type of hirudin-like factor, Hlf8. The recombinant form of Hlf8 was expressed using *E. coli* BL21 (DE3). The hirudin variants 1 and 2 of *Hirudo* sp. were expressed the same way to be used as positive controls for thrombin inhibition measured in a Siemens BFT II coagulation analyzer. Hlf8 and hirudins prevented clot formation in human and mallard plasma. Mallard plasma seemed to be less sensitive with respect to the tested proteins. For full inhibitory activity of the recombinant proteins, the N-terminal His-tag had to be removed. In vivo, Hlf8 seems to act as a thrombin inhibitor in a dose-dependent manner. It has, however, a somewhat lower effectiveness on thrombin inhibition compared with hirudins.



Main Meeting, FG Neurobiology*
Oral Presentation

Feedback signaling from mushroom body Kenyon cells to DANs during larval associative conditioning

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How brains organize behavior based on internal needs on the one hand and changing environmental information on the other is one of the key questions in neuroscience. Learning is defined as a process leading to a lasting alteration in behavior due to experience. *Drosophila melanogaster* larvae turned out to be very suitable model organism in studying memory formation in the mushroom bodies (MBs), the integration centers required for olfactory learning (Heisenberg 2003; Heisenberg et al. 1985). So far most research was done on olfactory conditioning, associating an odor (conditioned stimulus) with a gustatory (unconditioned) stimulus. During classical olfactory conditioning the unconditioned gustatory stimuli are mainly provided to the MBs via dopaminergic neurons (Selcho et al. 2009). Optogenetic activation of dopaminergic neurons was shown to be sufficient to substitute the unconditional stimulus (US) during conditioning (Rohwedder et al. 2016), while optogenetic activation of specific olfactory neurons was shown to be sufficient to substitute the conditional stimulus (CS) (Honda et al. 2014). Thus, we are interested in whether a conditional optogenetic activation of Kenyon cells is sufficient to induce an appetitive or aversive memory. Our results indicate that pairing odor information to a specific optogenetic activation of KCs during training is sufficient to induce appetitive memories. Based on our data we propose that a functional feedback loop exist from the KCs to dopaminergic input neurons. By that, recurrent activity between MB neurons and dopaminergic neurons elicits the formation of an appetitive memory in the *Drosophila* larva.

* Contribution also presented in: Symposium: 5th Meeting of the Arthropod Neuroscience Network (Poster: ANN 8)



Main Meeting, FG Ecology
Oral Presentation

Maintaining colony integrity in aggregation: A comparative study of CHC complexity and nestmate recognition in the Asian honey bee species *Apis florea* and *Apis dorsata*

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In social insects colony integrity is challenged by intruders from foreign colonies, e.g. non-nestmates might steal resources or transfer pathogens. To maintain colony integrity discrimination between nestmates and non-nestmates is required. Cuticular hydrocarbons (CHCs), long-chain non-polar substances attached to insects' cuticle, are known to serve as discrimination cues and trigger defens behaviour in many social insect species. Within the genus *Apis* almost all studies on nestmate recognition and CHC composition focus on *A. mellifera* while other honey bee species are poorly investigated. In our study, we investigate nestmate recognition in two Asian open nesting species, the dwarf honey bee, *A. florea* and the giant honey bee, *A. dorsata*. In comparison to *A. mellifera* and *A. cerana*, which nest in cavities and have only a small entrance to the nest with a few guard bees, the open nesting species have a larger colony surface exposed to the environment. Furthermore, the spatial distribution differs between *A. florea* and *A. dorsata* nests. *A. florea* colonies are distributed within the landscape while *A. dorsata* colonies accumulate in aggregations with up to 200 colonies in one tree. Due to the low spatial distance between colonies within an aggregation we assume that the integrity of these colonies is especially challenged. Therefore, we hypothesize that workers of *A. dorsata* show more fine-tuned nestmate discrimination ability than workers of *A. florea*. Evidence for our hypothesis was found linking the results of behavioural assays to the results of the analysis of CHC profiles of *A. florea* and *A. dorsata*.



Main Meeting, FG Evolutionary Biology

Poster: EvoBio 6

Characterization of the MHC class II loci in meerkats, *Suricata suricatta*

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The extremely polymorphic Major Histocompatibility Complex (MHC) gene family is intrinsically involved in the immune response of vertebrates. These genes code for cell surface receptors that present antigens to T-cells activating reaction chain leading to the immune response against parasites and other pathogens. In accordance with their specialized function, MHC genes are traditionally classified into three classes. MHC class II genes encode receptors that present the antigens of extracellular pathogens. The antigens of the pathogens are presented in the antigen binding site (ABS) of the receptors to the T-cells. The exon 2 of the MHC class II codes for part of the ABS (Klein J. (1979) Science 203, p. 516). Here I present the genetic characterization of the MHC class II of meerkats (*Suricata suricatta*). A sample of 60 individuals from South Africa had their DNA extracted, amplified and sequenced at the region of interest with two primer pairs. In total, 27 alleles were identified. Indels that lead to a shift in the reading frame were present in five alleles. As expected by phylogeny, the meerkat allele sequences found here were most similar to the MHC sequences of hyenas, cats and other feliformia carnivores. This work is the first step towards the characterization of the whole MHC region and its relevance concerning infections and population health. More can be learned about the social structure and behaviour of and between meerkats leading to a better understanding of infectious diseases and immune defence in social-living animals and of resulting conservation efforts.



Symposium: Adaptations to Hematophagy in Blood-feeding Parasites
Oral Presentation

Functional evolution at the tick-host interface: adaptive or neutral evolution?

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Hematophagous parasites need to modulate their vertebrate host's defense mechanisms (hemostatic and immune systems) for successful blood-feeding. These modulation mechanisms evolved independently as novel functions in salivary gland proteins in various blood-feeding lineages, as evident by comparative sialomics. Gene duplication played a large role in the evolution of new functions involved at the parasite-host interface. A central question in the evolution of new functions involved in modulation of host defences is whether they evolved via adaptive (positive selection) or neutral mechanisms, i.e. did parasites actively adapt in response to host defences (parasite-host arms races) or were adaptation a more random stochastic process? This question are explored with an overview of blood-feeding evolution in hematophagous arthropods with regard to evolution of new protein function and the role that gene duplication played in this. While some adaptive signatures do exist, existing data suggest that adaptation to a blood-feeding lifestyle may have been largely neutral. This has significant implications for our understanding of blood-feeding evolution, parasite-host arms races and future research directions in this field.



Main Meeting Keynote Lectures
Oral Presentation

Communication as a key feature in mammalian cooperation and competition

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How do animals decide when to cooperate and when to compete? What are the cues and signals that predict the change and timing in behaviours? In the daily encounters among conspecifics, decisions are made in how to interact with each other, depending on the benefits and costs of cooperating or competing in a given situation. These decisions are based on the experiences and intrinsic states of the individuals involved, as well as on the immediate context of that encounter. To make informed decisions, animals need to discriminate among individuals or categories of animals. In repeated interactions, it is beneficial to include information on past encounters in order to make optimal decisions. Cooperative breeding species perform a variety of cooperative tasks, but also need to minimize risky competitive interactions among group members. They have evolved numerous signals to coordinate social interactions. Focusing on meerkats (*Suricata suricatta*) and other mongoose species, I will discuss the functionality of signals within cooperative breeders, and also compare to other mammal species. Examples of vocal signals show that mammals produce individual signatures and respond differently depending on caller identity. Other case studies demonstrate how the decision to interact and interaction outcomes can be strongly influenced by information related to physical attributes and intrinsic factors reflecting a caller's intention. I will discuss the extent of selection for structural variation in signals related to these types of information on individuality, intrinsic state and context, and refer to difficulties identifying the selective processes underlying their evolution.



Main Meeting, FG Physiology*

Poster: Phy 5

Be still my beating heart: the influence of aminergic and peptidergic substances on heart beat frequency in the Indian stick insect *Carausius morosus*

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The dorsal heart of *Carausius morosus* is responsible for the anterograde flow of haemolymph to the aorta and into the body cavity. The contraction frequency of the insect heart is known to be influenced by several substances of neural source. We employed a semi-exposed heart assay to study the effect of an aminergic substance (octopamine) and three neuropeptides (*C. morosus* hypertrehalosaemic hormone, Carmo-HrTH; crustacean cardioactive peptide, CCAP, and proctolin) on heart contraction. The contraction frequency was measured as beats per minute in adults ligated between the head and the prothorax. All three investigated neuropeptides had a stimulatory effect on heart contraction that lasted approximately six minutes, after which the normal heart beat rate was restored. Curiously, proctolin and CCAP stimulated the rate of heart beat also in unligated stick insects, whereas Carmo-HrTH was active only in ligated insects. The latter could suggest that when the stick insect is not ligated a competing substance may be released from the head of *C. morosus*; the competing substance is, apparently, not physiologically active but it binds or blocks access to the receptor of Carmo-HrTH-II, thereby rendering the HrTH peptide “not active”. In ligated stick insects, 6.7×10^{-8} M Carmo-HrTH-II significantly increased the heart beat rate; higher doses resulted in no further increase, suggesting the saturation of the HrTH receptor. Octopamine inhibited the rate at which the heart contracted in a dose-dependent manner; inhibition was achieved with 10^{-4} M of octopamine. Our results will be discussed in a comparative manner. Funding: NRF, DAAD

* Contribution also presented in: Symposium: 5th Meeting of the Arthropod Neuroscience Network (Oral Presentation)



Workshop: Animal Welfare
Oral Presentation

Considering animal welfare and EU legislation in cephalopod research

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Cephalopods have come a long way from a simple molluscan ancestor to the most highly developed invertebrates on this planet. Due to their charismatic looks and behaviour and their cognitive abilities, they appear to the human eye to be more closely related to basic vertebrates (e.g. fish) than to other molluscs and invertebrates. This makes them an attractive animal group for evolutionary and behavioural biologists, neurologists and comparative physiologists, studying the diverging evolution of vertebrates and invertebrates. Being highly developed animals that are used in experimental animal research, they have been included in the 2013 EU Directive on the 'Protection of Animals used for Scientific Purposes'. They thus are given the same legal protection that was previously only offered to vertebrates and research on live cephalopods is now regulated EU wide. In principle, this is good news for cephalopods and researchers. However, there is still a relative scarcity of reliable and unequivocal data for cephalopods, on which judgements of the severity of specific experimental procedures can be based, and adoption of vertebrate standards may not always correctly account for their different invertebrate physiology. I will discuss several examples and point out critical pitfalls for researchers and animal welfare authorities alike.



Main Meeting, FG Morphology

Poster: Morph 10

Novel olfactory and mechanosensory neuropils in the brain of Onychophora (velvet worms)

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Olfactory systems occur in all major arthropod groups (i.e., chelicerates, myriapods, crustaceans and hexapods), yet they show a broad variety in morphology and segmental identity. Different from arthropods, onychophorans — one of their closest relatives — bear their olfactory organs (i.e., antennae) in the first/ocular head segment. Interestingly, the onychophoran antennae have been homologised with various structures of arthropods, such as the labrum or the frontal filaments of crustaceans, the latter based on a putatively similar neuronal innervation. However, little is known about the innervation pattern of the onychophoran antennae. We therefore performed neuronal tracing experiments on these appendages in the onychophoran *Euperipatoides rowelli* in order to yield a better understanding of their innervation. Additionally, we examined the protocerebral neuropil regions using immunohistochemistry to determine the exact number and position of olfactory glomeruli in the onychophoran brain. In doing so, we (i) localised the neuronal cell bodies associated with the antennae as well as the pathways of their fibres; (ii) revealed the existence of microglomeruli, hitherto unknown from onychophorans; and (iii) identified several paired neuropils associated with the onychophoran antennae, one of which resembles the mechanosensory neuropil of mandibulates. The striking similarities seen in the olfactory (i.e., glomeruli) and putative mechanosensory neuropils of onychophorans and arthropods might have resulted from convergent evolution of these structures. The new findings expand our understanding of the evolution of the panarthropod brain.



Main Meeting, FG Systematics, Biogeography and Diversity
Poster: Syst 12

A new species of *Newportia* (Scolopendromorpha: Scolopocryptopidae) from Cuba with a standardized terminology for cuticular structures and aspects on the transformation of ultimate legs

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Newportia Gervais, 1847 is the most diverse genus in the family Scolopocryptopidae Pocock, 1896, and also ranks first among New World Scolopendromorpha. Martínez-Muñoz & Tcherva (2017) counted 66 species, of which Chagas-Jr. (2018) synonymized two and Schileyko (2018) reduced one to a subspecific status. In this contribution we update the previous species number of *Newportia* sensu lato to 63 species, to which we add a species new to science. Eight specimens from five localities and four provinces of the island of Cuba were examined. SEM images of the ultimate legs of one paratype were taken and utilized for detailed examination of the cuticular structures, for which standardized terms are proposed. The new species is herein described and its affinities to *Newportia weyrauchi weyrauchi* and *Newportia weyrauchi thibaudi* are discussed. The list of Cuban *Newportia* is updated to eight species and two subspecies.



Main Meeting, FG Morphology
Oral Presentation

Masturbation-like behavior of male beetles let their long penis settle in a right position and makes them ready for copulation

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Many species of criocerine beetles have a hyper-elongated part of the intromittent organ called a flagellum. In an extreme case, males of the species *Lema* (*Lema*) *coronata* have a long flagellum as twice long as their body length. The flagellum is usually gripped along a margin of a membranous pocket located in the intromittent organ. This pocket had parallelly evolved with the flagellum. This specialized state of the flagellum and pocket is indispensable during copulation for flagellum insertion into the female spermathecal duct to transfer sperm. After hatching from the pupa, the flagellum is not in the active state. Rather, the flagellum is prepared in an inactive and completely coiled state. Males repeatedly evert and withdraw the internal sac multiple times before sexual maturation without mounting a female, which is masturbation-like behavior (MLB). This behavior serves the flagellum uncoiled and guides it into the active state. Systematically arranged projections on the internal surface of the pocket aids the rearrangement of the flagellum. The closely related species, *Lema dilecta*, also has a long flagellum and undergoes the same behavior to place the flagellum in the active position. However, some other species of criocerine beetles with much shorter flagella can attain the active state without exhibiting this behavior. Based on a previously proposed phylogenetic tree, I will discuss the evolutionary history of the hyper-elongation of the flagellum and associated behavior. This kind of “MLB” is also known for bugs, which serves their elongated sucking mouthparts into an active state after molting.



Main Meeting, FG Evolutionary Biology
Oral Presentation

ABCB transporters enable sequestration of secondary plant compounds in a highly specialized herbivorous insect

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Although sequestration of secondary plant metabolites is not a rare adaptation of herbivores to profit from the chemical defense of their host plants, little is known about the molecular and physiological mechanisms involved. The large milkweed bug, *Oncopeltus fasciatus* (Hemiptera: Lygaeidae) is a prime example of sequestration: it feeds on plants containing toxic cardenolides, potent Na,K-ATPase inhibitors, which they then store and concentrate in a specialized thoracic storage compartment. Not only are toxins eliminated from their target sites by sequestration, but furthermore the bugs exploit them for their own defense. HPLC analysis of released defense fluids showed that the polar cardenolide ouabain is efficiently taken up from the hemolymph into the storage compartment in a time-dependent manner. As membrane permeability is low for polar compounds, we hypothesized that ingested cardenolides are actively transported by carrier proteins. In mammals it is known that some ATP-binding cassette transporters (ABC) of subfamily B can transport cardenolides. Thus we investigated these proteins as potential candidates involved in cardenolide sequestration in our large milkweed bug. By transcriptome analysis we identified two ABCB full-transporters in *O. fasciatus*. Tissue-specific expression and localization by immunohistochemistry pointed toward the involvement of these transporters in tissue protection as well as in sequestration. RNAi mediated knockdown of these genes in adult bugs drastically reduced sequestration efficiency. Thus, our results indicate that ABCB transporters have a dual physiological function in *O. fasciatus*: in addition to protecting sensitive tissues ABCB proteins are key players involved in the sequestration and efficient storage of cardenolides.



Main Meeting, FG Morphology

Poster: Morph 8

***Denticeps clupeioides* (Teleostei, Clupeomorpha) – morphology and its relevance for the understanding of clupeoid and otomorph evolution**

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The denticle herring (*Denticeps clupeioides*) is the only extant member of the family, Denticipitidae, and occurs endemic in the Niger estuary and small coastal rivers in Nigeria and Benin. Furthermore, within this family, only a single fossil, *Palaeodenticeps tanganikae*, is known. Eponymous for *Denticeps* is the occurrence of real teeth distributed over several dermal bones of the skull. *Denticeps clupeioides* represents the sister-group of all other extant clupeomorphs, supported by morphologic and molecular data. Therefore, its morphology is of major importance for the understanding of the evolution in herring-like fish (Clupeiformes). A detailed study of its osteology displays a mosaic pattern of plesiomorphic characters, synapomorphies with the Clupeoidei and autapomorphies. Primitive characters also present in outgroups but absent in Clupeoidei are e.g., the absence of a pleurostyl, and an articulatory surface for the first vertebra on the neurocranium formed by exoccipital and basioccipital. Clupeomorph apomorphies present in *Denticeps* are e.g.: the recessus lateralis, ventral scutes and a fusion of the ural centrum I with the second hypural. Besides that, *Denticeps* is unique in extant clupeomorphs in having a temporal foramen that is built only by the frontal, the presence of a postsupracleithrum and the so called pelvic plate. By morphological comparison with other Otomorpha (Alepocephaliformes and Ostariophysii) and with basal Teleostei (Elopiformes and Osteoglossomorpha) a better understanding of the evolution of these groups and a characterization of the 'Grundplan' in Clupeiformes and in Otomorpha is possible.



Main Meeting, FG Developmental Biology

Poster: Dev 4

Ontogeny of the deutocerebral proliferative system in the crab *Carcinus maenas*: new insights into the evolution of adult neurogenesis in decapod crustaceans

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Adult neurogenesis, the persistent generation and integration of new neurons during adulthood, has been demonstrated in different representatives of malacostracan crustaceans. In the adult brains of these animals, new neurons are being integrated into somata clusters of the central olfactory system. This process is driven by the deutocerebral proliferative system that consists of a neurogenic niche and migratory streams which lead to proliferation zones. Previous studies have shown a high disparity of the deutocerebral proliferative system within decapod crustaceans. Suggesting an elaboration of the deutocerebral proliferative system from basally branching to more derived taxa of decapods, we have analyzed the deutocerebral proliferative system in the brachyuran crab *Carcinus maenas*, one of the most derived taxa of decapods. This organism displays a relatively well developed olfactory system, but in contrast to other reptant decapods, a reduced second order processing neuropil (the accessory lobe). We used Bromodeoxyuridine as S-phase marker in mitotically active cells combined with immunohistochemical detection to investigate the development of the deutocerebral proliferative system from larval stages to adult crabs. Until first metamorphosis, asymmetrically dividing neuroblasts and their progeny are patchily dispersed in the brain. During further development, the neuroblasts disappear and BrdU-positive cells concentrate as a transverse band consisting of two accumulations posterior to the olfactory lobes. However, in adult animals, there is only one proliferative zone left provided by a neurogenic niche. We assume that, initially, an elaborated deutocerebral proliferative system is developing in juveniles, but is being reduced again in adult brains of brachyurans.



Main Meeting, FG Behavioural Biology
Oral Presentation

Hard times for prey: the effects of weaver ant presence on foraging strategies in a fruit fly-parasitoid system

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Predator-prey interactions are often important to understand the dynamics observed at the population level of the involved species (Peacor (2003), *Oikos*, 100, 409). Predation can influence the reproductive success of the prey both through consumptive as well as non-consumptive effects (Lima (1998) *Bioscience*, 48, 25). Non-consumptive predation effects could have an equal or even higher impact than direct prey consumption (Suraci (2016) *Nature Communication*, 7, 1). In fact, the mere presence of a predator can induce the prey to adopt evasive strategies in order to avoid being predated. Detecting the presence of a predator may, for example, reduce the time a forager spends searching for resources, which, in turn, may reduce the forager's reproductive success (Roitberg (2010) *Behavioural Ecology Sociobiology*, 64, 627). Here, we used a predator-parasitoid-pest system to study whether the presence of an insect generalist predator (i.e. the weaver ants), influences the reproductive success of two fruit fly species (Tephritidae) and their parasitoids, respectively. We observed species interactions at two spatial levels, namely mesocosm and microcosm. At the former level, we analysed ant interference on parasitoid efficiency and, at the latter level, we analysed the mechanisms through which the ants affect the foraging behaviour of both, fruit flies and parasitoids.



Main Meeting, FG Physiology
Poster: Phy 13

Processing of the *Staphylococcus aureus* alpha-toxin in human airway epithelial cells via endocytosis

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The pore-forming alpha-toxin (hemolysin A, Hla) is one of the main virulence factors mediating *Staphylococcus aureus* (*S. aureus*)-induced pneumonia (Lowy 1998, N Engl J Med 339:520-32). Hla may diffuse through the mucus layer of the airways and bind to the surfaces of airway epithelial cells via plasma membrane receptors (e.g. ADAM10; Wilke and Bubeck Wardenburg 2010, Proc Natl Acad Sci USA. 107(30):13473-8). The toxin forms heptameric transmembrane pores (Montoya und Gouaux 2003, Biochim Biophys Acta. 1609(1):19-27). Ion fluxes through these pores and membrane potential changes may induce alterations in cell shape, in partial losses of focal and cell-cell contacts and to a disruption of the epithelial barrier function (Hermann 2015, Am J Respir Cell Mol Biol. 52(1):14-24). We hypothesize that S9 cells, immortalized human airway epithelial cells, may be able to defend themselves directly against the toxin by removal of pore-containing plasma membrane areas by endocytosis. To investigate the endocytic uptake of recombinant Hla (rHla) in these cells, cellular membranes from post nuclear supernatant (PNS) of rHla-treated S9 cells were separated using a continuous iodixanol gradient by ultracentrifugation. Individual fractions were analysed for endosomal or plasma membrane markers and for Hla by Western blotting. The results showed that rHla is present in fractions enriched with endosomes, which strongly suggests an active endocytic uptake of the toxin by S9 cells. Whether endocytic clearance of toxin pores from the surface membrane is a universal defense mechanism of airway epithelial cells or just of certain cell types has still to be investigated.



Main Meeting, FG Morphology
Oral Presentation

Unexpected diversity of median caudal cartilages in teleosts

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Caudal fin skeletons in teleosts have intensely been studied in the context of phylogenetic relationships. Small cartilages at the distal end of the diastema, the 'median caudal cartilages', have gained so far only little attention. Their taxa-dependent variable three-dimensional structure is reported herein for the first time. In some systematic groups shape and arrangement of these cartilages is quite uniform within the respective group, e.g. in Alepocephalidae, Platytrichtidae or Myctophyformes; in other taxa there is a high intrataxon variability, e.g. in Stomiiformes or Aulopiformes. Shape, number and presence/absence may even vary within certain species, e.g. *Osmerus eperlanus*, *Thymallus thymallus* or *Gymnocorymbus ternezi*. The function of median caudal cartilages remains unclear: they may be related to fin-ray support, but often an obvious relation to fin-rays or any other evident function becomes not visible. Their presence and size is not dependent on the size of the diastema. Median caudal cartilages seem to have evolved at the base of clupeocephalans and occur in many taxa up to about aulopiforms, as well as single beryciformes. Apparently they often have been reduced at different systematic levels and may have re-evolved within some taxa.



Main Meeting, FG Behavioural Biology

Poster: Behav 15

The evolution of female genital mutilation: implications of fitness costs and female mate preference

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Males may evolve traits that shift the remating or oviposition rate of the female from the female's optimum toward their own due to selection on competitive fertilization success. Defensive adaptations to sperm competition include mate guarding, copulatory plugs, manipulative seminal fluids and internal genital damage. These adaptations can manipulate the female by altering her behaviour or physiology, but also her genital anatomy. Examples of male-inflicted damages to female genitalia have been documented in numerous taxa, especially among arthropods. Most of these genital damages are inflicted internally by the male intromittent organ, and it is debated how these harmful traits have evolved. Recently, we described that males inflict external damage to the female genitalia in an orb-weaving spider as a defensive adaptation to sperm competition. In the course of copulation, males mutilate an external genital structure of the female that is necessary for genital coupling. The lack of this structure prevents the female from remating. Although probably widespread among spiders, the selection regime for external female genital mutilation is difficult to understand, since the mutilation may cause a fitness decrease for both sexual partners. By means of a theoretical model, we investigate how the fitness costs affect the selection on mutilation mating behaviour in males. Additionally, in a mating experiment, we show that some males are more likely to mutilate than others due to female mate preferences. We discuss the implications of the fitness costs and the female mate preference on the evolution of female genital mutilation.



Workshop: Animal Welfare
Oral Presentation

Fortbildung und Schulung von Mitarbeitern nach § 3 und § 4 der TierSchVerV

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In der TierschutzVersuchstierVerordnung (TierSchVersV) ist in den Paragraphen 3 und 4 eine Pflicht zur regelmäßigen Fortbildung von Mitarbeitern in Bezug auf Kenntnisse und Fähigkeiten zur Durchführung von Tierversuchen an Wirbeltieren und Kopffüßern verankert. Genauere Angaben zu möglichen Inhalten solcher Maßnahmen wie auch zu deren Häufigkeiten und zeitlichen Umfängen fehlen jedoch. Dies führt zu großer Unsicherheit sowohl bei den betroffenen Personen und Institutionen, als auch auf Seiten der genehmigenden und kontrollierenden Behörden. In meinem Beitrag möchte ich darlegen, welche innerbetrieblichen wie auch externen Möglichkeiten genutzt werden können, um der genannten Pflicht zur Fortbildung nachzukommen. Ein Blick in die Schweiz liefert Anhaltspunkte für zukünftige Anforderungen an den zeitlichen Umfang dieser Maßnahmen.



Symposium: Adaptations to Hematophagy in Blood-feeding Parasites
Oral Presentation

The hirudin superfamily

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Of all bioactive factors that are secreted by (medicinal) leeches during feeding on their vertebrate hosts, hirudin is the best studied. Originally it was purified from and described in members of the genus *Hirudo*, but since then it has been identified in a range of hematophagous leeches from several taxonomic groups. Hirudin is the one and only leech-derived factor that has found its way from bench to bedside. In *Hirudo medicinalis* three variants of hirudin (VV, IT and PA) have been described. They are encoded by different genes and can be expressed in parallel within one individual leech. The term hirudin, however, rather describes a concept than a unique entity. In this sense, hirudin is defined by both, its activity (the inhibition of thrombin) and a combination of structural (e.g. presence of six cysteine residues) and physico-chemical (e.g. pI value of about 4.1) properties. The essential structural features of hirudin do not belong to this particular protein exclusively, but can be found in other leech-derived factors as well: haemadin (a thrombin-inhibitor of the land-living leech genus *Haemadipsa*), decorsin and ornatin (inhibitors of platelet aggregation found in the North American leeches *Macrobodella decora* and *Placobdella ornata*) and the hirudin-like factors (factors of yet unknown function derived from members of the genera *Hirudo* and *Hirudinaria*). All these factors considerably differ in length (39 - 66 amino acids) and their respective pI value (3.1 - 9.2). Nevertheless, growing evidence clearly indicates that they share a common ancestor and hence form the hirudin superfamily.



Main Meeting, FG Evolutionary Biology
Oral Presentation

Evolution of viviparity in African toads (Anura: Bufonidae)

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Amphibians worldwide show a great diversity of reproductive modes and several of these are characterized by a complete independence from water. These terrestrial modes of reproduction include direct development, which is fairly widespread, and viviparity. While viviparity is relatively common in caecilian amphibians, it is comparatively rare in anurans and salamanders. Within anurans, only four taxa evolved ovoviviparity or viviparity and two of these are toads inhabiting montane areas in East and West Africa. Terrestrial reproductive modes are hypothesized to be more common in montane areas (Goin & Goin (1962) *Evolution* 16:364). Analyses confirm this hypothesis to be correct and reveal that terrestrial reproduction evolved in situ in montane areas. Additional factors influencing the evolution of viviparity in African bufonids are discussed.



Main Meeting, FG Morphology
Poster: Morph 3

A heart urchin hemorrhoid? Not quite, but close

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Heart urchins (Echinoidea: Spatangoida) form a highly specialized group within the irregular sea urchins (Echinoidea: Irregularia), a taxon characterized by a number of adaptations that evolved as a consequence to their predominantly infaunal lifestyle. In particular, the shift from an omnivorous or herbivorous diet in "regular" sea urchins to sediment feeding in irregular echinoids resulted in the digestive tract of these animals to undergo numerous changes, including the differentiation of specialized gut regions. During a recent, comprehensive survey of spatangoid caeca, the presence of a previously overlooked organ became apparent. Using dissection, photography, micro-computed tomography, histology, as well as scanning and transmission electron microscopy, this novel organ was studied both morphologically and anatomically to determine its characteristics, function, as well as evolutionary origin. The results show that the structure - tentatively termed the rectal caecum - is present only in a small number of genera within the family Schizasteridae (Spatangoida: Paleopneustina). As its preliminary name suggests, the rectal caecum is positioned relatively close to the anus and constitutes an outcrop of the rectum. Similar to all other currently known caeca of the spatangoid digestive tract, the wall of the rectal caecum differs from that of its host gut region, indicating physiological specialization. However, in contrast to other spatangoid caeca, the rectal caecum is permanently filled with sediment. Based on a comprehensive study of museum specimens as well as material freshly obtained in the Adriatic Sea, various anatomical, morphological, functional, and evolutionary aspects of this enigmatic new organ will be presented.



Main Meeting, FG Behavioural Biology
Oral Presentation

Quantity vs. quality: bat choices drive the evolution of copious but dilute floral nectars

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Hummingbirds and bats prefer sweet nectars, yet the plants they pollinate offer some of the most dilute nectars of all plants. The apparent paradox is resolved when we consider that pollinators evaluate not only the sweetness of the nectar they consume, but also the nectar amount and availability, independently from each other. When multiple reward dimensions influence choice, and when reward evaluation is based on proportional, rather than linear differences between options, a preference for dilute, but copious nectars emerges. We were able to support this theoretical prediction with a virtual evolution experiment in the tropical rainforest, where bats visited computer-automated flowers with simulated genomes and selected for relatively dilute nectars. Computer simulations allowed us to analyze how different reward evaluation mechanisms affected the evolutionary outcome. They also revealed that this outcome depended on the supply/demand ratio, so that food scarcity caused a stronger selection for dilute nectars. Indeed, this prediction was supported by results from laboratory experiments with bats and computer-automated flowers. Our findings illustrate that the integration of multiple reward dimensions that are evaluated proportionally, rather than linearly, results in choices that are not well explained by optimal foraging theory.



Main Meeting, FG Developmental Biology

Poster: Dev 5

Loss and re-evolution of the mechanosensory lateral line system in amphibians?

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The lateral line system (LLS) is a specialized sensory system composed of both mechano- and electroreceptors present in almost all anamniote aquatic vertebrates. Much is known about its anatomy, embryonic induction and physiological functioning but there is a clear lack about its developmental fate during the evolution of new life history strategies such as direct development. In amphibians the basal developmental mode is biphasic, including a free-living aquatic larva and a more-or-less terrestrial adult. However, in some groups direct development has evolved several times independently by reducing this free-living tadpole phase in varying degrees. Moss frogs (*Arthroleptella*) exhibit an intermediate stage between aquatic and direct development. The tadpole of *Arthroleptella* is not free-living but completes metamorphosis within the egg. African-squeaker frogs of the genus *Arthroleptis* have reduced the tadpole phase completely. We compare the development of the LLS of these taxa to ask whether the degree of direct development influences the pattern of LLS reduction. A reverse case where a biphasic developmental mode, including an aquatic larva, re-evolved from direct development is found in lungless salamanders of the genus *Desmognathus* (Plethodontidae). We compare the development of the lateral line system in *D. aeneus* (direct development), *D. ocoee* (short aquatic phase) and *D. quadramaculatus* (long aquatic phase) to elucidate if re-evolution of the LLS can be partial (e.g. only a few neuromasts) or only completely (full set of neuromasts).



Main Meeting, FG Behavioural Biology
Oral Presentation

Associative learning of recognition templates

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Elaborate division of labour is stable only when groups can be closed off to the outside. In eusocial species with often thousands of individuals per colony, the discrimination of nestmates from non-nestmates is thus a crucial process that needs to be precise and quick. Discrimination is based on colony-specific blends of cuticular chemicals. These are "labels" that are evaluated by e.g. guards at a nest entrance, in what is often described as a label-template-matching process. The template, some sort of neural representation of the nest-specific odour, is not yet well understood. New theoretical models of the template and its formation have been proposed based on existing data, but specific tests of the models are rare. The models range from simplistic ones that propose nestmate recognition to be a mere filter in the neural periphery, to models that favour complex templates in the brain that are learned by experience. We conducted a set of experiments testing the latter hypothesis in *Lasius* ants and found that (non)-nestmate recognition templates are learned associatively, which explains much of the inter-individual variation that has been observed in nestmate recognition behaviour.



Main Meeting, FG Neurobiology*

Poster: NB 11

Intracellular recordings from a time-compensated sun-compass in monarch butterflies

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The monarch butterfly (*Danaus plexippus*) is famous for its annual migration from North America to Central Mexico using a sun compass and the celestial polarization pattern as reference to maintain its southerly direction. In the butterfly's brain, these cues are processed in distinct brain areas, with the central complex acting as the internal compass for migration. How exactly the sun- and polarization-information are combined in the central complex is still unknown. In addition to these orientation cues, time of day information from the antennae is essential for the monarch butterfly to maintain its migratory direction. How celestial compass information, detected by the eyes, and time of day information from the antennae is combined in the monarch butterfly's brain is still a matter of speculation. To test this, we are performing intracellular recordings from central-complex neurons while stimulating the animal with different combinations of simulated skylight cues in natural (polarization angle perpendicular to the ersatz sun) and non-natural (in line with the ersatz sun) constellations. Our first data suggest that the combination of different skylight cues sharpens the neural tuning of central-complex cells. This generates a robust orientation compass that allows the monarch butterfly to maintain its southerly migratory direction with high precision. In addition, we are currently performing antennal backfills and brain injections to trace the time signals into the brain and to investigate where time of day information and skylight cues converge that allows the butterfly to compensate for the daily changes of the sun position.

* Contribution also presented in: *Symposium: 5th Meeting of the Arthropod Neuroscience Network* (Poster: ANN 9)



Main Meeting, FG Neurobiology*

Poster: NB 12

Spike pattern of auditory and ascending neurons in katydids

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Perception of sound is essential for reproduction and survival for many katydid species. Katydid use acoustic signals for example for mate finding and phonotactic behavior. Distinguishing between different sound sources and sound types requires acoustic stimuli to be received and characterized with regard to time and frequency components. The katydid ear, the so called crista acustica, is sensitive for airborne sound and located in the tibiae of the forelegs. To understand the spiking pattern of the auditory neurons in the crista acustica and ascending neurons in the ganglia, we analyzed the temporal structure of spiking in both types of neurons using pure tones with different frequencies and intensities. In the auditory neurons of the crista acustica of *Mecopoda elongata*, we found a spiking pattern with a high synchrony for the onset spike, timed precisely at about 2 ms after the sound reaches the organ. This timing of the first spike was independent of the used stimulus frequency and position of the auditory neuron along the crista acustica. With a stimulus duration of 20 ms, which is the typical length of a song syllable in this species, up to five more spikes can occur. The timing of these later spikes is highly regular and depends on how closely the stimulation frequency matches the most sensitive frequency of the respective cell. How differences in spike timing influence the spiking of the ascending neurons will be tested by extra- and intracellular recordings in the prothoracic ganglion, the projection area of the auditory neurons.

*Contribution also presented in: *Symposium: 5th Meeting of the Arthropod Neuroscience Network*
(Poster: ANN 10)



Main Meeting, FG Systematics, Biogeography and Diversity
Poster: Syst 7

Peptide mass fingerprints in combination with molecular phylogenetic analyses reveal genetic differentiation in *Psectrascelis* (Coleoptera, Tenebrionidae) from the Atacama

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The evolution of life in extremely water limited environments, such as the Atacama Desert in northern Chile has been poorly studied. Within the CRC 1211 (Earth - Evolution at the Dry Limit), we focus on the evolutionary patterns of darkling beetles (Tenebrionidae). These beetles belong to the most conspicuous biotic components in arid ecosystems worldwide. Here we summarize results obtained on the hyperdiverse genus *Psectrascelis*. Most species of *Psectrascelis* have a small area of distribution; particularly in the Atacama. Firstly, we analyzed by means of MALDI-TOF mass fingerprinting the structural diversity of neuropeptides in *Psectrascelis*. Selected tissue samples (antennal lobes) contained more than 50 neuropeptides detectable in a single spectrum; together these peptides contain at least 1000 amino acids. Isolated taxa naturally accumulate amino acid substitutions over time. Secondly, we analyzed the phylogenetic pattern using COI and 16S. Both approaches largely revealed congruent topologies. Analyses of COI provided the best phylogenetic signals at species level whereas high-throughput mass fingerprinting was useful to detect resolution at deeper nodes. Data suggest a very recent colonization of *P. intricaticollis* along the eastern Andes mountain range bordering the Atacama. We speculate that the disjunct distribution of many related *Psectrascelis* species is the result of (1) repeated expansions as presumed for *P. intricaticollis* and (2) long-lasting interruptions of migration corridors. The identification of abiotic key conditions that resulted in today's diversity and patterns of endemism will be performed by sharing data with geologists working in the same transects.



Main Meeting, FG Morphology
Oral Presentation

Structure and development of the tracheal system in Onychophora (velvet worms)

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The evolution of tracheal systems was pivotal for terrestrialisation within panarthropods. While the tracheae of arthropods (including spiders, millipedes and insects) have been extensively studied, those of onychophorans (velvet worms) remain largely unexplored, thus hampering conclusions about their evolution. We therefore analysed the structure and development of tracheae in representatives of Onychophora using scanning and transmission electron microscopy, histology, and histochemistry. Our data revealed a similar structure across the species, except that some species possess “Büscheltracheen”, with atria containing several tracheal openings, whereas in all remaining species the tracheae open individually. Our data confirm that the tracheal system of onychophorans develops postembryonically, as the first tracheal openings occur in four-day-old juveniles. In summary, our study revealed the following differences between the tracheal system of onychophorans and that of arthropods: (1) their tracheal tubes develop after birth; (2) the tracheal openings are distributed randomly along the body; (3) their atria possess no closing mechanism; (4) there is no evidence of tracheoles; (5) the taenidia rather than the intima face the tracheal lumen; and (6) the cuticular lining of tracheal tubes is not moulted. While our results support a single origin of the tracheal system in Onychophora, they show that there are several ways to organise tracheal systems, suggesting that there might be an evolutionary constraint for the similarities in structure of tracheal systems across the arthropod groups.



Main Meeting, FG Ecology
Oral Presentation

Microbes: ecological factors affecting reproductive traits in males and females

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Microbes are a universal ecological factor. They affect reproductive traits via several routes and their fitness impact link the environment directly to evolutionary change. Host fitness costs imposed by microbes include reproductive allocation due to the activation and maintenance of the immune system as well as direct microbe toxicity. Here I use the bedbug model system to make a case for studies in sexual selection, especially the ones investigating post-copulatory processes, to incorporate ecological, as well as genotypic variation, in reproductive traits. First, sexually transmitted diseases are universal and for example in bedbugs, genital microbes change with mating and vary between sexes and populations. Second, females seem to be particularly likely to have evolved adaptations to avoid or reduce opportunistic infections. However, I found bedbug seminal fluid contains antimicrobial compounds. The role of such antimicrobials in the reproductive process is not well understood. Third, I will provide evidence hinting at the protection of sperm against microbes using antimicrobials and at the coadaptation of sperm to microbes. This suggests a role for natural selection in shaping the evolution of reproductive traits in addition to sexual selection. In conclusion, microbes are an important but neglected ecological variable driving reproductive trait evolution.



Main Meeting, FG Systematics, Biogeography and Diversity
Poster: Syst 4

Distribution history of the palaemonid shrimp in the Baltic Sea based on the analysis of zoological collections

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The distribution of *Palaemon elegans* in the Baltic Sea is a highly discussed matter. Grabowski (2006) stated that *P. elegans* has performed a rapid colonization in the eastern Baltic Sea between 1990 and 2000 (Grabowski (2006) Aquatic Invasions, vol. 1, 116). However, the first occurrence of *P. elegans* in the Baltic Sea remains unclear because *P. elegans* was confused with *Palaemon adspersus* in older publications (Holthuis (1950) Decapoda of the Siboga Expedition, part 10, 1). The analysis of several Zoological Collections of the NORE-Association (the collection consortium of the North and Baltic Sea) reveals that *P. elegans* occurs much longer in the western Baltic Sea than assumed up to now. The earliest collections of egg-bearing females of *P. elegans* in the Baltic Sea come from Fehmarn coast and date back to 1925. The oldest distinct individuals of *P. elegans* were sampled 1874 in a Danish harbour in the western Baltic Sea. This is supported by further samples between 1874 and 1935 from the western Baltic. Additional findings regard the brackish water species *Palaemonetes varians*, which occurrence is presently explained by natural range extension (Nehring (2013) Invasive Aquatic Species of Europe. Distribution, Impacts and Management, 273). The presented collection data indicate, however, that this species already appeared in the Baltic in the middle of the 19th century and is in fact an autochthonic species in the Baltic Sea.



Main Meeting, FG Behavioural Biology

Poster: Behav 3

What does your neighbour do? – Electric signalling during different behavioural contexts in a weakly electric fish

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Weakly electric mormyrid fish emit brief, pulse-type electric organ discharges (EODs) that are used for both, active electrolocation and electro-communication. While inter-discharge intervals (IDIs) between EODs are important for active electrolocation, they also carry individual and social information during electro-communication. In previous studies, it has been suggested that the temporal variations of IDIs might be related to the behavioural context a fish is engaged in. Here, we aimed at finding whether certain IDI patterns are produced during distinct behaviours, and thus could inform neighbouring fish about the behavioural state of conspecifics. We established a reproducible experimental design to investigate the electric signalling behaviour of 20 *Mormyrus rume probosciostris* (siblings from the same clutch), which were kept solitarily under equal housing conditions and tested individually in the same experimental tank. We generated various behavioural contexts for each individual: resting, exploring of a novel environment and objects, foraging, feeding, reaction to an electric playback and startle response. Both, the motor and electric behaviours were recorded during the experiments. The analyses of recorded videos and electric signals revealed that individual *M. rume* seem to have distinct IDI characteristics. During some behavioural situations, e.g. during resting, feeding and startle responses, fish displayed characteristic IDI patterns. Our results suggest that fish could recognise the behavioural state of a neighbouring fish by solely “listening” to its EOD signalling behaviour even without seeing the fish. Further analysis might reveal additional influences of other parameters on electro-communication behaviour, e.g. a fish’s sex, age or reproductive state.



Main Meeting, FG Neurobiology*

Poster: NB 3

Cross-modal adaptation in a descending interneuron in the stick insect *Carausius morosus*

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Sensory systems adjust their sensitivity through adaptation, i.e., a history-dependent shift of the stimulus-response characteristic. For example, in motion-encoding proprioceptors, adaptation to constant stimulation during continuous active movement could ensure high responsiveness to changes in movement speed. In the stick insect *Carausius morosus*, continuous active movement occurs during active tactile exploration movements of the antennae. As walking stick insects reliably respond to antennal tactile cues with targeted leg movements, adaptation of neurons of the antennal-mechanosensory pathway should affect the information transfer from the head to the legs. Here, we measure adaptation in an identified descending interneuron that conveys antennal proprioceptive information to the thoracic ganglia: The contralateral ON-type velocity-sensitive (cONv) interneuron. This interneuron encodes antennal-joint velocity as well as substrate vibration (Ache et al., 2015, *J.Neurosci.*, 35:4081). Preliminary results showed that cONv reduces its response to repeated antennal deflection suggesting adaptation. Here, we ask whether multimodal activation of cONv can lead to a change in response intensity of the neuron when compared to unimodal stimulation. Using hook-electrode connective recordings, we examined the responses of the bilateral pair of cONv interneurons to antennal ramp-and-hold deflections at one of two ramp velocities. We found that cONv reached the same level of adaptation after 20 ramps irrespective of the velocity imposed, implying faster adaptation at higher velocity. Imposed movements of the opposite antenna did not affect the level of adaptation of cONv, while substrate vibration delivered at a rate comparable to footfall during walking set cONv into the adapted state, suggesting cross-modal adaptation.

*Contribution also presented in: *Symposium: 5th Meeting of the Arthropod Neuroscience Network (Poster: ANN 11)*



Main Meeting, FG Physiology
Poster: Phy 8

Comparison of tissue-specific transcriptomes of three *Danio* species

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Danio rerio, also known as “zebrafish”, has become a popular model organism for the study of gene function in vertebrates. Little is known about the molecular biology of other *Danio* species. In this study, we have compared the transcriptomes of *D. rerio* (zebrafish), *D. albolineatus* (pearl danio) and *D. aesusapii* (panther danio). About 40 million paired-end reads were obtained from individual transcriptomes of brain, liver, and gonads of females of the three *Danio* species. A total of 37,428 transcripts were identified by mapping of the reads to the *D. rerio* genome. The differentially expressed genes in each tissue were characterized and analyzed by gene ontology enrichment analysis tools. The results revealed species- and tissue-specific differences in the three *Danio* species.



Symposium: 5th Meeting of the Arthropod Neuroscience Network
Oral Presentation

Influence of wide-field motion on the signaling of sky compass cues in the locust central complex

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Navigation is a crucial task for many animals. During their long distance migratory flights locusts likely use a sky compass. Neurons of the central complex (CX) encode the direction of orientation relative to celestial cues such as sky polarization and the position of the sun (Pegel et al. 2018, *J. Exp. Biol.* 221:jeb171207). As compass cues are meaningful especially during self-motion, we asked whether neurons of the CX polarization network respond to wide-field motion. 5 out of 12 tested neurons of the protocerebral bridge (PB), a compartment of the CX, were responsive to progressive wide-field motion. CX neurons adapt to the stationary plane of polarized light (E-vector). When the preferred E-vector was presented together with progressive wide-field motion, the E-vector response disadapted in most neurons. In contrast, wide-field motion was largely ignored when presented in combination with the neuron's anti-preferred E-vector orientation. The data suggest that wide-field motion as experienced during flight strengthens the animal's internal representation of head direction relative to the zenithal E-vector in the PB. Three PB neurons were tested for wide-field motion simulating a right or left rotation around the yaw axis. Two of these neurons showed arborizations in one of the paired noduli of the CX and were previously termed CL2 neurons. They responded to rotational wide-field motion with excitation or inhibition, dependent on rotation direction and on the innervated nodulus. The neurons are suited to update the animal's internal head direction relative to a compass signal during right and left turns.



Symposium: Adaptations to Hematophagy in Blood-feeding Parasites
Oral Presentation

Biology of blood-feeding in kissing bugs (Hemiptera; Triatominae)

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The evolution of hematophagy within arthropods resulted in a series of convergent adaptations that favors the acquisition of blood from their hosts, including modifications in both their mouthparts' morphology as well as biological activities of saliva. Triatomines are vessel feeders that obtain their blood meals directly from blood vessels of their vertebrate hosts, while salivation occurs throughout the whole feeding. To investigate the impact of phenomena occurring in the host's skin and in the insect's intestinal during hematophagy, the triatomines feeding was monitored using the electromyogram of its cibarial pump and/or intravital microscopy techniques. Some alterations in mice's skin microcirculation (vascular permeability, hemorrhage and vasodilatation) were intensified along *Rhodnius prolixus* feeding process, while others such as the recruitment of platelets and leukocytes were more pronounced after withdrawing of insect's mouthparts. The analysis of blood flow through the bug's head showed that the reductions of pumping frequency observed along the engorgement phase was mainly due to the increased cibarial pump filling time. On the other hand, *Triatoma brasiliensis* knocked down for Braziliensin (intestinal anticoagulant) also presented a greater difficulty in maintaining the cibarial pump frequency along the blood-feeding on mice, when compared to appropriate controls. Both this difficulty during the blood intake as well as the presence of blood clots in the midgut content in Braziliensin knockdown insects were abolished by previous treatment of mice with heparin. These results suggested that both salivary and intestinal biomolecules are important to maintain the blood fluidity from the host microcirculation until the insect anterior midgut during the cibarial pump activity.



Symposium: Adaptations to Hematophagy in Blood-feeding Parasites
Oral Presentation

Haem - dietary vitamin for ticks

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Haem, an essential cellular cofactor, is synthesised endogenously in genetically encoded pathway in most eukaryotic organisms. Ticks, but not other mites, have lost most genes encoding the endogenous biosynthetic enzymes of haem. Using an artificial membrane feeding system of hard ticks, we demonstrated, that adult *I. ricinus* females acquire haem from host haemoglobin. Eggs of serum-fed ticks were devoid of host haem deposits and failed to undergo embryogenesis. Supplementing dietary serum with bovine haemoglobin restored haem deposits and facilitated the tick embryogenesis and larvae hatching. Supplementing dietary serum with haem only led to much smaller haem deposits in eggs, indicating that ticks express haemoglobin-specific receptor in their digestive tract enhancing the haemoglobin up-take. To sustain systemic inter-tissue distribution of haem across body, ticks transport haem on large lipoproteins throughout haemolymph. Juvenile stages, however, do not seem to be dependent on high supplementation of host haem as they feed and develop into next stages normally when fed on normal serum. We further demonstrated that ticks, as well as other mites, lack the gene encoding haem oxygenase, haem catabolising enzyme. We have experimentally shown that ticks, indeed, do not acquire iron from host haem/haemoglobin but rather from a host transferrin, a major non-haem iron transporter protein found in mammalian blood. Loss of haem oxygenase seems to be an ancestral trait in evolution of mites, followed by loss of haem biosynthesis in the origin of ticks.



Main Meeting, FG Morphology
Oral Presentation

Flesh and bone: an integrative approach towards sexual size dimorphism of a terrestrial salamander (*Salamandrina*)

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Males and females face different selection pressures due to a biased investment into reproduction. This does often result in different morphologies of the sexes. Sexual size dimorphisms (SSD) can give us important hints on the evolution and biology of a species. Salamanders are a well suited system investigating SSD including a diversity of reproductive modes and behaviours and patterns of SSD combined with life history traits including phylogeny help us to understand the evolution behind these processes. Because phylogenetically spectacled salamanders (genus *Salamandrina*) are the most basal taxon of the Salamandridae they have a key role for reconstructing the evolutionary pattern of SSD. Extensive morphological measurements on specimens of *Salamandrina perspicillata* gave us an overall overview of the expressed SSD in the external morphology but we employed high resolution micro CT scans of the skeleton to access SSD in skull, limbs and the pelvic girdle. Our investigations revealed a significant male-biased dimorphism in limbs, head and cloaca measurements relative to snout-vent length, while females showed larger trunks. Patterns of SSD on external and osteological measurements lead to the same results, but osteology uncovered further cryptic dimorphic traits. The novel dimorphic characters in the external morphology and osteology are likely linked to the different reproductive roles of the sexes of the salamanders.



Symposium: Adaptations to Hematophagy in Blood-feeding Parasites
Oral Presentation

Salivary gland transcriptome and salivary enzymes of *Sergentomyia schwetzi*

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Phlebotomine sand flies are blood sucking insects and vectors of *Leishmania* spp., parasites causing human and animal leishmaniases. Sand flies belong to three main genera – *Lutzomyia* (in Americas) and *Phlebotomus* and *Sergentomyia* (in Eurasia and Africa). *Lutzomyia* and *Phlebotomus* spp. bite mammals frequently and are well known for transmission of human diseases. Contrary, *Sergentomyia* spp. prefer to feed on reptiles, and their medical importance is rather unknown. However, some *Sergentomyia* species, especially *S. schwetzi*, can bite humans and domestic animals. During the blood feeding on vertebrate hosts, sand fly females inject saliva, which compounds have immunomodulatory and anti-hemostatic effects. These salivary components enable a sand fly female to complete the blood meal and also affect establishment of infection. Until now, all studies dealing with sand fly saliva were done with the representatives of the genera *Phlebotomus* and *Lutzomyia*. Moreover, out of more than 800 sand fly species described so far, salivary glands transcriptomic data were reported only for nine species of the *Phlebotomus* and four species of the *Lutzomyia*. We sequenced *S. schwetzi* salivary gland transcriptome. All main families of sand fly salivary proteins were found and phylogenetically compared with homologous proteins of *Phlebotomus* and *Lutzomyia* spp. Further we studied salivary enzymes, particularly hyaluronidase and apyrase, and found differences compare to other sand fly species studied previously. The activity of apyrase is lower than in any of *Phlebotomus* and *Lutzomyia* spp. studied thus far. Comparing to other sand fly species the Mw of hyaluronidase is lower, about 42 kDa.



Main Meeting, FG Developmental Biology
Oral Presentation

Evolution of visual system development - morphology meets genomics

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The great morphological diversity present in nature is the result of millions of years of evolution of the underlying developmental programs. Developmental gene regulatory networks (GRNs) need to be highly constraint to ensure consistent organ formation throughout varying environmental conditions. However, these networks also must be flexible enough to allow natural variation in morphology to occur. Since many developmental genes are highly conserved across distant animal phyla, it has been proposed that gene expression divergence plays an important role in phenotypic diversification. We study the evolution of the visual system in closely related *Drosophila* species to unravel the molecular basis underlying morphological diversification. Applying a combination of quantitative phenotyping, quantitative trait loci (QTL) mapping and comparative transcriptomics, we show that changes in the orthodenticle (otd) locus most likely contribute to eye size differences between *Drosophila simulans* and *D. mauritiana*. Further characterization of ommatidia morphology and the comparison of otd and rhodopsin gene expression suggest that differences in the onset of otd expression may result in variation in ommatidia size observed in nature.



Workshop: Animal Welfare
Oral Presentation

Nociception and pain in fish

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Fish are a widely exploited research model, second only to mice in numbers used, and are also important in a variety of other contexts. As such, we have an ethical and legal obligation to safeguard them from situations that might cause potential discomfort or suffering. Thus it is crucial we assess whether fish can experience the negative affective component of pain for improving their health and wellbeing. In order to define pain in animals, two key concepts have been recommended, firstly, neuro-, physiological and behavioural responses to potentially noxious stimuli should be markedly different compared to innocuous stimulation. Secondly, following a potentially painful experience, animals should demonstrate changes in motivation and behavioural outputs on future encounters. Nociception is the simple detection and reflex withdrawal response to noxious stimuli whether they be mechanical, thermal or chemical. Despite the nociceptor system having been well studied in mammals, there is relatively less known with regards to nociception in fish. Studies using anatomical and electrophysiological analysis have revealed that teleost fish possess nociceptors capable of detecting potentially painful stimuli and that these are physiologically similar to those found in mammals. Furthermore it has been demonstrated in fish that administration of analgesics can ameliorate the behavioural and physiological changes in response to noxious stimulation. These studies illustrate that fish possess the neural apparatus capable for nociception and behavioural responses that may be suggestive of pain. This system is remarkably similar to that of mammals, thus highlighting the wider implications for the humane use of fish.



Main Meeting, FG Behavioural Biology

Poster: Behav 16

Morphological investigation into cryptic female choice in *Argiope bruennichi* (Scopoli, 1772)

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The means of polyandrous females to choose between sperm of different males post copulation (i.e. cryptic female choice), has been an object of several studies over the last two decades. However, observations into the nature of the utilized mechanisms are difficult, due to the internal and mostly hidden processes at work. Several different means and places in the reproductive-tract provide opportunity for females to choose. Be it the allowed time to transfer sperm or the decision to dump, neutralise or digest sperm-cells. Even selective activation and controlled transport are possible tools to assign higher paternity to a chosen male. Entelegyne spider-females have paired spermatheca with complementary paired insemination-organs on the males' side. In *Argiope bruennichi*, effective postcopulatory plugging naturally prevents sperm-transfer from more than one male to each sperm-storage-site and thus provides an easy to manipulate and selectively observable platform to study CFC. Previous studies revealed CFC in three *Argiope* species, with females favouring sperm from smaller males, non-siblings' over those of siblings and courting males' over non-courting males'. The insemination-pattern of *A. bruennichi* is fixed and ipsilateral and we pre-determined the storage-site for each male's sperm by removing one of the pedipalps. Spermathecae of females, each with the sperm of one of the different males, were removed at three different times post copulation to be fixed and embedded for subsequent TEM-examination. We will present results on spatial and conditional differences of the sperm-cells inside spermathecae of females inseminated by males of different genetic relatedness (siblings and non-siblings).



Main Meeting, FG Developmental Biology

Poster: Dev 1

Origin and development of the male copulatory organ in the spider *Parasteatoda tepidariorum*

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Arthropods display an enormous diversity of morphology. Most of this diversity is produced by evolutionarily divergent developmental genetic mechanisms during both embryonic and postembryonic development. While embryonic development and its evolutionary diversification have been studied in great detail, postembryonic development remains far less understood. This is unfortunate, because many species specific morphological features develop only during postembryonic development. A striking example for species specific morphologies that form entirely during postembryonic stages is the male copulatory organ of spiders, the pedipalp bulb organ. This organ is especially interesting, not only because its shape is species specific, but also because this shape is involved in prezygous isolation mechanisms and thus links diversification of developmental mechanism with species recognition and speciation. We have studied the postembryonic development of the male bulb in the spider *Parasteatoda tepidariorum*. We were able to show that the primordium of the bulb forms from cells beneath the claw and thus from a modified claw fundament. In contrast to embryonic stages, postembryonic stages are surrounded by a rigid cuticle that limits the space for new organs. We provide evidence for an important role of hemolymph constituent coagulation in the expansion of the hypodermis of the early subadult stage in order to provide the space for bulb development. We were able to show that the species specific morphology of the bulb constituents forms during the final phase of postembryonic development. This provides a time-frame for our search for genes that likely control species specific bulb morphology.



Main Meeting, FG Evolutionary Biology
Oral Presentation

First neuropeptidome of Adephaga – Data from *Carabus problematicus* (Carabidae) shed new light on the evolutionary trends of neuropeptides in Coleoptera

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Neuropeptides are signaling molecules produced by neurosecretory cells of the central nervous system (CNS) and as such participate in the regulation of virtually all physiological functions in multicellular organisms. Compared with other speciose insect taxa, little is known about neuropeptide evolution in Coleoptera. In addition to it, the limited knowledge is restricted to members of Polyphaga suborder but indicates the loss of few common neuropeptide genes; such as genes coding for allatostatin A, corazonin, kinin, and pigment dispersing factor. In our study we analyzed for the first time the neuropeptidome of a member of the adephagean lineage, *Carabus problematicus*. Main purpose was separating features only typical of Polyphaga from those of Coleoptera in general. For that, we combined transcriptome analysis of CNS with mass spectrometry analyses for the identification of processed neuropeptides. Mature peptides and for the first time also protein hormones from about 50 precursors could be identified. Corazonin and allatostatin A were not detected both at the transcript and peptide level, which suggests a general absence of these peptides in Coleoptera. On the other hand, we detected for the first time in Coleoptera insect kinin and pigment dispersing factor, which indicates that these neuropeptides were lost in the Polyphaga lineage. Remarkable lineage-specific evolution of precursor sequences and also differential processing were found for CAPA precursors and their products, respectively.



Main Meeting, FG Neurobiology*

Poster: NB 24

Mass spectrometry imaging reveals distinct compartmentalization in neuroendocrine tissue of an insect

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Neuropeptides are signaling molecules regulating physiological functions in multicellular organisms. Many neuropeptides are produced in neurosecretory cells of the central nervous system (CNS) and released from neurohemal organs into the circulatory system. In insects, one of the major neuroendocrine tissues is the retrocerebral complex (RCC) which is constituted from different parts: a glandular part of the corpora cardiaca producing and releasing AKH, a neurohemal part of the corpora cardiaca which mostly stores neuropeptides produced in the brain, and the endocrine corpora allata which synthesize and release juvenile hormones. All of these tissues are crossed by axons from neurosecretory cells of the CNS. In our study, we optimized a protocol for the simultaneous detection of neuropeptides using Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry Imaging. Using our optimized protocol, we studied the distribution of neuropeptides at a 15 μm spatial resolution in 14 μm tissue sections of the RCC of the American cockroach *Periplaneta americana*. We detected more than 100 peptides with around 58 mature neuropeptides from 16 precursor genes in a single tissue section; thus obtaining for the first time a nearly complete coverage of insect neuropeptides by MSI. Based on the optimized protocol and differential distribution of neuropeptides in the RCC we were able to reconstruct the compartmentalization of the RCC and to detect differential neuropeptide processing. Thus, using our protocol, it is possible not only to investigate neuropeptide distributions but also to analyze differences in the neuropeptidome, e.g. in response to insecticide exposure or environmental stress in general.

*Contribution also presented in: Symposium: 5th Meeting of the Arthropod Neuroscience Network (Poster: ANN 18)



Workshop: From Gene to Function: Using CRISPR/Cas9 in Zoology
Oral Presentation

CRISPR-Cas: adaptive immune systems in prokaryotes and DNA scissors in eukaryotes

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CRISPR-Cas modules constitute adaptive and heritable immune systems found in many bacterial and most archaeal species. Cas proteins and processed CRISPR array transcripts, termed CRISPR RNAs (crRNAs), form ribonucleoprotein complexes that target and cleave foreign nucleic acids (Plagens, A. 2015) *FEMS Microbiol Rev*, 39, 442). Diversified CRISPR-Cas systems are found in nature and six types (I-VI) and sixteen subtypes have been classified. The DNA cleavage activity of Cas9 and related "DNA scissors" has been transferred into a variety of heterologous eukaryotic host cells facilitating elegant genome engineering approaches. I will provide an overview of CRISPR-Cas systems that are found in bacteria and give examples of their original antiviral activities. The coevolution of viruses with bacterial hosts promotes (i) diversification of CRISPR-Cas systems and (ii) the adaptation of viral anti-CRISPR measures. Abundant type I interference complexes, termed Cascade, and Cas9 variants have been reported to be inactivated by anti-CRISPR proteins. Recently solved structures and deduced mechanisms of crRNA maturation and crRNA-guided target recognition by Cas protein complexes will be described (Pausch, P. (2017) *Mol Cell*, 67, 622).



Main Meeting, FG Neurobiology*

Poster: NB 23

Identification of products from novel tryptopyrokinin genes in the locust, *Locusta migratoria* (Insecta)

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Almost 20 years after the release of the first insect genome, the discovery of novel neuropeptide genes becomes rare. In 2014, a thorough analysis of the genome of *Locusta migratoria* (Veenstra, 2014) suggested the presence of four novel neuropeptide genes, all encoding multiple tryptopyrokinins (tryptoPKs). Such peptides, which activate specific tryptoPK receptors, were already known from other insects and are typically encoded, together with other neuropeptides, in pyrokinin and capa genes. In our study, we identified for the first time mature products of two tryptopk genes from *L. migratoria* by MALDI-TOF mass spectrometric analysis up to a single cell level. The expression of tryptoPKs is restricted to two neurosecretory cells in the gnathal ganglion, exhibiting not only a unique neuropeptidome but also a very distinct axonal projection. In these cells, not less than 12 tryptoPKs could be identified. We also confirmed the existence of tryptopk genes in the cockroach *Periplaneta americana* and the stick insect *Carausius morosus*, thus providing hints for a lineage-specific polyneopteran origin of tryptopk genes. In addition, transcriptome data from CNS of *L. migratoria* revealed that the predicted tryptoPK precursors 3 and 4 are indeed partial sequences of a single precursor. Products of that precursor were not yet identified in the CNS. Comparative neuroendocrinology showed that homologous cells in holometabolous insects also contain tryptoPKs but use either capa or pyrokinin genes to reach this pattern.

*Contribution also presented in: Symposium: 5th Meeting of the Arthropod Neuroscience Network (Poster: ANN 12)



Main Meeting, FG Physiology
Oral Presentation

Metabolic mapping of *Drosophila* sperm

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Developmental biology (gonadal stem cells), infertility research and evolutionary biology (sperm competition, sperm ageing) rest on properly examining sperm metabolic rate. However, this trait is largely unexplored in most organisms, including in *Drosophila*. Here we borrow a method from cancer research and stem cell biology, fluorescence lifetime imaging (FLIM) and examine the metabolic state of *Drosophila melanogaster* sperm. We use the difference in autofluorescence lifetime between free and protein-bound NADH whereby a decreased proportion of free NAD(P)H indicates an increased employment of oxidative phosphorylation as the main cellular energy source, an increased proportion of free NAD(P)H would indicate increased glycolysis. In this poster we show how the ratio of free:protein-bound NAD(P)H changes with male age (0 to 35 days) and in the female (storage duration of 14 days) and across two different genotypes (Dahomey, Canton S). We discuss the implications of our results for sperm storage and for sperm competition.



Symposium: Adaptations to Hematophagy in Blood-feeding Parasites
Oral Presentation

The evolution of specialisation and generalism in bedbugs (Cimicidae)

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All 100+ bedbug species (Cimicidae) are obligate blood-sucking parasites but the evolutionary trajectory of blood-sucking and hosts are unknown. We constructed a new, fossil-dated, molecular phylogeny that estimates that ancestral Cimicidae evolved ca. 115 MYA as hematophagous specialists on an unidentified host (bats evolved ca. 50 MY later), switching to bats and birds several times thereafter. Humans were independently colonized three times, always from host specialist lineages that extended into host generalists. Our phylogeny rejects the idea that the divergence of the two current urban pests (*Cimex lectularius* and *C. hemipterus*) was associated with the divergence of *Homo sapiens* and *H. erectus*.



Symposium: Phenotypic Plasticity - RESPONSES of Animals to
Environmental Change
Oral Presentation

The costs of leaving early: Individual plasticity and mortality costs of emergence from hibernation in bats

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It is well documented that hibernation is crucial for temperate bat species to survive periods of food shortage during the winter. However, how differences in individual hibernation behaviour influence mortality and whether individuals are plastic with respect to their hibernation behaviour are largely unknown. Because bats are of high conservation concern it is of prime importance to understand their ability to respond to different climatic conditions and associated mortality costs. Here, we used a five-year data set of 1047 RFID-tagged individuals from two bat species, *Myotis nattereri* and *Myotis daubentonii*, that were automatically tracked when entering or leaving the joint hibernaculum. We investigated the impact of their individual hibernation behaviour, precisely the timing of departure in late winter and early spring, on mortality, their adjustment of departure timing to the North Atlantic Oscillation Index (NAO), as well as differences within and between the two species from 2011 until 2015. Our results suggest considerable differences among individuals within as well as between bat species with respect to emergence behaviour from the hibernaculum. In comparison to *M. daubentonii*, *M. nattereri* tuned emergence more closely to weather conditions and showed individual variation in plasticity. In both species, early departing individuals had an increased risk to die. Our results suggest that long-lived hibernating bat species have the potential to plastically adjust to changing climatic conditions, but this potential differs between species. Moreover, among-individual differences in emergence together with species-specific mortality costs of early emergence suggest the potential for natural selection to shape hibernation phenology.



Main Meeting, FG Morphology

Poster: Morph 9

The scale diversity in Pristigasteridae (Teleostei, Clupeiformes) with special focus on '*Ilisha*' *africana*

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Herring like fishes (Clupeiformes) are usually schooling fishes which live in marine, brackish and fresh waters with tropic, subtropic or moderate temperatures all over the world. Economically the order is very important for fishery including species which have the highest catch rate per year in the world. The order of Clupeiformes contains two suborders: the monotypic Denticipitoidei and the Clupeoidei with more than 400 species in five families. One of these families, the Pristigasteridae, is considered to be relatively basal in the phylogeny of Clupeiformes. Including the genus *Ilisha*, this family contains nine genera. However, Grande (1985) already considered the genus *Ilisha* as non-monophyletic, due to some character found in the species '*Ilisha*' *africana*. Recent, still unpublished, molecular data support the hypothesis, that '*Ilisha*' *africana* may not belong to the genus *Ilisha*, but shares only the external appearance. The scales of Clupeiformes are very diverse in size, shape and especially in the high number of ornamentations such as circuli, radii, and additional grooves. At least some of these characters may serve in phylogenetic analyses. In the present study we study and characterize the scales of the two pristigasterid subfamilies Pristigasterinae and Pelloninae. Then the scale characteristics of '*Ilisha*' *africana* were compared to the two subfamilies, to test if these characters can support or weaken the hypothesis of '*Ilisha*' *africana* not belonging to the genus *Ilisha*.



Main Meeting, FG Physiology
Oral Presentation

Impaired insulin signaling in response to ER stress in insulin producing cells

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Maintaining the homeostatic balance between the anabolism and catabolism is a major regulatory task that is achieved by hormonal systems such as the insulin signaling axis. Production and release of insulin from insulin producing cells is usually highly regulated in order to ensure constant blood sugar levels and to replenish a great variety of energy pools within the body. In humans, impairments of the insulin signaling system, either induced by reduced insulin production (T1D) or the inability of target organs to react appropriately to insulin (T2D), lead to diabetes, which developed into one of the most important diseases of industrialized countries. Here we show that induced activation of the endoplasmatic reticulum stress response (ER stress) within insulin producing cells induced phenotypic variations that resemble those observed in type 1 diabetes patients (T1D). The ER stress response is a universal cellular stress response to an overload of protein production in the ER. Using the fruit fly *Drosophila melanogaster* as a model, we could show that ectopic activation of different arms of the ER stress response in insulin producing cells only led to impaired insulin production and release, finally leading to enhanced glucose levels, reduced glucose tolerance and the reduced ability to store energy. Thus, this *Drosophila* model represents a valuable tool for the study of mechanisms underlying the development of diabetes.



Main Meeting, FG Evolutionary Biology
Oral Presentation

How it all (perhaps) began – insights into the origin of the coevolution between microbe management and insect sociality using *Drosophila*

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Along a gradient, ranging from small family groups to eusocial colonies, coevolution between social behaviours and mutualistic interactions with microbes seems to facilitate social complexity in insects and strengthen insect-microbe symbioses. However, we hardly understand how sociality and specific symbioses arise from an ancestral stage that lacks tight insect-microbe mutualisms and obvious social behaviours. Given the general assumption that parental care is a precursor of other social behaviours, we hypothesize that transmission of beneficial microbes during egg-laying represents a basic means by which (non-social) female insects could provide a non-genetic investment in their offspring. We propose a continuum of four phases describing the decoupling of various random effects on microbe transmission from those associated with reproductive behaviour; eventually, this leads to a more dedicated 'management' of beneficial microbes. By transmitting microscopic fungi (yeasts) to breeding sites, *Drosophila* fruit flies can provide a microbial 'start-up package' that sustainably support the developing larvae with food and protection from pathogenic microbes. Here we show that individual *Drosophila* females transmit more yeasts per patch visits when they lay eggs, yet the amount of yeasts transmitted is largely affected by additional factors, such as patch residence time. Our results meet the criteria of phase II of the proposed continuum of microbe-mediated parental care and suggest that the *Drosophila*-yeast interaction is a suitable model system to experimentally investigate the initial processes promoting mutualism-sociality feedbacks in insects.



Main Meeting, FG Evolutionary Biology
Oral Presentation

Does size matter? The evolution of highly exaggerated head humps in Midas cichlid fishes in the light of Zahavi's handicap-principle

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Highly exaggerated traits are of great interest because they evolved although imposing a major cost on their bearer. Zahavi's handicap-principle suggests that such traits evolve and spread through populations not albeit being a handicap, but exactly because they are one. These handicap-traits are used during communication to signal an individual's quality and must be costly to be reliable. For example, Midas cichlid fish develop a highly-exaggerated forehead swelling (hump) that has been predicted to increase mate attraction but also to impose severe swimming costs. However, this has not been empirically tested yet. We first explored if hump size contributes to inter- and intrasexual communication. In mate-choice experiments females showed a clear preference for males with large humps. Additionally, males with larger humps were more successful in securing territories when tested for dominance. Therefore, hump size provided a clear advantage when communicating with conspecifics of both sexes. We also found an associated swimming performance cost of humps. Males with larger humps required more fin-beats to hold position due to the additional drag imposed by the hump. Moreover, the larger a hump, the earlier its bearer came to exhaustion, probably due to the elevated energetic demand. This combination of increased energetic costs and decreased endurance especially aggravates behaviors that are highly important during territorial acquisition, defense and spawning. However, since males with exaggerated humps were still able to secure territories, hump size can be regarded as a proxy for male quality and represents a great example for Zahavi's handicap-principle.



Main Meeting, FG Physiology
Oral Presentation / Poster: Phy 2

Characterization of ABC transporters from the red flour beetle, *Tribolium castaneum*, involved in the elimination of diflubenzuron

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ATP-binding cassette (ABC) transporters are ubiquitous membrane proteins that translocate a wide range of physiological and xenobiotic substrates across membranes. In insects, they have been implicated in pesticide tolerance. The red flour beetle, *Tribolium castaneum*, is known to adapt readily to different classes of insecticides making it a suitable model for investigating insecticide resistance. The genome of this species harbors 73 ABC genes, which group into eight subfamilies ABCA-H. Subfamilies ABCA, ABCB, ABCC and ABCG contain genes that encode multidrug resistance proteins suggested to be involved in insecticide resistance. The aim of this study is to identify ABC transporters of *T. castaneum*, which mediate tolerance to insecticides, particularly to diflubenzuron inhibiting chitin biosynthesis. Treatment of mid-sized larvae with different ABC inhibitors resulted in an increased susceptibility to diflubenzuron suggesting that primarily genes of the ABCC subfamily, which is particularly large in *T. castaneum*, are involved in the elimination of this insecticide. Next, we determined the expression profiles of ABC genes from different subfamilies at different developmental stages and in different tissues. We found that some ABC genes had particularly high transcript levels in the midgut and the fat body. Then we analyzed transcript levels in response to diflubenzuron treatment and could identify several ABC genes from different subfamilies, which were upregulated in response to insecticide treatment. In summary, we provide evidence that multiple ABC transporters are involved in the elimination of diflubenzuron. However, we also obtained indications that other transporters like organic anion transporters are involved in this process.



Main Meeting, FG Neurobiology

Poster: NB 13

pERK as marker for neural activity after multimodal sensory stimulation in the weakly electric fish *Gnathonemus petersii*

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Neural activity induces certain biochemical events in neurons, which can be used to identify active neurons. One marker for visualizing neural activity is pERK, phosphorylated extracellular signal-related kinase. pERK plays a role during neural and synaptic plasticity, e.g. during learning and memory. Recent publications showed the successful use of pERK as an activity marker after sensory stimulation in zebrafish. We worked with the African weakly electric fish *Gnathonemus petersii*, which uses multiple sensory systems to perceive its environment, in particular its visual sense and active electrolocation. Primary visual sensory information is relayed to the optic tectum (OT) in the midbrain, which then projects to the valvula cerebelli and several other nuclei. The medullary electrosensory lateral line lobe (ELL) receives primary electrosensory input and conveys this information to the midbrain as well. Here, we tested whether in *G. petersii* the pERK method can be used to visualize neural activation in different brain areas after specific sensory stimulations. Three fish were kept in darkness for 24 hours, after which one individual was visually stimulated by illuminating it with a flash light. A second fish was exposed to an electrical short to stimulate its active electrolocation system. The third fish received no stimulation and served as a control. Immediately after stimulation, the brains were removed, sliced and pERK was visualized in the neurons by antibody staining. Brain sections were analysed based on pERK staining in the different brain regions, in particular in sensory brain areas of the visual and electrosensory pathways.



Main Meeting, FG Evolutionary Biology
Oral Presentation

The evolution of biting-chewing effectivity in non-holometabolan insects

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Insects show a plethora of different mandible shapes. It was advocated that these mandible shapes are mainly a function of different feeding habits, i.e. the ecological niche of a given taxon. We tested this hypothesis on a larger sampling of non-holometabolan biting-chewing insects in order to understand the interplay of mandible function, head biomechanics and phylogeny. Our results show that variation in mandible biting-chewing effectivity is regulated to a large extent by phylogenetic history and the configuration of the mandible joints rather than the food preference of a given taxon. Additionally, lineages with multiple mandibular joints such as primary wingless hexapods show a wider functional space occupation of mandibular effectivity than dicondylic insects (= silverfish+winged insects) and they evolved this variation at significantly different rates than Dicondylia. The occupation of a comparably narrow and stable functional performance space of dicondylic insects is surprising given the low effectivity values of this food uptake solution. Our results indicate that once functional dicondyly evolved, this biomechanical setup was stabilised due to phylogenetic effects.



Main Meeting, FG Evolutionary Biology
Oral Presentation

Selection on selfishness: The fitness of a selfish genetic element in different densities of wild house mice

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Life is conflict. Even within the highly cooperative individual genome, elements compete over transmission and some even manipulate the rules. For example, the t haplotype, a 40 Mb genomic variant in house mice, manipulates its transmission to offspring so that 90% instead of 50% will carry it (through male meiotic drive). However, it is much less frequent in natural populations than would be predicted based on this trait. The element carries recessive lethal mutations and male mice carrying this element perform poorly in sperm competition against other males. These two deleterious traits could explain the low frequency of this element in natural populations. However, these traits have such a strong negative fitness impact that it was unclear how the t haplotype could have survived for an estimated two million years. Our research suggests that the element manipulates the migration behaviour of its carrier, potentially to alleviate its low fitness in populations where the deleterious traits are most impactful. So far, this finding was based on simulations and correlational data from a long-term study population. To experimentally test this behavioural manipulation and the fitness differences of the t in different populations, we have setup artificial populations of genetically wild house mice. These populations differed in their initial population size and allowed the mice to emigrate from them. I will present insights into how the t haplotype, population density, and individual traits relate to variation in fitness and behaviour between house mice. This will aid our understanding of this interesting evolutionary conflict.



Main Meeting, FG Morphology

Poster: Morph 12

The prosomal endoskeleton and musculature in *Galeodes granti* (Solifugae)

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Solifugae are fast predators with a peculiar morphology of the locomotor system. With respect to the prosoma, this means that all coxae are immobilized and an endosternite is missing. In other arachnids, the endosternite generally serves as attachment site for the extrinsic musculature, which connects to the coxae of the walking legs. Both muscles groups are missing within the prosoma of Solifugae. Due to the immobilized coxae, the movement of the leg against the body is realized within the coxa-trochanter joint. The corresponding musculature therefore serves as (secondary) extrinsic musculature. Instead of the missing endosternite, Solifugae have a central endoskeleton, which is composed of dorsally elongated coxal apodemes. This endoskeletal system serves as attachment sites for muscles attaching to podomeres within the leg. We reinvestigated the complex prosomal morphology in *Galeodes granti* by conducting high-resolution micro-computed tomography. The 3-dimensional analysis aims at facilitating a better understanding of the complex morpho-functional interrelations of skeletal and muscular elements in the prosoma of Solifugae.



Main Meeting, FG Morphology
Oral Presentation

A morpho-functional comparison of antenniform legs in Pedipalpi

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Arthropodia are seen as key inventions having facilitated the evolutionary success of Arthropoda. The subdivisions in podomeres in combination with the segmental arrangement along the arthropod body are crucial aspects of their versatility. In association with tagmatization, arthropodia underwent large evolutionary changes thus enabling a variety of biological roles like swimming, prey capture or carrying sensory organs etc. With regard to the latter, antennae are the most specialized forms of appendages, which are only found in mandibulates, i.e. myriapods, crustaceans and hexapods. In chelicerates such specialized appendages are primarily missing. Nevertheless, within Arachnida several taxa evolved antenniform legs by transformation of the anterior-most walking leg. Most prominent example for well developed antenniform legs are the Pedipalpi (Amblypygi + Uropygi). Their antenniform legs are especially elongated, reduced in diameter and highly subdivided compared to walking legs. From a functional point of view, antenniform legs are characterized by a high motility. However, the reasons for this high motility remain uncertain as morphology of antenniform legs is sparsely studied. In our morpho-functional approach, we highlight joint morphology and the muscular arrangement of antenniform legs in representatives of Amblypygi and Uropygi. Using high-resolution micro-computed tomography and 3D-reconstruction we give detailed visualizations of leg morphology. The morphological comparison between these two groups reveals distinct morphological differences despite their proposed monophyly and the supposed homology of antenniform legs within Pedipalpi. Therefore, morphological differences will be discussed in the light of the two alternative evolutionary scenarios.



Main Meeting, FG Physiology
Oral Presentation

Calcium uptake from ingested exuviae in the terrestrial isopod *Porcellio scaber*

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The terrestrial isopod *Porcellio scaber* eats the anterior and posterior exuviae after each half moult of its biphasic moulting cycle. This suggests uptake of exuvial mineral by the hepatopancreas to minimize calcium loss. Using high-pressure frozen and freeze-substituted samples, we investigated ultrastructure, storage and transport of calcium within the B and S cells of the hepatopancreas, employing energy filtered TEM and electron probe microanalysis. We found: (1) Multivesicular bodies in the B and S cells of the hepatopancreas and numerous extracellular vesicles (exosomes) regardless of the moulting stage, which are not apparent in chemically fixed samples. (2) In lysosomal inclusion bodies containing copper and other metals (Prosi (1988) Cell Biology and Toxicology, 4, 81), the calcium and magnesium concentration decreases from inter- to postmoult. (3) Postmoult animals that have ingested both exuviae contain yet undescribed intracellular seams of calcium and phosphorus along apical and lateral plasma membranes of S-cells. Occasionally, extracellular calcium and phosphorus containing granules, about 70 nm in size, occur between cells and within the basal lamina. In intermoult animals such mineral seams and granules are less abundant and absent in control postmoult animals that have not consumed the exuviae. The results suggest that (1) calcium stored within inclusion bodies during intermoult is utilized for cuticle mineralisation in postmoult, that (2) calcium uptake from the ingested exuviae takes place across the apical plasma membrane of the S-cells and that (3) basolateral transport into the haemolymph occurs in form of calcium phosphate granules. Supported by the DFG ZI 368/11-1.



Main Meeting, FG Evolutionary Biology
Oral Presentation

Sex pheromone of *Urolepis rufipes* suggests saltational biosynthetic switch between fatty acid and isoprenoid metabolism within the *Nasonia* group

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Sex pheromones play a crucial role in the mate finding process of insects. The information has to be encoded in a species specific manner to prevent costly sexual interactions with unsuitable mates or even mismating with closely related species. Hence, sex pheromones typically diversify when new species evolve. Even when pheromones of closely related species differ considerably in their chemical composition, the compounds they use are typically biosynthetically related. The biosynthetic pathways of insect pheromones are often related to or variations of the conserved pathways leading to common metabolites of the primary and secondary metabolism. A saltational switch from one pathway to another, particularly in species that use the same type of pheromone glands, is the exception. Here we compare the male sex pheromones of the so-called “*Nasonia* group” consisting of the three genera *Nasonia*, *Trichomalopsis* and *Urolepis*. All *Nasonia* species and *T. sarcophagae*, the only *Trichomalopsis* species studied so far, produce fatty acid-derived hydroxylactones in their rectal vesicle. The pheromones are deposited on the ground and other substrates and attract virgin females. Chemical analyses and behavioral bioassays revealed that males of *U. rufipes* produce a sex pheromone in the same gland and use it in the same manner as the other species of the *Nasonia* group. Structure elucidation and stable isotope labelling experiments revealed, however, that the *U. rufipes* pheromone is an isoprenoid derived from the mevalonate pathway. This suggests a saltational biosynthetic switch between the fatty acid and isoprenoid metabolism in the *Nasonia* group.



Symposium: Phenotypic Plasticity - RESPONSES of Animals to
Environmental Change
Oral Presentation

Altered thyroid hormone levels and developmental temperature affect the capacity for physiological acclimation in tadpoles of *Rana temporaria* and *Xenopus laevis*

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Environmental variation induced by natural and anthropogenic processes and climate change treats species by causing environmental stress. Anuran larvae experiencing environmental stress may display altered thyroid hormone (TH) status with potential ramifications for metamorphic as well as physiological traits. Therefore, any capacity to adapt to environmental changes through plastic responses provides a key to determine species vulnerability to environmental variation. We investigated whether developmental temperature (Tdev), altered TH levels, and the interactive effect of both affect standard metabolic rate (SMR) and thermal tolerance in larvae of the Common frog (*Rana temporaria*) and the African clawed frog (*Xenopus laevis*) reared at five different temperatures. At metamorphosis, SMR was significantly affected by Tdev and TH status, intensified by the interaction effect of both. Larvae from warm temperatures revealed significantly higher SMRs indicating limited acclimation ability to temperature variation. Thermal limits were higher and thermal tolerance were narrower in tadpoles from warm temperatures but were not affected by altered TH levels. Thus, larvae may compensate for changes in Tdev as they increased their thermal limits at warmer developmental temperatures. Our results demonstrated that physiological traits in larvae of *X. laevis* and *R. temporaria* are strongly affected by increased TH levels and warmer temperatures. Altered TH levels and warmer Tdev due to global change may result in a reduced capacity for physiological plasticity. This is crucial since the energetic requirement at the onset of metamorphosis is known to determine metamorphic success and body condition and thus, individual fitness in later life stages.



Symposium: 5th Meeting of the Arthropod Neuroscience Network
Oral Presentation

Developmental and coding function of calcium channels in *Drosophila* motoneurons

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From fly to man voltage gated calcium channels (VGCCs) play fundamental roles in developing and mature neurons. These range from transcriptional regulation and growth cone turning during neuronal differentiation to amplification of synaptic input and vesicle release in mature neurons. Different functions depend on specific channel properties and sub-neuronal localization. We combine *Drosophila* genetics with electro- and optophysiology to unravel developmental and coding roles cacophony channels (Cav2 homolog) in motoneurons. In mature flight motoneurons cacophony mediates at least two different somatodendritic VGCCs, sustained high voltage activated and transient low voltage activated channels. In addition, cacophony encodes the presynaptic VGCC at the axon terminals. During differentiation dendritic VGCCs serve global growth control via transcriptional regulation, as well as local synaptotrophic functions. In the adult, these channels mediate postsynaptic amplification of excitatory input in dendrites and synaptic vesicle release in axon terminals. Toward identifying the mechanisms underlying different cacophony channel properties and their sub-neuronal localization we find that dendritic calcium channel targeting is augmented by $\alpha 2\delta 1$ -subunits, activation voltages are shifted by RNA editing, and CRISPR/Cas9 alternative exon removal hints to isoform specific channel properties. Therefore, specific combinations of RNA editing, differential splicing, and interaction with accessory subunits ensure cacophony channel functional diversity.



Symposium: Phenotypic Plasticity - RESPONSES of Animals to
Environmental Change

Poster: RESP 2

Resistance of crab larvae to abiotic stress: a multi- population comparison to explore phenotypic plasticity and local adaptations

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In most marine coastal organisms, the dynamics of pelagic larvae is essential for population persistence and dispersal. These early life history stages are typically more vulnerable than adults are, to fluctuating environmental conditions. With global ocean change, planktonic larvae are expected to experience increasing variations of key environmental parameters such as temperature, pH and salinity. An organism's capacity to tolerate current and future patterns of environmental fluctuation may vary across populations due to selection or developmental plastic responses to local environmental conditions. This project is aimed to evaluate the magnitude of inter-population variation in the tolerance to temperature and salinity of the shore crab *Carcinus maenas*, a species native to the European coast. Specifically, we will study responses from populations distributed across salinity gradients (Helgoland-German Bight versus Kiel-Baltic Sea) as well as thermal gradients (Bergen-North European Atlantic, Bangor-Irish Sea, Helgoland-North Sea, Cádiz-South European Atlantic). Larvae from each population are reared under several combinations of temperatures and salinities at the Marine station on Helgoland (Alfred Wegener Institute). We will measure larval survival and developmental rates, and also dry mass and elemental composition. Furthermore, we will quantify the level of mRNA and protein expression of various proteins related to ion regulation, oxidative stress and stress protection. The localization of proteins involved in ion regulation will be studied by immunohistochemistry. - Supported by DFG RTG 2010 RESPONSE. We thank Rebecca Meth, Alexander Kolb and Wladimir Escalante for help with rearing larvae, and Sophie Schindler and Dirk Brandis for contributing females from Kiel.



Main Meeting, FG Morphology
Oral Presentation

Enthesis deformation – comparison between a model and mechanical tests

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Fibrocartilaginous insertions of tendon into bone transfer loads between soft and hard tissues, and the angle between tendon and bone surface varies according to the angle of the bridged joint. From an adaptationist perspective, the insertional tissues are expected to (1) mitigate peak stresses occurring due to the abrupt change in tissue elastic behavior and to (2) homogenize spatial stress inhomogeneities that necessarily occur at extreme angles of force application. Based on the fibrous structure of entheses, a simplistic mechanical model was developed to predict entheses deformation. These predictions are compared to radiographic images of relaxed and loaded Achilles tendon entheses of mice [*Mus musculus*], acquired using synchrotron radiation-based micro-computed tomography. The model makes the following geometric assumptions: The tendon approaches the bone surface near tangentially and curves over a homogeneously convex bone surface for a certain arc length before it inserts into the hard tissues. According to the model, higher stress is expected to occur in the deep fibers of the entheses close to the convex bone surface, than in its superficial fibers. The deep fibrocartilage is expected to experience the highest compression. In contrast to the model, elongation is found to be nearly homogeneous among deep and superficial fibers of the entheses. Surprisingly, deformations in the unmineralized fibrocartilage are higher than in the tendon. We discuss whether hydrogel properties of the fibrocartilage are a possible explanation for the found deformation behavior.



Main Meeting, FG Evolutionary Biology
Oral Presentation

Location matters: Low-coverage exomewide sequencing reveals population divergence over extremely small spatial scales in a marine oligochaete worm

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Many marine interstitial invertebrate species appear to occur over large geographic ranges despite short lifespans and the lack of larval dispersal stages. Increasingly, molecular analyses have revealed that some of these morphospecies belong to cryptic species complexes. Geographic separation is a major driver of cryptic speciation, but the spatial scales at which reproductive isolation occurs and genetic divergence arises in marine invertebrates remain largely unknown. With the use of a recently developed low-coverage sequencing method, we show genetic divergence at a surprisingly small spatial scale in the marine oligochaete *Olavius algarvensis* from the island of Elba in the Mediterranean. Sequences of the nuclear 18S rRNA gene of *O. algarvensis* individuals collected around Elba were identical, while their mitochondrial cytochrome c oxidase I gene (COI) sequences varied within and between sites without any clear geographic separation. In contrast to these inconclusive single-gene analyses, our low-coverage exome sequencing of hundreds of *O. algarvensis* individuals revealed clear genetic divergence between sites as little as 5 km apart. Ancestry analyses based on individual admixture proportions also showed clear population stratification, indicating limited gene flow between neighboring sites. These results suggest that small-scale geographical separation acts as a strong reproductive barrier in *O. algarvensis*. With limited gene flow, microgeographic divergence may be further amplified through adaptation to the local environment. Our study raises the question whether the small-scale population divergence that we observed in *O. algarvensis* also occurs in other infaunal species, particularly those lacking effective dispersal mechanisms.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral Presentation

100 million years old insect larvae shed light on the ancestral morphology of Odonata (dragonflies and damselflies)

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The modern-day fauna is heavily dominated by insects, more precisely to a large degree by larval (and nymphal) stages of flying insects. Especially freshwater habitats are densely inhabited by aquatic insect larvae. Among these larvae, those of dragonflies and damselflies (Odonata) can be easily discriminated from others by the presence of a specialised lower lip (“Fangmaske”) and from each other based on distinct characters of their terminal end. Damselflies (Zygoptera) are characterised by three large caudal structures. These are generally interpreted as extensions (often incorrectly termed “appendages”) of the small tergite (epiproct) and the paired sternitic sclerotisations (paraprocts) of the 11th abdominal segment. These function as tracheal gills in most lineages. In dragonflies (Anisoptera) these three structures are smaller and more robust and in most species form an acute conical complex, the anal pyramid, which can be used for defense. We report here two relatively small insects in Cretaceous Burmese amber (100 million years old) that are unambiguously recognizable as larvae of Odonata as they possess the prominent raptorial mask that all dragon- and damselflies share. These larvae represent early instars and seem to differ from all known fossil and extant odonates (including *Epiophlebia* – “Anisozygoptera”) in the morphology of their posterior ends. They possess neither the specialised arrangement of damselfly larvae nor that of dragonfly larvae, but appear to retain a plesiomorphic morphology. With this, the fossils provide important character polarities for the reconstruction of the early differentiation within flying insects.



Main Meeting, FG Morphology

Poster: Morph 20

Does spinneret morphology in the spider *Argiope bruennichi* differ between developmental stages and populations?

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The spinning apparatus of spiders consists of the external spinnerets and the internal silk glands, which are essential for the production of silk. Each silk gland is associated with a spigot on the spinneret surface that release the silk. Spiders use their silk for different purposes (building webs, wrapping prey, dispersing via “ballooning”). The wasp spider *A. bruennichi* shows a palearctic distribution and is undergoing a northward range expansion. Spiderlings of this species can use ballooning for dispersal and are able to colonize new habitats. Since it has been shown that populations from three different European regions (Estonia, Southern France, Azores) strongly differ in ballooning propensity, we investigated, whether the behavioural differences are accompanied by morphological changes of the spinning apparatus in *A. bruennichi* spiderlings. For this aim, we performed ballooning experiments with freshly hatched spiderlings from Southern France, Estonia and the Azores, reared them to the next developmental stage and examined the spinning apparatus using scanning electron microscopy. Our first results showed no differences in spinneret morphology between non-ballooning and ballooning spiderlings from the same region nor between spiderlings from different regions. Previous ballooning experiments in other species revealed that the silk for ballooning is produced by aciniform and minor-ampullate silk glands and we want to investigate, whether *A. bruennichi* spiderlings use the same glands for ballooning. Furthermore, we found out, that the numbers of piriform and aciniform spigots increase during spiderling development, whereas the number of minor-ampullate, major-ampullate, aggregate and flaggeliform spigots remain unchanged in juvenile wasp spiders.



Main Meeting, FG Ecology

Poster: Ecol 6

Colonisation history of a fragmented *Bombina variegata* population: Genetic vs. capture-mark-recapture data

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Colonisation, dispersal and fragmentation history of a yellow-bellied toad (*Bombina variegata*) population inhabiting a former military training area is reconstructed using historical, molecular and recapture data. The “Schmidtenhöhe” near Koblenz, situated in Rhineland-Palatinate, Germany (ca. 700ha, 279m-338m a.s.l.), was a mixed pasture-woodland with a clay pit established during the late 19th century. From 1937-1992, most of the area has been used for military training, tanks shaped landscape and numerous ponds. Today, a small part of the area is still used in that manner; the rest consists of the clay pit, pasture land and a succession area. At these four localities (0.5-2.5km in between), capture-mark-recapture analysis (CMR, n=835) of *B. variegata* was conducted during reproductive seasons in 2016 and 2017. Photographs of the ventral pattern enabled to identify individuals using Wild-ID Software. Genotyping (10 microsatellite markers) of 100 individuals from the four breeding assemblages was conducted to test for genetic substructuring. Results of the CMR-analysis gave no evidence for exchange among localities, indicating isolated local populations. In contrast, microsatellite analysis did not show any genetic differentiation, suggesting a single panmictic population. Consequently, a colonisation of the Schmidtenhöhe by a small founder population, originating in the clay pit as only suitable habitat connected to the next stream (Lahn) by a cableway around 1900 is likely. We hypothesize dispersal via stepping stone biotopes created by tanks until the 1980ies and subsequent fragmentation of this initially panmictic population caused by succession in the post-military period, creating areas impermeable for dispersal.



Main Meeting, FG Behavioural Biology
Oral Presentation

The link between habitat preference and performance in pit-building predators

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Pit-building insects are sit-and-wait predators that construct pit-traps in loose soil to capture prey. Wormlion larvae are such predators, common in cities all over Israel under man-made shelters. Together with pit-building antlions, they present a fine example of convergent evolution. My goal was to examine which habitats wormlions prefer and whether they perform better in their preferred habitats. I first demonstrated that wormlions prefer dry over wet sand, deep over shallow sand and fine over coarse sand. I then examined whether such preferences match performance, i.e., whether wormlions construct larger pits and hunt more successfully in the preferred habitats. While wormlions' preference matched their performance regarding dry and deep sand, I could not detect any benefit of the wormlions' existing preference for fine sand. However, preference for fine sand was the strongest pattern detected not only in the lab but also in field observations, suggesting that other factors dictate this preference. Wormlion preference for specific habitats decreased with increasing conspecific density, as common in other systems. However, the effect of density interacted with the shape of the habitat, and was weaker in habitats that enabled wormlions to increase the distance to their nearest neighbor. Habitat shape is rarely tested in habitat selection experiments, but can interact with density to affect preference. In short, wormlions usually prefer habitats in which they can hunt prey more successfully. They also consider several habitat features, including their body size, when choosing a suitable habitat, leading to a complex procedure of habitat selection.



Main Meeting, FG Behavioural Biology
Oral Presentation

Linking personality, parasite-induced behavioural manipulation and immunity in two populations of three-spined sticklebacks (*Gasterosteus aculeatus*)

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Many parasites manipulate behaviors of their hosts to facilitate transmission to the next host. Accordingly animal behavioural types (personality) might change upon parasite infection. On the other hand, host infection probability might vary with behavioural type and certain personalities might be more prone to infection. We wanted to address these questions and used the infection of three-spined sticklebacks with the cestode *Schistocephalus solidus*. This parasite makes its stickleback host bolder, to facilitate its transmission to the final host, a fish eating bird. We used sticklebacks from an Icelandic origin with high and a German origin with low *S. solidus* infection pressure. We assessed behavioural responses of individual sticklebacks in the context of confinement stress, activity, aggression and boldness four times during the course of six months. We exposed the sticklebacks to *S. solidus* halfway through the experiment. After the last observation we assessed basic immune functions. If the *S. solidus* infection developed, sticklebacks from both origins developed higher boldness. Sticklebacks from Iceland were generally bolder and got infected less often with *S. solidus* than sticklebacks from Germany. In fact about one third of Icelandic sticklebacks even refused to eat copepods, and female Icelandic sticklebacks particularly avoided copepods harboring their sympatric *S. solidus*. Male Icelandic stickleback, which had ingested infected copepods, were more likely to defend the infection if they had high boldness and low aggression scores before the parasite exposure. Thus for Icelandic male sticklebacks we could predict future probability of becoming infected with *S. solidus* by their behavioural profile.



Symposium: Adaptations to Hematophagy in Blood-feeding Parasites
Oral Presentation

Blood digestion in the the reduviid bug *Triatoma infestans* and the human body louse *Pediculus humanus corporis* – A review

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Physiology of blood digestion triatomines and lice is completely different. Triatomines approach their hosts only for a short period of time to feed, take up an enormous amount of blood and digest very slowly. Lice spend their entire life cycle on the host, require frequent small blood meals and have a fast digestion. Triatomines have an acidic midgut lumen and digest blood via cysteine and/or aspartic proteinases and then aminopeptidases and carboxypeptidases [1]. In *Triatoma infestans*, cathepsin B- and cathepsin L-like activities in gut extracts are high at 5 and 10 days after feeding. One of the two cloned cathepsin B-like genes is expressed at low, constitutive levels in unfed and fed *T. infestans*. According to in situ hybridizations on the gut, cathepsin B mRNA is present in a distinct region at the anterior part of the midgut and patchy distributed in the posterior part of the midgut. Like the majority of hematophagous insects, lice use a range of alkaline digestive proteases, trypsin and aminopeptidases. The glutamyl-aminopeptidase gene is constitutively expressed after feeding. According to *in situ* hybridisations on whole guts, the aminopeptidase gene is expressed in the posterior part of the midgut. The trypsinogen gene is constitutively expressed in adults 2–24 h after the bloodmeal. Trypsin is activated by cleavage of chymotrypsin, a so far undescribed phenomenon in trypsin activation [2]. [1] Ribeiro et al. (2014) PLoS Negl. Trop. Dis. 8(1); [2] Schaub et al. (2012) Arthropods as vectors of emerging diseases. Springer, 255



Main Meeting, FG Morphology
Oral Presentation

Cross sectional properties of Sciurormorph femora and their relation to lifestyle and phylogeny

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Members of the Sciuromorpha (“squirrel-like” rodents) occupy a variety of habitats, ranging from plains to forests, and evolved different lifestyles according to these habitats. Within the group, arboreal and fossorial lifestyles independently evolved several times in parallel. Previous studies of several mammalian taxa documented that long bone cross-sectional properties (CSPs) reflect adaptations of the locomotor apparatus to the differing functional demands posed by diverse lifestyles. In order to gain insight into sciurormorph locomotor postcranial adaptation, we here tested how femoral CSPs are determined by the lifestyle (i.e., ecology) when the phylogenetic correlation among species and body mass are taken into account. In this study, 69 species of Sciuromorpha were categorized into four lifestyles, “fossorial”, “semi-fossorial”, “arboreal” and “aerial” according to foraging, nest-building and fleeing behaviour. High resolution computed tomography (CT) scans of the specimens’ femora were obtained. For each digitized bone, cross-sections in 5% increments were analysed using the freely available “BoneJ” plugin for “ImageJ”. The following parameters were obtained: i) Cross-sectional area (CSA), which determines the ability to withstand compression along the dorso-ventral axis; ii) the mediolateral second moment of area (SMA_{ml}), which determines the ability to withstand bending about the mediolateral axis; and iii) the craniocaudal second moment of area (SMA_{cc}), which determines the ability to withstand bending about the craniocaudal axis. Preliminary results suggest a mosaic pattern of femoral CSP evolution within the Sciuromorpha that only partly reflects adaptations to functional demands of specific lifestyles.



Main Meeting, FG Evolutionary Biology
Oral Presentation

A taxonomic renaissance in the narrow-mouthed frogs of Madagascar is opening a new model system to understand ecomorphological evolution in amphibians

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Two thirds of the 102 species of narrow-mouthed frogs in the Madagascar-endemic subfamily Cophylinae have been described in the last 20 years, with a dramatic increase in description rate in the last five years. The acceleration of taxonomic progress on this subfamily coincides with intensified fieldwork, growing museum reference collections and methodological advances (e.g. molecular barcoding, micro-computed tomography, and integrative taxonomy). As the known taxonomic gap is closing, patterns of evolution in form and ecology are emerging, such as repeated niche swapping and dramatic and repeated miniaturisation. Using phylogenomics paired with 'museomics', we are developing these frogs as a new model system for the study of the evolution of body size, skeletal morphology, and the repeated evolution of similar ecological niches.



Main Meeting, FG Neurobiology
Oral Presentation

Jaws with brains – Cognition in elasmobranchs

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While most people associate sharks with a whole bunch of action-filled attributes, being clever is not usually one of them. Over the last 10 years we have been assessing learning and memory functions in bamboo sharks (*Chiloscyllium griseum*) and freshwater stingrays (*Potamotrygon motoro*) on a behavioural and neuronal level. Most behavioural studies were performed as two-alternative forced choice experiments, in which the designated positive stimulus was reinforced by a food reward. Sharks and rays successfully master object recognition and categorization tasks and show visual perception and discrimination abilities of numerical information, illusionary contours, symmetry and movement, as well as spatial orientation and memory retention capabilities. Results of these studies indicate that the here assessed cognitive abilities in bamboo sharks and freshwater stingrays are as well developed as in other vertebrates, aiding them in activities such as food retrieval, predator avoidance, mate choice and habitat selection.



Main Meeting, FG Neurobiology*

Poster: NB 19

Modulation of neuronal processing and behavior due to uni- and multi-modal learning in the honeybee *Apis mellifera*

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During their daily foraging flights, honeybees have to process environmental stimuli of different modalities, as vision, e.g. colorful petals, or olfaction, e.g. flower bouquets. The integration of the optical and olfactory input takes place in the Mushroom Bodies (MB), brain centers for sensory integration and memory formation. Each MB is formed by 170,000 Kenyon cells (KC). At its input region (calyx), the MB is organized in different layers, each mainly innervated by one sensory modality. The KC converge in approximately 400 MB-Output Neurons (MBON), which form several clusters near the vertical lobe. Lately we characterized MBON response behaviors and found unimodal MBONs (responding to light or odor), multimodal MBONs (responding to both modalities) and MBONs that did not respond at all (Strube-Bloss and Rössler, 2018, R Soc Open Sci,5). In an ongoing project we perform extracellular multi-unit long-term recordings to examine the MBON activity in this area and to extract single unit activity. The recording position is visualized by immunohistochemical stainings that allow a subsequent 3D reconstruction of neuropils and the electrode position. Currently, we record MBONs before, during and after classical conditioning to a rewarded olfactory-visual compound stimulus and examine MBON response patterns and their changes separately in all experimental phases. Funding: This work is supported by DFG grand STR1334/3-1 to MSB

*Contribution also presented in: *Symposium: 5th Meeting of the Arthropod Neuroscience Network* (Poster: ANN 13)



Main Meeting, FG Morphology
Poster: Morph 25

Under pressure they're breaking - force resistance measurements in ptychoid oribatid mites

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The soil is a hazardous environment filled with a multitude of predators and to ensure survival herbivorous species evolved numerous defensive mechanisms. In oribatid mites, morphological defense begins with a thick (hardened) cuticle and ends with ptychoidity: a defensive mechanism enabling the animals to encapsulate themselves. The two super-families of Ptyctima, Euphthiracaroida and Phthiracaroida, are both ptychoid and have a hardened cuticle. Euphthiracaroida, however, additionally feature predator-repelling chemical secretions. Since Phthiracaroida evolved within the glandulate group of Oribatida (possessing chemical secretions), how can they afford to give up this additional protection? In earlier predation experiments, chemically disarmed specimens of Euphthiracaroida were easily cracked by the staphylinid beetle *Othius punctulatus*, whereas equally sized Phthiracaroida specimens survived. We thus hypothesize that the specific body form (and way of pressure build-up) of each group is key. To measure force resistance, we placed animals of both groups on a small test bench and constantly added weight to a container placed on top of the mites until they cracked. Surprisingly some Phthiracaroida could sustain more than 120 g – 200,000 times their body weight. And as expected, there is a significant difference between Euphthiracaroida and Phthiracaroida of the same size. The force needed to crack Euphthiracaroida would fall well into the bite force range known for predatory beetles, but they are still defended by chemistry, whereas Phthiracaroida could sustain forces higher than that. Thus, we can conclude, that Phthiracaroida could afford to give up chemical secretions simply because they simply don't need it anymore.



Main Meeting, FG Evolutionary Biology
Oral Presentation

Regulation, synteny and functional novelties in cephalopod genomes

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Cephalopods not only evolved complex body plans and behaviours, but are also fascinating in regard to their genome architecture and its regulation. While vertebrates enlarged their genomes through two whole genome duplications, cephalopods found a different way to evolve complexity. The action of a huge number of transposable elements drove cephalopod genomes to being largely rearranged, which in its course led to the loss of locally clustered gene order (synteny) that is otherwise conserved between most bilaterians. In the case of the Hawaiian bobtail squid *Euprymna scolopes* genes associated to the establishment of its symbiosis to the bioluminescent bacterium *Vibrio fischeri* and the specialized light organ that harbours it are largely expanded and show species-specific expression patterns. The accessory nidamental gland, another symbiotic organ of the squid, likely evolved by different means and expresses a large number of orphan genes. With this project we aim to decipher the regulatory mechanisms that evolved with cephalopod- and species-specific novelties. Using chromatin confirmation capture (Hi-C) and open chromatin profiling (ATAC-seq) we can identify functional co-regulated units in the squid genome. Preliminary results show that the structure of topologically associated domains (TADs) differs between novel, cephalopod-specific gene clusters and ancestral, bilaterian clusters. Moreover, local gene linkages are co-regulated in TADs. Further studies using both in-situs and RNA-seq will allow us to correlate novel, tissue-specific expression patterns with the emergence of novel regulatory architecture of the genome.



Main Meeting, FG Physiology
Oral Presentation

Metal responsive hemocyanin genes in the gastropod *Cantareus aspersus*?

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Hemocyanins are copper-containing respiratory proteins found in the hemolymph of many molluscs. In gastropods, hemocyanins are cylindrical, decameric macromolecules composed of polypeptide subunits of ~400 kDa. These decamers are assembled into didecamers or even multidecamers in most gastropod species investigated so far. It has been shown that in gastropods hemocyanin synthesis occurs in rhogocytes, a mollusc-specific cell type located in the connective tissue that also plays a significant role in heavy metal detoxification. In the present study, we wanted to address the question, whether exposure to elevated metal concentrations may have an influence on the mRNA expression of hemocyanin subunits. We have identified three different hemocyanin isoforms in the helioid gastropod *Cantareus aspersus*, namely α D, α N and β . In a quantitative Real-Time PCR approach, we were able to show that in the midgut gland of this species, β is expressed highest among the three different isoforms. Upon exposure of snails to a Cd or Cu enriched food source through 10 days, both metals were strongly accumulated in the midgut gland. After Cu exposure, the total mRNA expression level of α D increased significantly to about two-fold compared to control animals. On the other hand, expression levels of β mRNA significantly increased about two-fold after Cd exposure. No alteration of α N mRNA was detected under neither of the applied exposure conditions. The significance of these findings still remains elusive.



Main Meeting, FG Evolutionary Biology
Oral Presentation

Swimming performances in a sympatric species pair: Is body shape an adaptive trait driving sympatric speciation in neotropical Midas cichlid fishes?

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Sympatric speciation remains debated controversially in evolutionary biology and a natural model system to study this process is the Nicaraguan crater lakes' Midas cichlid fishes' radiation. Differences in species' body shapes are thought to be adaptations accompanying habitat divergence along a benthic – limnetic axis that was suggested to drive the speciation of Lake Apoyo's species pair *Amphilophus astorquii* and *A. zaliosus*. Here, we tested whether these two species perform differently in cruising swimming performance and maneuverability, and if observed variation in performance can be linked to morphology, as suggested. Our study confirms different cruising swimming abilities, with *A. zaliosus* being superior to *A. astorquii*, and that main morphological differences associate with these differences in performance. However, we find that with increasing swimming speed *A. zaliosus* has an increasing oxygen demand relative to *A. astorquii*, suggesting diverging metabolic rates or oxygen uptake capabilities during exercise. Surprisingly, these species did not perform differently in maneuverability (estimated by burst swimming), although *A. zaliosus* again consumed more oxygen. RNA-seq analyses of gill tissues at rest and after exercise revealed that the transcriptomes are more different between species during exercise, reflecting the different oxygen levels in the species' respective foraging grounds. We conclude that morphological and metabolic differences might both represent adaptations to the different habitats used by these fishes for feeding. Ecological, physiological, and genetic constraints may jointly facilitate the rapid accumulation of divergence despite gene flow, leading to speciation in sympatry as by-product of ecological adaptation and habitat specialization in Midas cichlids.



Main Meeting, FG Behavioural Biology

Poster: Behav 17

Behavioral observations and animal welfare implications of lab housing conditions in red foxes (*Vulpes vulpes*) in the frame of oral rabies vaccine testing

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Oral rabies vaccines for red foxes (*Vulpes vulpes*) need to be assessed for their efficacy prior to licensure. To this end, foxes are housed under experimental settings for a longer period of time, i.e. longer than 400 days. However, there are no defined housing conditions and little is known on the influence of long term housing and sampling on recipient behaviour and locomotor activity. The aim of this project therefore is to investigate short- and long-term effects on behaviour and locomotor patterns of 23 single housed captive red foxes after vaccination and subsequent challenge infection. Furthermore, we will assess physical and cognitive enrichments in order to improve animal welfare of captive foxes in such a laboratory setting. In a first step, video recordings of individuals (24 hours per day splitted in 15 min intervals) were evaluated against automated motion detection devices. While there was an overall agreement of 88% between the detected activity or inactivity, the agreement was nearly 100% for inactivity, whereas less than 35% of activity seen on video was correctly detected by motion detection devices. Other preliminary results indicate a slight change of the daily cycle of activity after sampling. Further data on the behavioural patterns over time of captive foxes and the effects in response to sampling routines and rabies challenge infection will be gathered and evaluated.



Main Meeting, FG Developmental Biology

Poster: Dev 2

Analyzing bioelectric phenomena during *Drosophila* oogenesis: Quantification of changes in membrane potential and intracellular pH by genetically encoded sensors expressed in epithelial cells

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Changes in the activities of ion transport mechanisms that result in transcellular bioelectric signals are known to play important roles during developmental and regenerative processes. In order to study their functions as well as cellular mechanisms, *Drosophila* oogenesis provides a suitable model system. In previous studies, we used various inhibitors and two fluorescent dyes to investigate the role of specific ion transport mechanisms in the generation of membrane potentials (V_{mem}) and intracellular pH (pH_i) in *Drosophila* ovarian follicles. The changes in V_{mem} and pH_i , as revealed by the fluorescent indicators DiBAC4(3) and 5-CFDA,AM, were now evaluated using the genetically encoded fluorescent V_{mem} sensor ArcLight and the genetically encoded pH_i sensor pHluorin, respectively. Both pHluorin and ArcLight, which consists of a voltage-sensing domain and a pHluorin-GFP variant, were cell-specifically activated by the Gal4-UAS-system. We found that both genetically encoded sensors reliably revealed changes of bioelectrical properties in the follicular epithelium resulting from the specific inhibition of various ion transport mechanisms. The results obtained with ArcLight-expressing follicle cells correspond to those observed with DiBAC4(3). For example, while the inhibition of sodium transporters and voltage-dependent calcium channels resulted in relatively hyperpolarized cells, the inhibition of cytochrome C oxidase resulted in relatively depolarized cells. Comparable effects were observed using pHluorin or 5-CFDA,AM. For instance, the inhibition of sodium-potassium-chloride cotransporters and ATP-sensitive potassium channels both resulted in relatively alkalized cells. In further experiments, we want to analyze the knock down of various ion transport mechanisms in the follicular epithelium using RNAi.



Main Meeting, FG Developmental Biology
Poster: Dev 11

The roles of the Wnt-antagonists Axin and Lrp4 during embryogenesis of the red flour beetle *Tribolium castaneum*

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In both vertebrates and invertebrates, the Wnt-signaling pathway is essential for numerous processes in embryogenesis and during adult life. Wnt activity is fine-tuned at various levels by the interplay of a number of Wnt-agonists (Wnt ligands, Frizzled-receptors, Lrp5/6 coreceptors) and Wnt-antagonists (among them Axin, Secreted frizzled and Lrp4) to define anterior–posterior polarity of the early embryo and specify cell fate in organogenesis. So far, the functional analysis of Wnt-pathway components in insects has concentrated on the roles of Wnt-agonists and on the Wnt-antagonist Axin. We depict here additional features of the Wnt-antagonist Axin in the flour beetle *Tribolium castaneum*. We show that Tc-axin is dynamically expressed throughout embryogenesis and confirm its essential role in head development. In addition, we describe an as yet undetected, more extreme Tc-axin Ai-phenotype, the ectopic formation of posterior abdominal segments in reverse polarity and a second hindgut at the anterior. For the first time, we describe here that an Lrp4 ortholog is involved in axis formation in an insect. The *Tribolium* Lrp4 ortholog is ubiquitously expressed throughout embryogenesis. Its downregulation via maternal RNAi results in the reduction of head structures but not in axis polarity reversal. Furthermore, segmentation is impaired and larvae develop with a severe gap-phenotype. We conclude that, as in vertebrates, Tc-lrp4 functions as a Wnt-inhibitor in *Tribolium* during various stages of embryogenesis. We discuss the role of both components as negative modulators of Wnt signaling in respect to axis formation and segmentation in *Tribolium*.



Main Meeting, FG Behavioural Biology

Poster: Behav 19

Dispersal in the spider *Argiope bruennichi*: do density and kinship matter?

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Dispersal is an important mechanism to maintain genetic diversity, escape unfavorable environments and colonize new habitats. There are many factors known to influence dispersal decisions, such as population density or relatedness between individuals. Different types of dispersal modes are employed by different animal groups. A mode of passive dispersal termed “ballooning” is used by many spider species. One or more silk threads are released as a sail to catch the wind and become airborne. To date, it is unclear whether this behaviour is influenced by population density and/or relatedness. Individuals might balloon to escape from overcrowding or to avoid competition between kin. We investigated the dispersal behaviour of spiderlings of the wasp spider *Argiope bruennichi* with regard to density and kin. To accomplish this, we conducted experiments with four different treatment groups: (1) low density, all kin; (2) high density, all kin; (3) low density, kin and non-kin and (4) high density, kin and non-kin. We found no consistent effect of density or relatedness on ballooning behavior of *A. bruennichi*. However, there were differences in activity and space use: spiders in high density treatments (2, 4) grouped together more strongly than those from low density treatments (1, 3). An analysis of picture series was used to estimate the activity in the rearing boxes. Groups consisting of only related spiderlings (1, 2) showed greater activity than groups from mixed kin treatments (3, 4). We conclude that density and kin have little influence on dispersal decisions in the wasp spider.



Main Meeting, FG Behavioural Biology
Poster: Behav 18

Plasticity of the start decisions of hunting archerfish

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Only 100 ms after prey falls ballistically, archerfish elicit a rapid start that is adjusted in turn angle and speed to where and when prey can later be caught on the water surface. The start decisions are accurately made based on initial speed, height and direction of prey movement and are appropriate for any combination of these variables and for any orientation of the responding fish. Moreover, in a newly developed setup the fish start in response to planar movement of items on an appropriate screen just as they would for real ballistically falling objects. This allowed us to explore if the start decisions somehow intrinsically 'assume' ballistic motion patterns. We challenged the fish with situations in which a systematic deflection of the path occurred, but only after the fish had already made their start decision. Expectedly, the fish initially aimed to the expected ballistic landing point and made large errors which they then had to correct later. However, the fish learned to adjust their start decisions so that they were now no longer appropriate for ballistic patterns of falling but for the occurrence of the later deflections. Surprisingly, this did not mean that the fish now no longer could handle ballistically falling objects and had to re-learn how to handle them: When we mimicked two types of objects, one that fell ballistically, the other with a later deflection, and presented the fish at random with the two types the fish readily made the appropriate decision as required.



Main Meeting, FG Morphology
Oral Presentation

The more they chew the more is lost: jaw kinematics, tooth wear and digestive physiology in equids

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Despite copious documentation of wear patterns of numerous vertebrates, the etiology of dental wear is not completely understood. Central questions are whether wear features can be attributed to food properties or chewing movements, and the interplay of wear, chewing efficiency and digestibility. In an 18-month feeding study with six Shetland ponies, we explored the impact of alfalfa chaff and grass hay on the geometry of the postcanine wear surface and mandible movements. After removing the ectoloph, we applied mesowear and surface texture analyses to periodically quantify macro- and microscopic wear, we quantified the chewing movements using marker-based 3D high-frequency cinematography (XROMM), and we measured the fecal particle size (FPS) as an indicator of chewing efficiency and the crude fiber and lignin contents as indicators of nutrient digestibility. Thus, we found a diet-specific tooth wear pattern. When feeding on alfalfa chaff, the occlusal surfaces renewed after 2-3 weeks, when feeding on grass hay, after 4-7 weeks. We found a higher chewing frequency for alfalfa chaff compared to grass hay, with smaller rotational antero-posterior but similar medio-lateral jaw movements. The degree of particle comminution was correlated with nutrient digestibility, and FPS decreased once the animals, given dental treatment, had regained their occlusal profile. Our study suggests that a decreased fiber digestibility is tolerated within physiological limits and fiber digestibility improves with increasing chewing efficiency. Tooth wear is clearly the result of food properties, while chewing movements vary chew by chew.



Main Meeting, FG Systematics, Biogeography and Diversity
Poster: Syst 9

Effective detection ranges of porpoise click loggers: an important step towards estimating abundance from click loggers

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The Baltic Sea subpopulation of harbour porpoises (*Phocoena phocoena*) is critically endangered with only 500 remaining individuals. Therefore, information about habitat use, migration behaviour and distribution are necessary to regulate anthropogenic stressors like noise, pollution or bycatch in order to facilitate conservation of the residual animals. The only resident whale in German waters can be observed by aerial surveys using line transects procedures with human observers or digital equipment. However, cost of these surveys limits their application and causes large variability in abundance estimation, due to low effort. Another possibility is using acoustic detections of odontocetes. Porpoises produce high frequency clicks at 130 kHz to echolocate during hunt and orientation. Click detectors (C-PODs, chelonia.co.uk) and hydrophones (SM3M, www.wildlifeacoustics.com and Soundtrap, www.oceaninstruments.co.nz) can be used for monitoring efforts. In contrast to aerial surveys they provide long-term data on movements and occurrence continuously over the years. They have an effective range of a few hundred meters, depending on the deployment area and hydrographic conditions. However, their effective detection ranges have not been measured in detail yet. Therefore, it is not possible to calculate densities or abundance from these devices. We tested three different systems in the field to compare effective detection radii. Preliminary data analysis suggests that the Soundtrap has an expanded effective detection range and therefore outperforms the C-POD and the SM3M. Effective detection ranges are one necessary step to estimate abundance from acoustic data and therefore will provide one crucial step towards an integrated assessment of porpoise abundance.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral Presentation

Impact and potential benefit of hybridization in teleost fishes

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Hybridization between different species or divergent populations is increasingly recognized as a common phenomenon in the animal kingdom. Discordant patterns (e.g., conflicting phylogenetic signal between different cell organelles or along the genome) and other strong indicators for gene flow play a much more prominent role in recent phylogenetic studies than they did in the past. Approaches like D- or F4- statistics or coalescent models allowing for further disentangling incomplete lineage sorting from hybridization increased our knowledge on the impact of hybridization on species diversification. Especially in species rich groups like teleost fishes hybridization is common, and in some groups suggested as potential driver of speciation through the generation of variation, which might then act as substrate for species diversification. Here, I will present data on riverine cichlid radiations (Cichlidae) that diverged along a steep riverine gradient in the lower Congo River within a complex network of recent and ancient gene flow and preliminary data on a young species assemblage of Ricefishes (Adrianichthyidae) from Sulawesi. I will highlight the great potential of natural as well as experimental hybrids for understanding the evolution of complex traits and the emergence of evolutionary innovations potentially preceding species diversification.



Main Meeting, FG Neurobiology*

Poster: NB 4

Tactile and visual orientation of the stick insect *Carausius morosus* during climbing

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As nocturnal animals, stick insects sample near-range information by active tactile exploration using their antennae. A previous study on the use of visual and tactile cues showed that antennectomy in stick insects strongly affects climbing efficiency, whereas blindfolding does not (Dürr et al., 2003, *Int.J.Robot.Res.*, 22:151-167). However, this study used a setup with very low luminance and visual contrast. Since it is known that stick insects reliably orient themselves towards visual landmarks (Kalmus, 1937, *Z.vergl.Physiol.*, 25:494-508), we wondered whether stick insects can exploit visual cues during climbing, provided that visual contrast and luminance were similar to experimental conditions of visual orientation experiments. To test this, we let animals climb an obstacle (height: 24 mm). On the front of the obstacle we placed one of three visual patterns (a horizontal or vertical black bar on white background, or a checkerboard). Stick insects were first tested intact and then grouped into two cohorts: In cohort 1 animals were tested with both antennae cut, then retested after blindfolding. In cohort 2, animals were tested blindfolded first, then with additional antennectomy. For each cohort and test session, we analysed the minimum distance to the obstacle, head orientation, and foot placement. Our expectation was that sighted animals with cut antennae would react similarly to intact animals, and differently from blindfolded, antennectomized animals. Our results proved both expectations wrong in that blindfolding had little or no effect on the parameters observed. We conclude that stick insects make little or no use of visual cues during climbing.

* Contribution also presented in: *Symposium: 5th Meeting of the Arthropod Neuroscience Network* (Poster: ANN 19)



Main Meeting, FG Morphology

Poster: Morph 4

Sustained function despite constant wear – structural and mechanical reinforcements of the tooth plates in chimaeroid fish (Holocephali)

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Chimaera (Holocephali) exhibit a peculiar unmineralized cartilaginous endoskeleton and unusual dentition, comprised of three pairs of large, permanent tooth plates that grow constantly at the base. Unlike shark and ray teeth, chimaeroid tooth plates are continually worn away at the occlusal surface, exposing inner tooth material, and yet they continue to be capable of withstanding the high stresses associated with eating hard foods. To understand the mechanisms that regulate growth and abrasion rates and tooth structural reinforcements, we investigate the design strategies of the tooth plates of *Chimaera monstrosa* by combining chemical and materials characterization techniques such as SEM, μ CT, EDX, Raman spectroscopy and nanoindentation. Our data show that the major portion of chimaera tooth plates is composed of a network of low mineralized trabecular dentine that is infilled and thickened during growth by successive mineral accretion from the base towards the tip. The trabecular dentine is reinforced with two distinct hypermineralized structures embedded in the trabecular dentine—long, slender rods (in adults, comprised of separate ovoid masses in series) and thickened, vascularized tritoral pads—both appearing to develop continuously. The hypermineralized features in the tooth plates appear to increase the hardness and abrasion resistance of the biting surface, and the rigidity of the tooth plates along their primary axis likely preventing catastrophic damage when feeding on hard prey. This first quantitative characterization of *Chimaera* tooth plate composition and properties enables hypotheses of structure-function relationships of the several mineralized tissues forming this unusual type of vertebrate dentition.



Main Meeting, FG Morphology
Oral Presentation

A peculiar vertebrate skeleton – an ultrastructural survey of the cartilaginous endoskeleton in sharks and rays

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The endoskeleton of elasmobranchs (sharks and rays) is comprised largely of unmineralized cartilage, differing fundamentally from the bony skeletons in the rest (~98%) of the vertebrates. Elasmobranch skeletons are further distinguished by a tessellated surface mineralization, a layer of minute, mineralized tiles called tesserae. This 'tessellation' has defined the elasmobranch group for more than 400 million years, yet data on tesserae development (e.g. if tesserae grow in size or number with age), ultrastructure and mechanical properties are scarce. We characterize tessellated cartilage from the stingray *Urolophus halleri* using a variety of high-resolution, 2D and 3D biological tissue and materials characterization techniques. We outline distinct growth phases for tesserae, define features of mineral density variation appearing to be related to growth and mechanics, and characterize tissue compositions allowing for comparison with bony skeletons. Despite large variation in tesseral shape and size, we observe commonalities in tesseral structural features among species of all major elasmobranch groups. This suggests universal principles of tesseral growth and form across elasmobranchs, and reveals that tessellated cartilage lacks some features believed to be associated with vertebrate cartilage mineralization (e.g. chondrocyte hypertrophy, type-X-collagen expression). Based on our data, we propose hypotheses of accretive growth and local inhibition that explain the tessellated pattern distinct to these fishes. Our results lay groundwork for our current modeling work, aimed not only at understanding the contribution of tesserae to whole skeleton mechanics (e.g. to localize regions of high/low reinforcement or flexibility), but also to understand fundamental concepts of tiled composites in general.



Main Meeting, FG Behavioural Biology
Oral Presentation

Immature mating and male mate choice in the cannibalistic brown widow spider *Latrodectus geometricus*

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Males of many spider species cohabit with immature females. Mating, however, has been considered to occur only after maturation of the female, which is connected to a suite of changes in morphology, physiology and behaviour. In the brown widow spider *Latrodectus geometricus*, however, mating with immature females is common and even results in successful production of offspring. These females moult to adult stage and then produce viable eggs fertilized by sperm from mating while immature. Mature females generally cannibalise males and thereby limit them to a single copulation. From the male perspective, immature mating is beneficial, because males that mate with immature females are not cannibalized and can achieve more than one mating. We conducted choice experiments in order to elucidate whether males are able to distinguish immature from mature females and whether they prefer to mate with immature, non-cannibalistic females. In contrast to our expectations, males showed no preference for immature females. One possible explanation is that there are no cues or signals indicating female developmental stage. However, there may also be costs arising from immature mating. These costs can vary from loss of sperm in the moulting process to disadvantages in sperm storage due to unfavourable storage conditions. Therefore, we compared the morphology of the copulatory organs of immature and mature females by means of micro-computed tomography as well as classical histology. We discuss our results in the light of male mate choice, and potential costs and benefits of the immature mating.



Main Meeting, FG Evolutionary Biology
Poster: EvoBio 7

Zooming in on range expansion: insights into the microbiome of the European wasp spider, *Argiope bruennichi*

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The European wasp spider, *Argiope bruennichi*, has expanded its range in the last century from warm, oceanic and Mediterranean climate zones into the continental climate zone of the Baltic States and Scandinavia. We are interested in factors contributing to this rapid range expansion. The speed of expansion outpaces the rate of warming due to climate change, meaning the species is not tracking its preferred climate, but rather adapting to novel climates. Animals evolved in a bacterial world, and it is well documented that endosymbiotic bacteria can have dramatic effects on arthropod demography, dispersal, and even thermal tolerance. Therefore, we employed 16S rRNA sequencing to compare the microbiome of a population of *A. bruennichi* in Germany to a population in Estonia, the range edge of the species. Additionally, we dissected the spiders before extraction to investigate if different tissue types have different microbial communities. Lastly, we sampled spiderlings to look for evidence of a vertically transmitted microbiome. We found a significant effect of region and tissue type on the microbial community, as well as a distinctive community within spiderlings. Intriguingly, the most abundant bacterium in all samples cannot be assigned taxonomically, with <85% identity to all named species. Data exploration shows that this bacterium has a homogenizing effect on the regional signal, and increases differentiation of tissue types. This result fits the expectation of an endosymbiont. Overall, we found differences in the microbiome of the populations, preliminary evidence of vertical transmission, and a candidate for a novel endosymbiont within spiders.



Symposium: Adaptations to Hematophagy in Blood-feeding Parasites
Oral Presentation

Haematophagous insects and their vector capacity for diverse pathogens

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Mosquitoes are important transmitters of pathogens with dramatic effects on human health. Alongside human disease agents such as Dengue and Chikungunya virus, zoonotic pathogens are transmitted by mosquitoes, such as the West Nile fever virus circulating endemically between mosquito and bird populations, and also mosquito-borne nematodes. Mosquito-borne pathogens have long been thought to mainly occur in the tropical habitats of their most common insect vectors, but recent developments showed that mosquitoes are capable of invading new habitats. In Europe, for example, established populations of *Aedes albopictus*, the Asian tiger mosquito, and of *Aedes japonicus*, the Asian bush mosquito, have been described. These container-breeding mosquito species can be transported long distances as desiccated eggs and can therefore potentially establish in new geographic locations. To assess the risk of vector-borne pathogen transmission, certain parameters such as vector capacity of certain mosquito species have to be considered. This value contains factors such as vector competence, host preference and biting behaviour and several other biometric data. We study the mosquito-borne nematodes *Dirofilaria immitis* and *Dirofilaria repens* as well as several mosquito-borne viruses as a model for vector-pathogen interactions including assessment of vector competence in local and invasive mosquito species through experimental infections under different temperature conditions. With continuing global changes, the challenges posed by insect vectors and transmitted pathogens are likely to grow rather than diminish. To assess the risk and develop control tools for these future challenges, extensive studies on the epidemiology and on fundamental vector-pathogen-interaction continue to be of utmost importance.



Symposium: 5th Meeting of the Arthropod Neuroscience Network
Oral Presentation

Distinct roles of parallel visual pathways

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Many animals use visual motion cues to navigate through the environment, find prey or escape predators. Long-standing theoretical models have made predictions about the computations that compare light signals across space and time to detect motion. Over the past years, core circuits that can implement such motion computations in *Drosophila* have been worked out. In the fly visual system, separate ON and OFF pathways exist that are specialized to detect the movement of light or dark edges. These pathways already split downstream of photoreceptors in the lamina, where L1 provides input to the ON pathway, and L2 and L3 are the major inputs to the OFF pathway. These input neurons synapse onto a set of second order interneurons which connect to the direction-selective in the ON and OFF pathways. We aimed to understand why the fly visual system utilizes parallel pathways to process OFF motion cues. We explored several possibilities, including redundant circuit mechanisms, differential speed tuning or processing of different features of the visual scene. Using *in vivo* two photon calcium imaging, we showed that the two OFF pathways exhibit distinct temporal filtering properties which provide fast and slow inputs to OFF edge motion detection. Strikingly, the two visual OFF pathways are furthermore sensitive to fundamentally different features of the visual scene, namely contrast and luminance. Using a variety of genetic tools we could show that the initial L2 and L3 response kinetics are established by cell-autonomous mechanisms, whereas a slow, luminance-sensitive component depends on circuit interactions. We are currently investigating the circuit implementation and biophysical mechanisms that shape the distinct properties of the two parallel OFF pathways. We will also report how their physiological specializations are differentially required for visually-guided behaviors. In summary, we aim to link biophysical mechanisms of individual cells, as well as organization in visual circuit organization to animal behavior.



Symposium: Adaptations to Hematophagy in Blood-feeding Parasites
Oral Presentation

Blood digestion in ticks

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Host blood that is majorly represented by hemoglobin and serum albumin represents the ultimate source of nutrients and energy for ticks. Interruption of these essential processes might thus lead to limited development and reproduction of ticks and thus offers a way to combat ticks and the diseases they transmit. Using the major European Lyme disease vector *Ixodes ricinus* as a model we have made a substantial progress in the determination of a gut-associated proteolytic machinery, which is based on a dynamic multienzyme network of cysteine and aspartic peptidases. Here we summarize the current knowledge on tick hematophagy and we highlight the analogies to other parasitic invertebrates - platyhelminthes, nematodes and triatomine insects. Uptake and processing of serum albumin and hemoglobin are further compared using ticks membrane fed on whole blood and pure serum. We employ microscopic comparisons to demonstrate the separate trafficking routes of albumin and hemoglobin in tick gut cells and we monitor individual digestive peptidases at the transcriptional (qPCR), protein (Western blot) and enzymatic activity (assays, activity based probes) levels. We further examine the relation of gut proteolytic network regulation and female fertilization as well as we propose specific roles of individual peptidase isoenzymes by RNAi, tick membrane feeding on blood with containing specific enzyme inhibitors and not least feeding of ticks on animals immunized with recombinantly expressed tick gut peptidases. Future research perspectives, including the potential for rational control of ticks and tick-transmitted diseases, are also discussed. Acknowledgements: GACR 17-14631S631S



Main Meeting, FG Morphology

Poster: Morph 16

On the secretory ultimate legs in *Haplophilus subterraneus* (Chilopoda, Geophilomorpha)

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In comparison to walking legs, the last pair of legs in Chilopoda – the ultimate legs – are particularly unique as no other leg in centipedes is of a comparable functional, morphological, and behavioral heterogeneity. They are never or only rarely used for locomotion, but hold a variety of different functions. One particular aspect of ultimate legs are sexually dimorphic characteristics found in many centipedes, most eye-catching in Geophilomorpha. Here, males possess substantially thickened ultimate legs featuring an intensive coverage with trichomes, sensilla, and other cuticular protuberances, indicating an elaborated sensory performance. We used histology, scanning- and transmission electron microscopy, as well as microCT analysis in order to explore characteristics of sexually dimorphic ultimate legs of *Haplophilus subterraneus* in terms of leg morphology, diversity of sensory organs, and glandular structures. In contrast to earlier descriptions, our analyses revealed that the majority of the 3,000 plus cuticular structures do not represent sensilla, but rather elongated epidermal glandular shafts similar to spigots. In addition, the entire leg is packed with glandular tissue. As it is known that male geophilomorphs produce a silk web for spermatophore transfer, one possible explanation is that the ultimate legs might be the silk production- and secretion site. Another hypothesis might be the secretion of a sex specific compound in order to attract potential mates. This is the first detailed account on centipede ultimate legs demonstrating the transformation from a former walking into a "secretory" leg.



Symposium: MorphoEvoDevo - A happy threesome?
Oral Presentation

The sensory pathways in arthropods – convergent evolutionary transformation or corollary of serial homology?

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Arthropod sensory appendages exhibit a high abundance of cuticular sensilla or specialized sensory organs which contribute to processing centers in the associated neuromere of the nervous system. As a general consequence, a pronounced input of sensory information is correlated with the shaping of elaborate and discrete primary processing neuropils. This plasticity cascade is mostly known and well documented for the mandibulate deutocerebrum that is characterized by the bipartite nature of how sensory information is processed. Innervated by axons of a variety of antennal sensilla of different modalities, it is typically composed of a glomerular domain as the first order processing area of chemosensory information, and at least one somatotopically organized domain in which mechanosensory information is processed. Apart from the antennae, arthropods feature other sensory appendages, like the first walking legs in mites or amblypygids, pectines and malleoli in scorpions and solifugids, or the last pair of legs in various centipedes. Accordingly, modality specific neuropilar domains are present in the associated ganglia of the ventral nerve cord that show a strong structural resemblance with the bipartite organization of the mandibulate deutocerebrum. We will present data on different sensory pathways in arthropods, and discuss issues of specific location and architecture of primary processing neuropils with regard to plasticity of ventral nerve cord ganglia, evolutionary transformations, serial homology versus morphological coherence, and constructional constraints.



Main Meeting, FG Physiology
Poster: Phy 6

The Down syndrome cell adhesion molecule (Dscam) in innate immunity: Proof of Dscam in phagocytic haemocytes of *Manduca sexta*

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The Down syndrome cell adhesion molecule (Dscam) is an alternatively spliced hypervariable member of the immunoglobulin-superfamily, which plays a dual role in neuronal differentiation and in insect innate immunity (Watson et al. (2005) *Science*, 309, 1874). Thus, Dscam is ubiquitously required for neuronal wiring and axon guidance in invertebrates and vertebrates (Schmucker et al. (2000) *Cell*, 101, 671; Fuerst et al. (2008) *Nature*, 451, 470), and acts as a pattern recognition receptor (PRR) in phagocytosis of bacteria *in vitro* in *Drosophila* and *Anopheles* (Dong et al. (2006) *PLoS Biology*, 4, 1137). However, the function of Dscam in phagocytosis still remains unclear *in vivo*, which is suggested to be more complex than *in vitro* since secreted protein isoforms of Dscam in the haemolymph of *Drosophila* are supposed to function as opsonins binding homophilic to membrane-bound Dscam on phagocytes (Watson et al. (2005)). Therefore, the aim of our study is to investigate the function of Dscam as a PRR in phagocytosis of bacteria *in vivo* in *Manduca sexta* larvae. Our recent findings reveal that Dscam is broadly expressed in the nervous system as well as in immune competent tissues of *M. sexta* larvae. In addition, a systemic infection with *E. coli* leads to a higher Dscam-mRNA level in haemocytes. But antibody labelling of haemocytes results in a differential pattern of Dscam on certain larval haemocytes. In summary, our data indicate that MsDscam pattern of haemocytes changes after bacterial challenge and might serve as a highly variable and therefore potent phagocytosis mediating factor.



Main Meeting, FG Ecology

Poster: Ecol 8

Will climate change threaten early life-history of the European shore crab *Carcinus maenas* Linnaeus 1758 (Brachyura: Portunidae)?

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Planktonic larvae of benthic invertebrates like the European shore crab *Carcinus maenas* are considered highly sensitive to environmental fluctuations. We wanted to gain insights into larval responses to climate driven environmental variables, more specifically, on how tolerance to low salinity is affected by increased temperatures. Larvae of *C. maenas* were reared at twelve different temperature and salinity combinations; larval performance as well as changes in morphological traits were measured. The interaction of temperature and salinity had strong effects on larval performance, but allowed for successful development to the megalopa stage in all treatment combinations. High temperature and low salinity generally caused increased mortality. Duration of development was shorter with increasing temperature while low salinity had delaying effects. The negative effects of low salinity were most distinct at extreme temperatures, while moderately high temperatures ameliorated the negative effects of low salinity on larval performance. Furthermore, the tested combinations of abiotic factors induced morphological changes mostly manifested in size with stressed larvae being smaller. In addition, all measured parameters showed significant differences among larvae hatched from different females of origin indicating strong maternal influence. Overall, slight increases in temperature, driven by climate change may enable larvae to tolerate exposure to moderately low salinity and, in combination with intra-population variability, potentially allows for population persistence. This study was supported by the DFG Research Training Group 2010 RESPONSE and DFG INST 292/119-1 FUGG, DFG INST 292/120-1 FUGG.



Symposium: MorphoEvoDevo - A happy threesome?
Oral Presentation

**Maybe a metamorphosis is not such a big thing?
Reconstructing the larval organogenesis of *Carcinus
maenas* (Decapoda: Brachyura)**

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The life history of brachyuran crustaceans includes pelagic larvae of the Zoea type, which develop through a series of molts from one instar to the next. The last zoeal stage molts to the semi-benthic Megalopa including dramatic changes in ecology, habitat, behavior, feeding, morphology, physiology. Contrary to e.g. holometabolous insects, these metamorphic transformations must occur highly sudden. Are these sudden and erratic metamorphic changes also mirrored in the animals' internal anatomy? In order to investigate ontogenetic changes, larvae of the European shore crab *Carcinus maenas* were analyzed using classical histological methods and microCT combined with 3D-reconstruction. Our results demonstrate that despite their different life styles and external morphology, brachyuran larvae are smaller versions of the adults when regarding their inner organization: the adult bauplan unfolds from organ anlagen compressed into miniature organisms. Our results also provide an overall picture of seemingly gradual organogenesis across larval development and the metamorphic molt, an insight that contrasts with the abrupt morphological changes during metamorphosis. This study was supported by the DFG Research Training Group 2010 RESPONSE and DFG INST 292/119-1 FUGG, DFG INST 292/120-1 FUGG.



Symposium: MorphoEvoDevo - A happy threesome? – Keynote Lecture
Oral Presentation

Some thoughts on threesomes, MorphoEvoDevo and happiness

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Morphology: The science of organismal forms.

Evolution: The theory that species change over time as a consequence of variation during self-replication followed by subsequent selection.

Development: All changes of an individual during its entire lifetime from fertilization (or initiation of budding) to death.

EvoDevo: A research area where molecular techniques are applied to elucidate developmental mechanisms. Often, results are interpreted against a molecular phylogenetic background.

Morphology is a descriptive science. This does not distinguish Morphology from other natural sciences because, as I argue, all natural sciences are descriptive. Morphology is intrinsically analytical and comparative. In an evolutionary framework, Morphology is also synthetic: it unites different aspects and approaches in its central evolutionary concept, homology. Homology might be the most debated single term in Morphology, yet it can be simply characterized as sameness due to common ancestry. Similarity is an indication of such sameness. Cladistics offers a recipe how to transparently resolve conflicts in competing homology hypotheses in complex data sets.

Morphology is not restricted to a specific technique, method, explanatory level, or life-history period. Therefore on a logical and historical basis it has precedence and EvoDevo in this view becomes a part of Morphology.

I present recent results on deuterostome and tunicate evolution from my laboratory in order to discuss contrasting perspectives derived from different conceptual research strategies.



Main Meeting, FG Developmental Biology
Poster: Dev 7

Stain alive: Illuminating embryology with a fluorescent dye

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4D-microscopy that is relying on time series of z-stacks of DIC micrographs is a fast and easy method to obtain comparative embryological data for evo-devo studies. However, the method is limited by light scattering and subsequent degradation of the images, especially in more advanced developmental stages. Therefore, fluorescent labeling that could be followed more easily through advanced developmental stages presents a convenient solution. Here, we present an easy method of in vivo staining of nuclei with the membrane permeable dye Hoechst 33342. By assessing the effect of the stain on development of the model organism *Platynereis dumerilii*, we are able to provide a critical dye-concentration that is non-toxic but well detectable with fluorescent imaging systems (confocal laser-scanning microscope, spinning-disc microscope). Extension of the staining protocol onto non-model organisms provides an innovative method to obtain comparative developmental data on the presently understudied metazoan lineages.



Symposium: 5th Meeting of the Arthropod Neuroscience Network
Oral Presentation

Genes, channels and neuromodulation: how neurons remain functional as temperature changes

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Neurons and networks are constantly challenged by changing internal and environmental conditions. Yet, despite substantial differences in network structure, cell physiology and ion channel complement, neuronal activity is surprisingly robust against perturbations. How this important trait is achieved is poorly understood because neuroscientists face the problem of deciphering mechanisms of robustness across diverse neurons and networks - a topic requiring knowledge of neuronal physiology and connectivity, ionic currents, channels, genes, and their modulation and evolution. I will use the example of temperature perturbations to demonstrate how small arthropod networks allow us to assess mechanisms of robustness and how recent advances in molecular and genetic approaches will further facilitate this. Temperature changes can disrupt the well-balanced ion flow across the cell membrane but neurons also possess compensatory mechanisms that counterbalance detrimental effects, to sustain neuronal function and animal survival. We show that extrinsic neuromodulation counterbalances temperature-induced changes in ion flow in pattern generating neurons of the crustacean stomatogastric ganglion, enabling a quick and flexible temperature compensation. Crustacean neurons and circuits can be traced across species with substantially diverse temperature tolerances allowing us to recognize evolutionarily conserved mechanisms, which will ultimately enable us to understand how animals survive in continuously changing environments.



Main Meeting, FG Evolutionary Biology
Oral Presentation

Population dynamics - an evolutionary demographic process

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Evolutionary change and population dynamics are driven by simple demographic events, the reproduction and survival of individuals. These processes have been intensively studied with a genetic and environmental (ecological) focus. However, heterogeneity in survival and survival of individuals is not only driven by genetics and the environment, but also by often not quantified stochastic events. In parameterizing population models using data from highly controlled single cell bacteria microfluidic experiments, I will show how large amounts of individual heterogeneity can be generated by such stochastic events. Such neutral heterogeneity influences ecological and evolutionary processes by slowing adaptive processes. I will end with discussing why we might be only at the beginning of understanding the evolution and maintenance of such neutral heterogeneity.



Main Meeting, FG Neurobiology
Oral Presentation

Complex integration of visual information: The secondary eye pathway of the jumping spider brain

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Jumping spiders are known for a large repertoire of complex behaviors. They perform multimodal courtship displays and possess extraordinary cognitive abilities including planning, learning and reversal learning. Their eyes, which display the highest-known spatial acuity among all terrestrial invertebrates, aid in generating such behaviors. Jumping spiders have one pair of large anterior median eyes (primary eyes) and three pairs of smaller secondary eyes, all of which serve a different, specific task. We explored structure, arrangement and connectivity of visual neuropils within the brain of the jumping spider *Marpissa muscosa* by means of paraffin-histology, microCT analysis and immunohistochemistry. We found that every eye supplies its own specific first order visual neuropil. While the primary eyes are also associated with an individual second order visual neuropil, the second order visual neuropils of the lateral eyes are fused. Furthermore, *M. muscosa* possesses an additional visual neuropil not found in other spiders. This neuropil receives input from the first order neuropils of all three pairs of secondary eyes and is connected to the mushroom body. The mushroom bodies are considered to be the higher order integration center for visual information in the spider brain. Our results show that the visual system in the brain of *M. muscosa* differs in number, arrangement and connectivity of neuropils from that of other spiders. We suggest that the unique visual capabilities of jumping spiders demand a similarly complex visual system within the brain that enables a fast integration of incoming information from the different eyes.



Symposium: 5th Meeting of the Arthropod Neuroscience Network
Oral Presentation

Neuroanatomy of Chelicerata – bringing the understudied into the spotlight

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Based on traditional external morphology and modern sequence information numerous and often contradictory hypotheses concerning arthropod phylogeny have been postulated. Independent data are needed to evaluate these hypotheses and supplement our knowledge of arthropod evolution. One promising approach deals with the morphology and development of the nervous system, a discipline termed neurophylogeny. Research has been focussing on insect and crustacean species, whereas myriapods and chelicerates have largely been ignored. Information on these taxa is thus of particular interest to assess existing neuroanatomical data and identify apomorphic versus plesiomorphic characters as well as presumptive evolutionary transformations. In this context, the distribution and projection patterns of serotonin-immunoreactive neurons are well suited for phylogenetic comparisons because of low numbers of these individually identifiable neurons and large amounts of data available for several arthropod taxa. Data on chelicerates are nonetheless extremely limited, but crucial for meaningful conclusions. Further, analyses of chemosensory processing in Chelicerata are also scarce, not least since Chelicerata do not possess antennae, as do Mandibulata, but evolved dedicated chemosensory organs in several other body regions. The conspicuous raquet organs of camel spiders are prominent examples here. They would appear as perfect model systems to investigate anatomical characters, which may be functional prerequisites for chemosensory systems, and thus may or may not provide phylogenetic information (e.g., glomerular organization of chemosensory neuropils). The presentation will give insights into the evolutionary morphology of individually identifiable neurons and chemosensory organs in Chelicerata and will highlight the neurophylogenetic approach to unravel nervous system evolution in arthropods.



Main Meeting, FG Neurobiology*

Poster: NB 6

Neuronal innervation of trunk appendages in Remipedia (Crustacea)

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Many aspects of the natural history of the enigmatic crustacean taxon Remipedia remain unresolved. However, the general morphology of the central nervous system as well as the distribution of serotonergic neurons have been investigated in detail, revealing a complex brain with affinities to Malacostraca and Hexapoda. The peripheral nervous system has not yet been investigated, by contrast. Interestingly, Remipedia are supposed to grow throughout life, adding functional body segments at a posterior growth zone. This assumption is supported by different developmental stages of limbs along the body. Since only few larvae have as yet been collected, study of limb development in the adult organism appears as a promising approach. To provide a basis for such studies, knowledge of the fully developed appendage innervation is crucial, allowing meaningful comparisons to the developing limbs near the posterior growth zone. I will describe the fully functional adult system in the context of limb innervation by using antisera against acetylated-alpha-tubulin, horseradish peroxidase, and glutamic acid decarboxylase (GAD, the synthesizing enzyme of GABA). In combination with lipophilic dye tracing of efferent fibers, GAD labeling reveals the presence and distribution of common inhibitory motoneurons in Remipedia. Common inhibitors have been studied in several representatives of Euarthropoda and have been shown to be suitable for phylogenetic comparison. In summary, I will characterise branching patterns of peripheral nerves as well as the distribution of common inhibitors in Remipedia, a key taxon for arthropod phylogeny.

*Contribution also presented in: *Symposium: 5th Meeting of the Arthropod Neuroscience Network* (Poster: ANN 20)



Main Meeting, FG Neurobiology
Oral Presentation

Neuromuscular transmitters in myriapods

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The neuromuscular junction is the chemical synapse where motor neurons communicate with skeletal muscle fibers. Whereas vertebrates and many invertebrates use acetylcholine as neuromuscular transmitter, in those arthropods examined up to now, glutamate and GABA are used instead. With respect to taxon sampling in a phylogenetic context, there is, however, only a limited amount of data available, focusing mainly on crustaceans and insects, and neglecting other arthropod groups. Here we investigate the neurotransmitter equipment of neuromuscular synapses of myriapods, using immunofluorescence and histochemical staining. Glutamate and GABA could be found colocalised with synapsin in synaptic boutons of body wall and leg muscles of the chilopod *Lithobius*. Acetylcholinesterase activity as a marker for cholinergic synapses was found abundantly in the central nervous system and also in some peripheral nerves, but not at neuromuscular junctions. Furthermore, a large number of leg mechanosensory neurons displayed GABA-immunofluorescence and was also labeled with an antiserum against the GABA-synthesizing enzyme, glutamate decarboxylase. In diplopods (*Julus scandinavicus*, *Polydesmus angustus*) however, only glutamate, but not GABA was colocalized on body wall and skeletal muscles. Our data indicate that glutamate and GABA are likely neurotransmitters at neuromuscular junctions, whereas acetylcholine is very unlikely to play a role here. This is in line with the concept of glutamate as excitatory and GABA as the main inhibitory neuromuscular transmitters in arthropods. Furthermore, we have localized GABA in arthropod mechanosensory neurons, indicating the possibility that neurotransmitter equipment in arthropod sensory systems may be more diverse than hitherto assumed.



Main Meeting, FG Behavioural Biology

Poster: Behav 20

Righty or Lefty: About the consistency of lateralized behavior across time and context in mice

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Lateralized behavior is not unique to humans. In the last decades, numerous studies detected lateral biases in various vertebrate and invertebrate species. Food-reaching tasks are the most widely used method for assessing behavioral asymmetries in forelimb use in rodents. However, lateralization of spontaneous behaviors has been largely neglected. This study investigates the consistency of the direction and strength of a set of spontaneous lateralized behaviors in two strains of mice. Paw and/or body-side preferences of male and female CD-1 and C57BL/6 mice are observed during a traditionally used food-reaching task and during spontaneous grid-climbing, barrier-climbing and self-grooming. Additionally, to test for temporal consistency, mice are re-observed five weeks later. We assume that mice show consistent lateral biases across the four behavioral observations. Presumed that mice show paw and/or body-side preferences, we hypothesize the direction and strength of lateral biases to be consistent over time. First pilot results reveal paw and/or body-side preferences in all behavioral observations. Furthermore, lateral biases are consistent over time in at least two of the above mentioned behaviors.



Main Meeting, FG Behavioural Biology
Oral Presentation

The gentlemen's club: Vocal communication in male African elephants

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The prevailing theory about male African elephants (*Loxodonta africana*) was that, once sexually mature, males are solitary and mainly targeted at finding oestrous females. While this might be true during the competitive state of 'musth' (a condition characterized by increased aggressive behaviour and elevated androgen levels), male elephants generally are companionable animals exhibiting social relationships and long-distance communication. Our current results on male vocal behavior reveal that similar to females living in matriarchal family groups, individuality and context is transferred via bull vocalizations and that acoustic cues to size are particularly pronounced. Further, male elephants have a distinct network of vocal recognition discriminating and preferentially moving towards the vocalizations of unfamiliar females. Males might use acoustic cues to assess mating opportunities, which may involve selection to identify individuals or kin in order to avoid inbreeding. Social knowledge, companionship, hierarchy, reproductive competition and the need to communicate over long distances are the aspects that drive male elephant vocal behavior. Examples of vocal learning and sound invention (in both, African and Asian elephants) that occur particularly often in male individuals further highlight their extraordinary vocal plasticity and complexity. By increasing our knowledge on male vocal abilities we might finally achieve a more complete picture of elephant vocal behavior and how it relates to the specific life history of these iconic species.



Symposium: 5th Meeting of the Arthropod Neuroscience Network
Oral Presentation

The apical brain enigma

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Evolutionary stability extending through over half a billion years is suggested by two cardinal centers in the arthropod forebrain, the central complex and mushroom bodies, the neuroanatomical divergences of which correlate to the times of origin of the five major arthropod lineages originating during the onset of the Cambrian. An even earlier origin for these centers is suggested by observations of extant lophotrochozoans, particularly Annelida and Platyhelminthes, both revealing structural and molecular homologues of the central complex and mushroom bodies in their apical brains. Developmental, genetic, and functional studies additionally provide evidence that in modern craniates the basal ganglia and hippocampal formation share numerous characters with the arthropod central complex and mushroom bodies. Because these lines of evidence suggest their genealogical correspondence across Lophotrochozoa, Deuterostomia and Ecdysozoa, it is plausible that these centers evolved early in animal evolution independently of the later convergent evolution of body segments. Although basal ganglia and hippocampus, and the central complex and mushroom bodies, are located in corresponding vertebrate and arthropod neuromeres that require homologous homeotic gene expression for their development, these centers themselves need not be considered as segment-related. The more plausible suggestion, that they are ancestrally asegmental, explains their presence in asegmental brains and brains that are segmentally organized. The prediction is that circuits that define the central complex and mushroom bodies, should occur in asegmental cycloneuralians and asegmental spiralian, as well as in the most basal Arthropoda. This is Tardigrada, for which there is accumulating evidence for a cycloneuralian-like asegmental brain. Such findings would add support to the proposition that two circuits, one responsible for action selection and pathfinding, the other for associative memory of place and valence, were present in the first exploratory bilaterians. The relatively abrupt switch from simple to goal-directed foraging and interactive behaviors evidenced by trace bilaterian fossils in the late Ediacaran further supports to this hypothesis.



Main Meeting, FG Neurobiology
Oral Presentation

Olfactory-visual integration and reward association in mushroom body output neurons

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Brains are fascinating miracles with a multitude of adaptations across the animal kingdom. They receive a tangle of multi-modal input and hold the capacity to simultaneously select adequate stimuli while ignoring others. The resulting percept reflects a multi-modal construct rather than the neural representation of a single modality. Multi-modal integration involves convergence of different sensory pathways at a higher brain level. The bee's mushroom body (MB) represents such an integration center. Its ~170.000 Kenyon Cells are organized in layers each receiving input from a different modality. MB output is conveyed to ~400 MB output neurons (MBON), which we record from on a reliable basis. We characterized olfactory, visual, as well as olfactory-visual (OV) induced activity in the same MBONs. We can show that the layered input of the MB is conserved in a subpopulation of MBONs responding to either odors or light stimulation, whereas a substantial proportion of MBONs was sensitive to both modalities and thus integrated OV information across MB input layers. Another subpopulation of MBONs did not respond to any of the presented stimuli. Previously we showed that such units become recruited after a classical conditioning experiment. We therefore propose that reward association to an OV compound stimulus may recruit initially non sensitive MBONs which will encode the OV-reward association during memory retention. Funding: This work is supported by DFG grand STR1334/3-1 to MSB.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral Presentation

What is a catshark? On the taxonomy and systematics of Mesozoic Carcharhiniformes (Elasmobranchii)

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Elasmobranchii forms a highly diversified monophyletic group of marine vertebrates comprising all living sharks and rays, as well as their fossil relatives, which first appeared in the Early Permian (~297 Ma), if not earlier. Within crown-group Elasmobranchii, two major shark groups, Galeomorphii and Squalomorphii, are repeatedly supported by different published morphological and molecular studies, and with more than 280 recognized extant species, the galeomorph order Carcharhiniformes (ground sharks) constitutes the most speciose clade of living elasmobranchs. The oldest known fossil records of Carcharhiniformes date back to the Middle Jurassic (~167 Ma) and these sharks seemingly diversified during the Cretaceous onwards to the Cenozoic, where most of the more modern forms became abundant in the fossil record (i.e., Carcharhinidae, Proscyllidae, Hemigalidae, Sphyrnidae). The great majority of described Mesozoic carcharhiniforms, which are in fact based on isolated teeth only, have been attributed to Scyliorhinidae (catsharks) due to close dental similarities to extant forms traditionally kept within this family. However, controversial issues concerning the taxonomic content of Scyliorhinidae and its longevity still prevail, particularly in the light of recently published molecular phylogenies, where Scyliorhinidae was repeatedly found to represent a paraphyletic assemblage, thus rendering the reception of fossil carcharhiniforms and their familial affinities difficult. We present a new carcharhiniform shark from the Late Cretaceous (~97 Ma) of Germany, which is represented by two partial skeletons with dentitions, and discuss its familial placement within the framework of recently proposed molecular phylogenies of Carcharhiniformes, providing new insights into the taxonomy and systematics of Mesozoic elasmobranchs.



Symposium: Adaptations to Hematophagy in Blood-feeding Parasites
Oral Presentation

Yellow-related proteins from sand fly saliva act as binders of biogenic amines

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Yellow-related proteins (YRPs) are a family of proteins present only in insects. In each sand fly species, 1-5 YRPs with molecular weight in range of 41-46 kDa were described. In sand fly saliva, these proteins are supposed to play a role in blood-feeding, as they act as binders of host pro-inflammatory and pro-haemostatic biogenic amines, such as serotonin, histamine and catecholamines. Previously, this binding was experimentally verified only for *Lutzomyia longipalpis*. Here, we demonstrate by homology modelling that all 37 sand fly salivary YRPs known up to date (originating from 15 species) share similar folding of six-bladed beta-propeller structure with a tunnel connecting the amine-binding site with the outer surface. To experimentally confirm binding of different amines in genus *Phlebotomus*, we employed the microscale thermophoresis method. High pure salivary YRPs (OriYRP and PerYRP) of two closely related species of *Larrousius* subgenus (*P. orientalis* and *P. perniciosus*) were prepared in recombinant form and used for quantification of binding affinity with various amines. While both proteins were shown as strong binders of serotonin and poor binders of histamine, only OriYRP strongly binds also dopamine, moderately binds norepinephrine and octopamine and poorly binds epinephrine. Binding properties of OriYRP correspond to the ones previously shown for LJM11 YRP from *L. longipalpis*. In competitive assay, however, OriYRP was shown to bind amines on a first-come, first-served basis, independently of their binding affinity. Since both *P. orientalis* and *P. perniciosus* are important vectors of *Leishmania* parasites, these findings might contribute to better understanding of parasite-host-vector interactions.



Main Meeting, FG Neurobiology
Oral Presentation

How insects find food in turbulent odor environments

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Insects rely on their sense of smell to find food. To find a food source, an insect needs to separate odorants from different sources. This is because odorants distribute in turbulent plumes and plumes of different sources intermingle. I will show that insects can exploit the fine-scale temporal differences between odor plumes from different sources to separate them (similar as we use short differences in sound arrival to separate sound sources). These fast smelling capabilities imply a rapid neural coding mechanism for odors. Because the speed at which sensory systems can encode stimuli depends on the temporal precision of stimulus-evoked spikes, we probed the temporal precision of olfactory receptor neurons in *Drosophila*. Olfactory receptor neurons responded with first spike latencies (time between odorant arrival and first spike) as short as 3 ms and with a standard deviation (jitter) well below 1 ms. Such a high spike timing precision is comparable to the precision of insect photoreceptor cells and auditory receptor cells. Using a neural network model of the insect olfactory system we demonstrate the plausibility of a rapid, spike timing code for odors, which could explain insects' rapid processing of temporal stimuli when encountering turbulent odor plumes.



Main Meeting, FG Developmental Biology
Oral Presentation

Understanding cellular mechanisms driving skull morphogenesis through *ex vivo* imaging

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As an organ's physiology and function are often linked to its shape; understanding how tissue shape is generated is, therefore, essential and a core question in developmental biology. A common feature in shape generation, or morphogenesis, is anisotropic growth, where tissues do not grow equally in all directions, however, the cellular and physical cues that drive anisotropy in developing tissues are poorly understood. Amongst the simplest tissue shapes are sheets which can be derived either from epithelia or mesenchyme. While epithelial sheets have been well studied, shape generation in mesenchymal sheets has been entirely overlooked. Such sheets include the intramembranous bones of the skull which are indispensable for human life. The frontal bone is an example of one such understudied skeletal element that is particularly intriguing as it undergoes anisotropic expansion from the base of the brain to the apex of the head. To address the cellular mechanisms that drive expansion of the frontal bones, we developed a novel live imaging system for performing quantitative *ex vivo* analyses of early skull growth. We find that oriented cell division, spatiotemporally controlled progressive differentiation and possibly tissue stiffness cooperate to drive the collective movement of osteoblasts during anisotropic skull expansion. Our *ex vivo* imaging system provides insights into mechanisms of morphogenesis in a mesenchymal-derived, sheet-shaped tissue.



Symposium: MorphoEvoDevo - A happy threesome?

Oral Presentation

Supraneurals – What are they and what can we learn from them?

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“Supraneural” is a well-established term in fish morphology. It describes bony or cartilaginous structures in the median septum between head and dorsal fin in actinopterygians and dipnoans. However, its history and origin is complicated. Goodrich first mentioned the term in 1930 characterizing free pieces of the “neural spines” (not to be confused with the “true neural spines found in amniotes and Amphibia”) above the neural arches. The elements, which we define as supraneurals, have been termed “radials” in *Amia* by Goodrich, implying a homology to the dorsal fin pterygiophores. Later, Eaton (1945) interpreted these “radials” as supraneurals while Smith & Bailey (1961) proposed that supraneurals are homologues to pterygiophores, naming them “predorsals”. Today the term “predorsals” is outdated and again replaced with “supraneurals”. Similarly to the back and forth concerning the name of the structures between the head and the dorsal fin, their origin and homology still remains unclear. We aim to unravel this problem, to find out their ontogenetic origin as well as their evolutionary history. In a first attempt, we look at the distribution and pattern of supraneurals in lower teleostean fishes. Especially within the Otomorpha, there is a consistent pattern as well as an evolutionary trend. This is particularly helpful in context with new phylogenetic hypothesis placing the Alepocephaliformes inside the Otomorpha. Such a placement, based on molecular data, was problematic to substantiate with the available morphological data. However, supraneural patterns offer a morphological clue on the phylogenetic position of alepocephaliforms and other lower teleostean taxa.



Main Meeting Keynote Lectures
Oral Presentation

Biodiversity in the Anthropocene: a story of biological gains as well as losses

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All ecological and evolutionary processes are dynamic: the birth, death and movement of individuals, the changing distributions of species and composition of biological assemblages in space and time, through to evolutionary adaptation and diversification. These dynamic events have always generated a kaleidoscope of biological diversity across our planet, particularly during periods when the physical environment was changing. Then humans evolved, natural event for sure, but one with surprising consequences. The resultant changes to the world's ecosystems, the distributions of species, the atmosphere, and the climate could not have been imagined. In this talk, I will discuss how two processes are generating changing biological assemblages, climate change and biological invasions. Whilst both are clearly negative in some situations (e.g. local endemics threatened by climate change, isolated island endemics unable to survive in the presence of continental-origin species), the perhaps surprising result is regional diversity is increasing in many parts of the world. Human-altered ecosystems contain different sets of species, but not always fewer. Even more surprising, new hybrid and other species are coming into existence because humans. This Anthropocene realisation that humans are generators as well as destroyers of diversity requires a reappraisal of the relationship between humans and nature. Humans are part of nature and it is as legitimate for us to facilitate novel biological diversity as it is for us to try to save the old.



Main Meeting, FG Evolutionary Biology
Oral Presentation

Effects of genetic relatedness on intra- and inter-sexual selection in a cichlid fish

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Kin selection theory (inclusive fitness theory) predicts that conflicts are reduced, and cooperation is increased among genetic relatives. The role of relatedness has been generally recognised for its importance of explaining the evolution of animal social behaviour and group living. However, the impact of relatedness on sexual selection is less well studied although conflicts during intra- as well as inter-sexual interactions are assumed to be ubiquitously present. Here, we examined the impact of relatedness on sexual selection in *Pelvicachromis taeniatus*, a West African cichlid fish with mutual mate choice and biparental brood care. Previous studies showed that this species prefers kin as mating partner (active inbreeding) and suggest this behaviour to be adaptive. Although in this species kin can be recognised alone by olfactory cues, visual cues may play a role as well. We present the results of a series of experiments in which we examined the effects of relatedness on reproductive behaviour in different sexual selection contexts, including male-male and female-female competition, mate choice and within-pair courtship and aggression. To assess the importance of the different sensory modalities for kin recognition, we focus on the relevance of visual cues for kin-mating preferences.



Main Meeting, FG Evolutionary Biology
Oral Presentation

Phylogeny and life-history evolution of Sabellidae (Annelida)

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Sabellidae are tube-dwelling polychaete worms, often with a colorful radiolar crown giving them the common name feather-duster worms. This charismatic group of marine invertebrates displays a large variety of life-history strategies, making their biology fascinating to study. However, the phylogeny of sabellids is yet to be resolved. Molecular phylogenies of Sabellidae show significantly different topologies to the morphology-based phylogeny, and the relationships between the internal sabellid lineages were only partially resolved. Herein we present the results of our phylogenomic analyses using 17 new and 2 previously published transcriptomes spanning the diversity of Sabellidae. The transcriptome assemblies were translated into amino-acid sequences by longest open reading frame. All of the translated transcriptomes were run through the Agalma pipeline to find homologous sequences across the species. The data was concatenated using amino acid sequences, as well as DNA sequences. Additionally, the data was analyzed using ASTRAL for a gene tree analysis. The resulting tree topologies were highly supported and congruent regardless of the method used. This new and robust sabellid phylogeny will not only allow the necessary taxonomic revision of this taxon, but will also provide a backbone to explore the evolution of the diverse life-history strategies and morphological characters within Sabellidae.



Symposium: 5th Meeting of the Arthropod Neuroscience Network
Oral Presentation

Activity dependent adult neurogenesis in the mushroom bodies of the red flour beetle (*Tribolium castaneum*)

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With its fully annotated genome, the susceptibility for genetic tools and its relative longevity (up to 2-3 years), *T. castaneum* is ideally suited to study the development and plasticity of the nervous system. In the current study, we focus on cell proliferation in the adult mushroom bodies (MB). To visualize cell proliferation in adult *T. castaneum* MB, we successfully combined the 5-ethyl-2'-deoxyuridine (EdU) technique with immunohistochemistry against the glia-cell marker reversed-polarity and the use of transgenic lines expressing neuron-specific markers. We reliably labeled the progenies of the adult persisting MB neuroblasts, determined their identity and counted the newborn Kenyon cells within the first week after adult eclosion to determine the proliferation rate. In several studies it was proposed that newborn neurons of MBs may play a role during olfactory processing and learning. To address the question whether adult proliferation of Kenyon cells depends on olfactory input, we used two approaches. First, we enriched the environment of group-reared beetles during their adult life with the food related odor cis-3-hexenol or the beetle aggregation pheromone 4,8-dimethyldecenal (DMD). Secondly, we repeated those stimulation experiments, but knocked down the common odorant co-receptor (Orco) by systemic RNAi. Our data suggest at least two proliferation phases in the early adult. A first phase, direct after adult eclosion that lasts for 3 to 4 days, seems to be independent from olfactory stimulation. In contrast, a second phase that directly follows the first phase seems to depend on olfactory stimulation.



Symposium: Phenotypic Plasticity - RESPONSES of Animals to
Environmental Change
Oral Presentation

Clonal variability in reaction norms of plasticity in prey defences and predator offences

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Inducible defences are known to enhance the effects of predation on coexistence and promote population stability, by dampening predator-prey oscillations. Prey species have evolved defensive strategies that reduce predation risk. They may show adaptive morphological features, behavioural traits or shifts of life history parameters. Yet, some predators are able to counter prey plasticity, by being plastic themselves. This has been described for ciliate species. The prey protist *Euplotes* spp is known to develop protective lateral wings in the presence of the predatory ciliate *Lembadion* spp. In turn *Lembadion* is able to gradually increase its peristome size, to the increased size of its prey, facilitating ingestion of defended prey. We studied the reaction norms of morphological defences and offences in *Euplotes* and *Lembadion*. We find differences in reaction norms of plasticity between clonal strains in prey and predator. This high degree of trait variability, complicates trophic system interactions. Thus, we will use this system in community experiments and study eco-evolutionary effects of inducible defences and offences.



Main Meeting, FG Evolutionary Biology
Oral Presentation

Oxidative stress in sperm: effects of metabolic pathways, male and gamete age, and storage duration

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Sperm age is an understudied trait that may account for much of the currently unexplained across-male variation in fertilization success. As sperm cells undergo metabolism, they produce reactive oxygen species (ROS) that can in excess lead to cellular damage and accelerate the aging process. In species where sperm is stored for any length of time, both males and females should be under selection to minimize such damage. Here, we use *Drosophila* to investigate the relationships between sperm ROS production and (i) metabolic rate; (ii) sperm age and male age; and (iii) sperm storage duration. Applying autofluorescence lifetime measurements in two metabolic mutants with above-normal and below-normal somatic ROS production, we investigate oxidative stress in sperm. We also use genetically encoded redox probes to disentangle the relationships between metabolic rate, male age, sperm age, and the location of ROS production (mitochondria vs. cytoplasm). Finally, we measure sperm ROS production in a range of species that differ in their mating frequency and in the duration of male and female sperm storage; preliminary results support the hypothesis that less frequent mating and longer sperm storage durations have selected for lower ROS production. Our findings synthesize the field of sexual selection and the theory of cellular senescence, an area of research that has major but as yet largely overlooked implications for sperm use and competition.



Main Meeting, FG Physiology

Poster: Phy 9

Activity of FoxO transcription factors are involved in airway epithelial remodeling processes

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Bronchial asthma is a chronic disease of the airways characterized by inflammation and remodeling of the airways, mucus hyperproduction, and airway hyperresponsiveness. The bronchial epithelium is involved in the development of all these hallmarks and, thus, plays a critical role in the pathogenesis of the disease. Due to the lack of an adaptive immune system and a relatively simple structure of its airway system the model organism *Drosophila melanogaster* offers the unique opportunity to exclusively investigate the immunobiology of airway epithelial cells *in vivo*. This study aims to elucidate the role of the inflammation-related transcription factor NF- κ B and the stress-activated transcription factor dFoxO in remodeling processes of the airway epithelium. Overexpression of the NF- κ B-activating receptor peptidoglycan-recognition protein PGRP-LC in airway epithelium resulted in hyper- and metaplasia of airway epithelial cells accompanied by massive epithelial thickening. An equivalent phenotype could be induced in animals overexpressing the transcription factor dFoxO in the airway epithelium. Using transgenic animals expressing a dFoxO-GFP-construct in the airway epithelium, we could show that an activation of NF- κ B results in a translocation of dFoxO-GFP into the nucleus. These data indicate that translocation of dFoxo mediates NF- κ B-triggered remodeling processes of the airway epithelium of the fly. Based on these findings we suggest that the transcription factor FoxO could also be involved in the development of airway remodeling in asthma.



Main Meeting, FG Neurobiology
Oral Presentation

Neural mechanisms underlying song learning in zebra finches

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Zebra finches learn their songs by listening to and imitating a tutor. During development, sensory input is necessary in order to effectively imitate the tutor's song. Here, we measured the impact of the tutor song on HVC neurons during and after learning. We recorded intracellularly from premotor cells and found that the tutor song has the potential to drive precise spiking responses in the awake juvenile zebra finch, but not in the adult bird. Local application of the GABAA antagonist gabazine led to a reemergence of tutor song-driven spiking responses in premotor neurons suggesting that inhibition suppresses this activity. We measured inhibitory currents evoked by the tutor song throughout the critical period for song learning while simultaneously quantifying each bird's learning trajectory. Synaptic inhibition onto premotor neurons in HVC became significantly more precisely timed to the tutor song depending on the learning stage of the bird. We further trained zebra finches with a synthetic tutor song consisting of four identical syllables (AAAA). After the birds gained proficiency in the performance of syllable A, we extended the tutor song by adding syllable B (ABAB). We recorded interneuron activity and inhibitory currents onto premotor neurons in zebra finches that copied A well and copied B poorly, and found that inhibition was selectively stronger during syllable A versus syllable B. Taken together, these data suggest that inhibition within HVC progressively blocks an instructive signal in an accurate manner during motor learning, potentially to 'write protect' that motor skill.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral Presentation

In quest of contact: phylogeography of helmeted terrapins (*Pelomedusa galeata*, *P. subrufa* sensu stricto)

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Based on rangewide sampling and three mitochondrial and two nuclear markers, we examine the phylogeography of two helmeted terrapin species (*Pelomedusa galeata* and *P. subrufa* sensu stricto) and infer shifts of climatically suitable spaces since the Last Glacial Maximum using a modeling approach. Whilst *P. galeata* displays significant phylogeographic structuring across its range and consists of two deeply divergent lineages that could represent distinct species, *P. subrufa* shows no obvious phylogeographic differentiation. This seems to be related to historically stable or fluctuating ranges. One of the lineages within *P. galeata* appears to be confined to the westernmost winter-rainfall region of South Africa and deserves special conservational attention due to the scarcity of surface water. The other lineage is distributed further east and is differentiated in three weakly supported subclades with parapatric distribution; one occurring inland, and two along the south and east coasts, respectively. A sympatric occurrence of *P. galeata* and *P. subrufa* is possible in the northeast of South Africa. Another putative contact zone, for the two lineages within *P. galeata*, must be located in the Western Cape region, and further contact zones are likely for the eastern subclades within *P. galeata*. The nuclear loci provided no evidence for gene flow across taxa or genetic clusters within taxa. Future investigations should use denser sampling from putative contact zones and more nuclear markers to re-examine this situation.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral Presentation

A transcriptomic approach to investigate the phylogeny of Dytiscoidea (Coleoptera: Adepaga)

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Transcriptomic data offer the possibility to obtain a huge number protein-coding markers suitable for exploring the phylogenetic relationships of the taxa of interest. Accordingly, phylotranscriptomics has contributed to the phylogenetic resolution of many major insect groups. The beetle superfamily Dytiscoidea comprises six aquatic families whose evolutionary affinities remain contentious. Specifically, the monophyletic origin of the two species of the highly disjunct Aspdytidae (China and South Africa) remains an open question. Here we use phylotranscriptomic methods along with Four Cluster Likelihood Mapping to show that compositional heterogeneity among taxa and data-type effects may mislead the phylogenetic inference within Dytiscoidea. In particular, supermatrix and coalescent-based analyses of amino acid data as well as supermatrix analyses of second codon positions suggest a monophyletic origin of Aspdytidae. On the other hand, when all codon positions were included, Aspdytidae were rendered as paraphyletic. Subsequent removal of the most compositionally heterogeneous genes from the codon-based nucleotide alignments restored the monophyly of Aspdytidae. The family Hygrobiidae was either recovered as the sister to a clade comprising Amphizoidae + Aspdytidae in the analysis of the compositionally non-homogeneous amino acid datasets or as the the sister group to a clade consisting of (Amphizoidae + Aspdytidae) + Dytiscidae in the compositionally homogeneous amino-acid datasets. Our preliminary results highlight the detrimental effects of model violations on large scale phylogenies. Despite a very large data set and advanced analytical methods, a solid reconstruction of interrelationships within Dytiscoidea remains an intricate problem, especially but not only concerning the small relict group Hygrobiidae.



Symposium: Phenotypic Plasticity - RESPONSES of Animals to
Environmental Change
Oral Presentation

Adaptation against dislodgement through phenotypic plasticity in shell morphology of a clonal aquatic gastropod?

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Organisms featuring wide trait variability and occurring in a wide range of habitats are ideal models to study adaptation. Since the mid-19th century, the ovoviviparous New Zealand snail *Potamopyrgus antipodarum*, characterized by extremely variable shell morphology, has successfully invaded freshwater areas on four continents. Because these asexual invasive populations should harbour low genetic diversity, we hypothesized that the observed morphological variation must at least in part be the result of adaptive phenotypic plasticity. Controlling for genetic background, we tested the effects of the environment on the shell morphology and brood size of 425 snails collected at 21 European localities in a geometric morphometric framework. We found the two main components of shell morphology, shape and size, to be differentially controlled, the former mainly genetically and the latter predominantly by phenotypic plasticity. Integrating computational fluid dynamics simulations and a flow tank experiment with living snails, we then tested if the more globular shells with larger aperture observed in lotic habitats are an adaptation against dislodgement risk by 1) reducing lift rather than drag forces, and 2) increasing the attachment area by allowing for a larger foot size, hypothesizing the latter can be predicted by shell morphology. We found drag and lift forces to increase with shell size, globularity, and with increasing rotation of the snails out of the flow direction. Both our hypotheses were rejected. We concluded that globular shells must play another adaptive role in lotic habitats, e.g. diminishing damage caused by tumbling after dislodgement or against lotic crush-type predators.



Main Meeting, FG Evolutionary Biology*

Poster: EvoBio 8

DNA methylation as a mechanism of transgenerational phenotypic plasticity in *Daphnia*.

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Phenotypic plasticity is defined as the ability of an organism with a given genotype to respond to environmental changes by the adaption of its phenotype increasing organism fitness. Organisms can respond quickly to environmental changes within one generation, but also transgenerational plasticity has been observed. The freshwater crustacean *Daphnia* is well known for its high degree of plasticity. For example, it responds to an increased predation risk by developing defensive morphological features. Transgenerationally, the clonal offspring of defended mothers display even stronger defences when the predation risk remains high. As *Daphnia* reproduce via parthenogenesis, this transgenerational plasticity is non-genetic. We here want to elucidate the molecular mechanisms of transgenerational activation of predator-induced phenotypic plasticity focussing on differential DNA methylation patterns in *D. lumholtzi* and *D. pulex*. We compare DNA methyltransferase (DNMT) activity by measuring differential gene expression of the DNMT genes in two successive generations of predator exposed and control daphniids. This will provide first insights into whether DNA methylation is involved in coding transgenerational plasticity in *Daphnia*. With this, we want to set the basis for future methylation studies using whole genome bisulfite sequencing.



Main Meeting, FG Morphology
Oral Presentation

Fossil colours and the evolution of predator-prey landscapes

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Melanins and other pigments have been found to preserve under exceptional circumstances in fossils and in recent years developed into a distinct discipline. In this talk I will outline the discovery that melanin is responsible for the soft tissue outlines of exceptional vertebrate fossils and how we have developed microscopic and chemical methods for inferring colour and colour patterns from fossils. Reconstructing ancient colour patterns allow us to understand novel aspects of dinosaurian ecology and the nature of predator prey landscapes. Colour patterns evolve due to the nature of the eye of the beholder. Here I will outline periods in the past where the visual systems and the nature of predators was markedly different from what we today think is normal.



Symposium: MorphoEvoDevo - A happy threesome?

Oral Presentation

Palaeontological evidence for the origin of ctenophores

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Comb jellies have recently come under a hefty debate surrounding their place in the tree of life. Some molecular analyses place comb jellies as the sister to all other metazoans, and others place sponges as more traditionally held. Here I will present a series of Cambrian fossils, including the famous “weird wonder” *Dinomischus* and demonstrate their ctenophore affinity. These sessile, polypoid forms possess tentacles with pinnules carrying unique and particularly large compound cilia. Such a feature is unique to living ctenophores. The tentacle-ciliary apparatus can be shown to be homologous to the ctene-ciliary apparatus. Through these forms, we can trace the transformation from a sessile polypoid form with an internal sclerotised skeleton to ctenophores. We can demonstrate the successive transformation of the tentacle organ into ribbon shaped ctene structures as well as the formation of the main body compartment and the aboral organ. The evidence from these Cambrian fossils is mirrored by ctenophore development. The fossils furthermore possess a coelenterate-like digestive cavity possessing mesenterial divisions echoing cnidarian morphology. Our cladistic analyses find these forms to be successive stem groups to ctenophores in a clade with cnidarians (Coelenterata).



Main Meeting, FG Behavioural Biology

Poster: Behav 21

Kinship promotes exploratory behavior in the West African cichlid *Pelvicachromis taeniatus*

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Kin selection theory (inclusive fitness theory) predicts facilitated cooperation between genetic relatives. Consequently, an adjustment of social behavior in accordance to the genetic relatedness of encountered individuals is a widespread phenomenon in the animal kingdom and is especially pronounced in risk-taking behaviors like exploration, foraging or predator inspection. We investigated the effect of genetic relatedness on the exploratory behavior in the West African cichlid *Pelvicachromis taeniatus*. In this species, non-reproductive individuals live in groups and the exploration of novel environments is essential, e.g. to gain information about foraging locations and future territories which is likely affecting individual's fitness. *P. taeniatus* is able to recognize unfamiliar kin, and kinship influences social behaviour and mate choice (active inbreeding). In our study, fish were exposed to either unfamiliar kin or unfamiliar non-kin before they were allowed to explore a novel environment solitary. *P. taeniatus* showed promoted exploratory behavior after being exposed to unfamiliar kin compared to individuals exposed to unfamiliar non-kin. Thus, our results suggest an enhanced willingness to cooperate with kin and thereby potentially increasing their inclusive fitness.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral Presentation

Semantic morphological descriptions using Morph·D·Base

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A significant amount of morphological data is still provided as unstructured text. This is unfortunate in times of eScience in which data are increasingly available in a semantically structured format. Here we report on ongoing development of a new description module for Morph·D·Base (<https://proto.morphdbase.de>) that is based on semantic programming technology. The module enables users generating highly standardized and formalized morphological descriptions. The main organizational backbone of a description is a partonomy, to which users can add all the anatomical parts of the specimen that they want to describe. Each element (=anatomical part) of this partonomy is an instance of an ontology class and can be further described in three different ways: (i) in a semantically and thus highly formalized way through defined input forms, resulting in what we call a Semantic Instance Anatomy; (ii) as semantically enriched free-text; and (iii) through images with specified regions of interest which can be semantically annotated. Each description of each element of the partonomy, with its Semantic Instance Anatomy, free text and image annotations, is saved in the tuple store of Morph·D·Base. All data associated with a description entry can be accessed through a web-based interface and a SPARQL endpoint. The data are meaningfully fragmented using a sophisticated scheme of named graph resources, which additionally supports subsequent data retrieval and data analyses. We conclude the presentation with discussing potential applications of the resulting data and the possible overall impact of the semantic approach to morphology in general.



Main Meeting, FG Neurobiology
Poster: NB 25

Reproductive status-dependent Kisspeptin and RFamide-related peptide (Rfrp) gene expression in female Damaraland mole-rats

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Damaraland mole rats (*Fukomys damarensis*) are cooperatively breeding, subterranean mammals, which exhibit high reproductive skew. Reproduction is monopolized by the dominant female while subordinates are physiologically suppressed to the extent that they are anovulatory. It is thought that in these latter animals normal GnRH secretion from the hypothalamus is disrupted. The RFamide peptides kisspeptin (Kiss1) and RFamide-related peptide-3 (RFRP-3) are considered potent regulators of gonadotropin release. To assess whether these neuropeptides are involved in the mechanism of reproductive suppression we investigated the gene expression of Kiss1 and Rfrp by means of *in situ* hybridisation in wild-caught females with different reproductive status. In both reproductive phenotypes, substantial Kiss1 expression was found in the arcuate nucleus (ARC) and only few Kiss1-expressing cells were detected in the anteroventral periventricular nucleus (AVPV), potentially due to low circulating oestradiol concentrations in breeding and non-breeding females. Rfrp expression occurred in the dorsomedial nucleus, the paraventricular nucleus and the periventricular nucleus. Quantitative analysis revealed significant differences in relation to reproductive status. Reproductively active females had more Kiss1-expressing cells and a higher number of silver grains per cell in the ARC compared to non-reproductive females. Furthermore, breeding status was associated with a reduced number of Rfrp-expressing cells in the anterior hypothalamus. This reproductive status-dependent expression pattern of Kiss1 and Rfrp suggests that both neuropeptides play a role in the regulation of reproduction in Damaraland mole-rats. Enhanced long-term negative feedback effects of oestradiol could be responsible for the lower Kiss1 expression in the ARC of reproductively suppressed females.



Main Meeting, FG Developmental Biology

Poster: Dev 3

***Manduca sexta* haematopoiesis: the role of the haematopoietic organ in larval haemocyte formation**

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Insect haematopoiesis comprises two phases of formation and differentiation of haemocytes, the embryonic haematopoiesis and the larval haematopoiesis (Holz et al. (2003) *Development*, 130, 4955). In lepidopteran insects four haematopoietic organs located around the wing imaginal discs are thought to contribute to the larval haematopoiesis (Grigorian and Hartenstein (2013) *Dev Genes Evol.*, 223, 103). Haematopoietic organs of *Bombyx mori* form plasmacytes, granular cells, and oenocytoids (Akai and Sato (1971) *J Insect Physiol.*, 17, 1665; Han et al. (1998) *Zool Sci.*, 15, 371), whereas in *Pseudaletia includens*, *Spodoptera frugiperda* (Gardiner & Strand (2000) *Arch Insect Biochem Physiol.*, 43, 147) and *Manduca sexta* (Nardi et al. (2003) *Dev Genes Evol.*, 213, 477) they contain especially plasmacytes. We conducted experiments in *M. sexta* that proved a) that exclusively plasmacytes and putative prohaemocytes are found within or released by the haematopoietic organs, b) that the organs release plasmacytes during larval development rather than only in (pre-) metamorphic stages, as opposed to *D. melanogaster*, and c) that histological traits and different markers for plasmacytes and the newly identified phagocytosis receptor Ms-Eater reveal a strict zonation of the organ into a putative stem cell region located proximally to the wing disc, a median region of differentiation, and a zone containing terminally differentiated plasmacytes beneath the distal surface. In a nutshell, the haematopoietic organs of *M. sexta* form plasmacytes which most likely differentiate within the organ into a functionally differentiated state, i.e. capable of phagocytosis and other immune responses, and these cells are released during larval development.



Main Meeting, FG Developmental Biology

Poster: Dev 8

Identification of a GATA transcription factor coding mRNA in *Manduca sexta* and its localisation in haemocytes

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Evolutionary conserved transcription factors play a major role in determination and differentiation of the haematopoietic lineage (Evans et al. (2003) *Developmental cell*, 5(5), 673). GATA family transcription factors (GATA-TFs) are characterised by the presence of zinc finger motifs (Cys-X-X-Cys-X17-Cys-X-X-Cys) allowing to bind specific nucleic acid motifs (Waltzer et al. 2002 *The EMBO journal*, 21(20), 5477; Orkin (1992) *Blood*, 80(3), 575). It is known that GATA-TFs are responsible for the proper differentiation of haemocytes or blood cells in both, invertebrates and vertebrates (Rehorn et al. (1996) *Development*, 122(12), 4023). The *Drosophila melanogaster* GATA-TF Serpent (Dm-Serpent) plays a key role in the haematopoietic system and development of other immune competent tissues (Senger et al. (2004) *Mol Cell.*, 13, 19). Here, we present a GATA-TF of *Manduca sexta* (Ms-Serpent) with a high similarity to Dm-Serpent, identified by *in silico* analyses and *in-situ*-hybridisation. We show Ms-serpent mRNA in larval haemocytes and haematopoietic organs as well as in early developmental stages during embryogenesis. A region next to the stomodaeum, the putative intercalary segment, shows a strong Ms-serpent expression. Within this region, the earliest embryonic haemocytes form, which also contain the Ms-serpent mRNA. Additionally, the putative fat body anlagen contain Ms-serpent mRNA, which is in accordance with the role of Dm-serpent in fat body development in *D. melanogaster* (Hayes et al. (2001) *Development*, 128(7), 1193). Due to the localisation in haematopoietic organs, larval and embryonic haemocytes and haematopoietic regions we suggest a role of Ms-Serpent in the haematopoiesis and organogenesis similar to Dm-Serpent in *D. melanogaster*.



Symposium: MorphoEvoDevo - A happy threesome?
Oral Presentation

First larva intercalated? – Evolutionary developmental morphology in Nemertea

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The evolution of larvae has been a recurrent question in evolutionary biology. Two conflicting hypotheses prevail until today: the larva-first and the intercalation hypothesis. The larva-first hypothesis assumes a primary larva to have appeared with Metazoa. The intercalation hypothesis, on the other hand, states that larval stages have evolved independently within the life-cycle of several lineages. The trochophore-larva found in Spiralia (=Lophotrochozoa) is taken as an example by advocates of either hypothesis to support their respective case. Investigations in the development of previously neglected spiralian taxa such as Nemertea (ribbon worms) reveals that the trochophore-larva has not evolved at once, already endowed with all of its pivotal characters, but that the larval organs have different, independent evolutionary histories. The obtained results prove the validity of comparative morphological studies in developmental stages and underline the importance of morpho evo-devo data on previously neglected taxa for formulating evolutionary hypotheses.



Main Meeting, FG Neurobiology*

Poster: NB 10

Anatomical analysis of tangential neurons of the central complex based on the desert locust brain atlas

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Insects show exceptional abilities for spatial orientation that in many respects parallel those of vertebrates. The diversity of navigational strategies like landmark-aided orientation, path integration and sky compass orientation reflects adaptations to different living conditions of insects. Being a long-range migratory species, neural mechanisms underlying sky compass orientation have been studied in *Schistocerca gregaria* in detail. We have analyzed the cerebrum, of the desert locust and provide a digital three-dimensional atlas of 48 distinguishable brain compartments and 7 major fiber tracts and commissures. In many navigational tasks, an assembly of midline-spanning neuropils, the central complex (CX), is involved. We have studied the organization of tangential neurons within the CX and used the brain atlas to analyze arborizations of those neurons in detail. With few exceptions, tangential neurons have putatively dendritic ramifications outside the CX and axonal terminals within the CX. Ramifications of tangential neurons outside the CX are largely subdivision-specific. Tangential neurons of the lower division of the central body have dendritic processes in the bulbs of the lateral complex and surrounding areas. Tangential neurons of the upper division of the central body showed the largest variety of cell types. Their ramifications outside the CX were concentrated in subfields of the lateral accessory lobes, the superior medial protocerebrum and the lateral protocerebrum. The data suggests specific input to the protocerebral bridge, the noduli, and the lower division of the central body and, in contrast, a large variety of brain areas directly connected to the upper division of the central body.

* Contribution also presented in: Symposium: 5th Meeting of the Arthropod Neuroscience Network (Poster: ANN 14)



Main Meeting, FG Behavioural Biology
Oral Presentation

Female *Drosophila* copulatory song impacts strategic ejaculate allocation and sperm competition

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Male *Drosophila melanogaster* sing elaborate wing songs during courtship. Genes and neuronal circuits underlying this sex specific behaviour have been extensively studied. Females do not sing during courtship, presumably because they lack critical neuronal components. We recently discovered, however, that females produce highly structured sounds during copulation by vibrating both wings. Female copulation songs are actively produced by several identified wing motor neurons. Furthermore, they depend on interneurons expressing the sex determination factor Doublesex. We find indication that female sound production is correlated with male ejaculate quality and/or quantity. Males depleted of ejaculate by multiple recent matings, very young or small males, all of which have less seminal fluid proteins, elicit fewer sounds. Sperm and products of the male accessory gland main cells are not necessary for sound production, but manipulation of accessory gland secondary cells leads to less sounds. In playback experiments, female copulatory song affects locomotion of single males. When played back during copulation, female songs increase the reproductive success of a first male compared to the success of subsequent males. This suggests that songs solicit strategic ejaculate allocation and by this impact on sperm competition in a remating scenario. In summary, we discovered a new signal during *Drosophila* reproduction. Female song can be considered an instance of female copulatory courtship and female cryptic choice. It provides new insight into sexual dimorphisms of courtship circuits, mate choice strategies, animal communication and sexual selection.



Main Meeting, FG Ecology*
Oral Presentation

How multiple-resource limitation (co-limitation) of consumer growth manifests in a fluctuating environment

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It is increasingly recognized that consumers tend to respond differently to fluctuating versus constant resource supply even when the average supply is the same. Even though resource variability (e.g. food species' spatiotemporal diversity) is crucial for consumer performance, its physiological underpinnings are poorly understood. For example, how does the capacity of consumers to store resources, or to acclimate their digestive physiology to the diet affect their performance in nutritionally complex environments? How do these traits interact? Perhaps, one of the most interesting, yet elusive questions is how multiple-resource limitation (co-limitation) of consumer growth manifests in a fluctuating environment? Here, we combine modelling and experiments to understand how consumer growth, at the organismal level, is affected by the nutritional variability of the environment. We use a two-resource Dynamic Energy Budget model to study how single or multiple resource-limited consumers with the ability to store resources and to adjust their digestive physiology respond to the temporal structure of resource fluctuations (i.e., frequency, amplitude, phase and covariance). In a second step, we confirm the model predictions in laboratory experiments using an aquatic model organism, *Daphnia magna*, limited by either dietary phosphorus, cholesterol, or both. We show, how physiological adaptive mechanisms such as reserves and acclimation of resource assimilation, may shape the growth response of *Daphnia* to environmental resource fluctuations.

* Contribution also presented in: Symposium: Phenotypic Plasticity - RESPONSES of Animals to Environmental Change (Oral Presentation)



Main Meeting, FG Morphology
Oral Presentation

Differentiation of trunk segments in the early euchelicerate lineage: First results of an evolutionary historical approach

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Chelicerate arthropods (about 100,000 extant species), today well known as spiders, scorpions, mites and alike, have a long evolutionary history. Since their early beginnings, numerous distinct chelicerate groups evolved, but also vanished, only leaving behind their fossil footprint. Chelicerates are known from terrestrial habitats all over the world, but also marine (sea spiders, “swordtails”) and freshwater (e.g., water mites) representatives are known. Their sizes range from microscopic scale, smaller than 0.1 mm (mites), to the largest forms of over 2 meters (extinct sea scorpions). However, morphological diversity is not only represented by size, but also by body organization. Chelicerates, as all arthropods, possess a segmented body, with several segments being organized into functional units, termed tagmata. These tagmata are specialized in their morphology to perform different functional tasks, such as walking or food uptake. In euchelicerates, especially the transition area between anterior and posterior tagma shows a high morphological variability, including compression of segments, functional integration of segments of one tagma into the other, and also appendage differentiation. We are therefore aiming at reconstructing the evolutionary history of body organisation within chelicerates with a focus on this very region. We use a combination of several methods including investigations of inner structures, e.g., muscles, using μ CT and histological staining and sectioning, but also of ontogenetic and fossil data. We here present first results and discuss in how far this approach is improving our understanding of the diversification of Euchelicerata in an evolutionary historical context.



Symposium: MorphoEvoDevo - A happy threesome? – Keynote Lecture
Oral Presentation

The need for a revised, multi-level view on homology and parsimony for reconstructing morphological evolution in the genomic era

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The importance of reliable phylogenies for parsimony-based ground pattern reconstruction is a widely accepted dogma in evolutionary biology. However, in times of growing numbers of phylogenetic trees that challenge traditional concepts, yet fail to produce consistent alternative topologies, hypotheses on evolutionary scenarios are particularly prone to change. This appears frustrating because the “morphological revolution” has seen a delightful increase in high-quality data on all taxonomic levels including hitherto neglected taxa, whose relevance is downgraded by too much focus on (changing) phylogenies and their impact on reconstructing character evolution. I argue that more tribute should be paid to original data by refining (primary) homology assessments in a Hennigian sense, using unbiased character analyses that are unconstrained by precast phylogenetic concepts. Darwin’s theory of evolution renders homology a fact (although homology propositions remain a hypothesis), while parsimony constitutes a mental construct without any claim for universal validity. Therefore, arguments for or against origin by common descent (i.e., homology) should be based on real data, rather than on indirect assessment by changes in character states (parsimony) in an algorithm-based tree. I will also discuss recent examples where long-standing homology hypotheses are challenged by molecular (gene expression) data and will point towards difficulties in assessing homology on organ system level using gene expression data alone. I argue that, rather than deducing homology of characters directly from cladograms, the true value of phylogenies is as sources to identify characters with a hitherto unrecognized potential for homology that can be tested using state-of-the art methods.



Main Meeting, FG Physiology

Poster: Phy 11

Characterization of fluorescent-labeled Chitosan-wtCFTR-mRNA complexes and tracking their uptake in human bronchial epithelial cells

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Cystic fibrosis (CF) is the most lethal autosomal recessive disease due to mutations in the cystic fibrosis transmembrane conductance regulator (CFTR) gene. Non-viral vehicles like chitosan (CS) are of special interest for gene therapy purposes. Due to its polycationic character CS is able to form nanocomplexes with mRNA via self-assembly. In previous studies we generated unlabeled CS-wtCFTR-mRNA complexes and successfully transfected human CF airway epithelial cells to restore CFTR function. The aim of this study is to characterize labeled CS-wtCFTR-mRNA complexes, track their uptake and determine the time point of mRNA expression. Thus, wtCFTR-mRNA fused with GFP as well as wtCFTR-mRNA labeled with fluorescent UTPs were used to form complexes with CS. Hence, complexes of varying charge ratios (+/-) were characterized for their physicochemical properties, e.g. size, polydispersity index and zeta potential. Afterwards, using these optimized complexes, CF cells (CFBE41o-) were transfected at different time points. Our results revealed that the complexes enter the cells after 2h of incubation in a lower amount compared to the positive control (Lipofectamine® 2000 transfection reagent), which lead to a slightly higher uptake of mRNA after the same time. Furthermore, the imported mRNA with CS as delivery system shows nearly the same expression level than the transfection with the positive control. These findings demonstrate that the non-toxic CS transfection reagent is suitable to form proper complexes with wtCFTR-mRNA, restore CFTR function and show almost the same transfection efficiency as the conventional but cell toxic transfection reagent Lipofectamine®2000.



Main Meeting, FG Neurobiology*

Poster: NB 22

Carboxypeptidase D (SILVER) is required for neuropeptide production and peptide-dependent behaviour in *Drosophila*

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Metalloproteases (CPs) of the N/E subfamily are involved in the processing of proteins and peptides in the secretory pathway. They remove specific residues from biologically inactive processing intermediates, rendering them active. In mammals, carboxypeptidase E (CPE) is the primary CP involved in neuropeptide processing, while carboxypeptidase D (CPD) can to some extent substitute CPE action. *Drosophila* lacks CPE, but contains the dCPD-encoding gene silver. It is therefore likely that dCis the main CP involved in neuropeptide processing in the fruit fly. This hypothesis is supported by the expression of *svr* in the CNS and endocrine tissues such as the midgut, and the direct transactivation of *svr* by the transcription factor DIMMED which confers a neuroendocrine peptidergic phenotype. Ectopic expression of *svr* transgenes also affects processing of adipokinetic hormone. Yet, direct and comprehensive evidence for a role of dCin neuropeptide processing is lacking. To identify whether and to which extent dCis required for neuropeptide and peptide hormone processing, we performed a peptidomic analysis in the central nervous system and midgut of larval and adult *Drosophila svr* mutants that were conditionally rescued during development. Our results indicate that dCis a major if not the sole fruit fly CP involved in neuropeptide processing. To test for the functional significance of dCin peptide-regulated behaviour, we performed several behavioural assays in constitutive and conditional *svr* mutants. These flies showed impairment in most of these behaviour, further strengthening the key role of dCin *Drosophila* neuropeptide and peptide hormone processing.

* Contribution also presented in: Symposium: 5th Meeting of the Arthropod Neuroscience Network (Poster: ANN 15)



Main Meeting, FG Morphology
Oral Presentation

Spatial imaging of wing flexing in flies by force deflection analysis

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Flies exhibit sophisticated flight behaviors in complex environments. The required aerodynamic forces result from active wing flapping. Fly wings are elastic composite structures that allow bending and twisting in chord- and spanwise direction. The benefit of wing deformation for force production and body posture control is under debate because previous results produce inconsistent results. Our research aims to determine wing deformation in flight using a comprehensive, mechanical fly wing model and computational fluid dynamics. We conducted elaborate stiffness measurements in fly wings by local application of forces similar to those occurring in flight and estimation of local 3-dimensional wing deformation using imaging methods. We found that spanwise wing bending widely follows simple beam theory with spring stiffness ranging from ~0.02 to 1.0 N/m in fruit flies and ~0.2 and 2.8 N/m in blow-flies. We did not find dorso-ventral anisotropy during wing bending in fruit and blow-flies. Wings of house flies, however, are ~1.5 times stiffer when loaded from the ventral than from the dorsal wing side. Surface analyses show that fly wings also buckle along longitudinal veins when appropriately loaded, which increases chordwise wing camber and thus aerodynamic angle of attack. Our findings help to explain wing deformation in flapping fly wings and are essential for any detailed evaluation of the aerodynamic impact resulting from wing flexing.



Main Meeting, FG Behavioural Biology
Oral Presentation

Stochastic variations in gait patterns and their effect on body dynamics in multilegged locomotor systems

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In legged terrestrial locomotion, different gaits and energetic economy are determined by the dynamics of the centre of mass (COM). However, COM dynamics are largely determined by the degree of leg synchronization and the resulting overall vertical ground reaction forces (GRF). The degree of leg synchronisation within sets of legs, like the typical tripod sets of insects, are determined by ipsilateral phase relations of the legs and stochastic irregularities of the legs' touch down and take off. While ipsilateral phase shifts can be controlled deliberately, the degree of stochasticity depends on the extent of internal and external disturbances. In a numerical model approach, the combined effects of ipsilateral phase shifts and stochasticity on total vertical ground reaction forces and body dynamics have been examined for locomotor systems with two to four pairs of walking legs. The calculations show that both, ipsilateral phase shift and stochasticity result in decreased leg synchronisation in the putative alternating sets of legs. While stochasticity mainly affects the phase range around 0.5, i.e. the proximity of alternating leg coordination, the effect of increasing ipsilateral phase shifts is larger for higher deviations from the alternating gait pattern. Temporal dissociation of the sets of legs, results in low amplitudes of the total vertical GRF. With increasing disturbances, the synchrony factor declines even when the sets of legs are modelled in perfectly synchronised fashion. Depending on the duty factor, thus, vertical GRF amplitudes can drop significantly, which prevents the effective use of elastic energy recovery on rugged substrates.



Main Meeting, FG Developmental Biology
Poster: Dev 10

Electrochemical gradients as regulators of cytoskeletal patterns during oogenesis of *Drosophila melanogaster*

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Drosophila oogenesis provides an excellent model system for studying the potential role of electrochemical signals during development. In the somatic follicle-cell epithelium, stage specific transcellular anteroposterior and dorsoventral gradients of intracellular pH (pHi) and membrane potential (Vmem) establish that depend on the asymmetrical distribution and/or activity of various ion transport mechanisms. Alterations of the electrochemical properties of cells and tissues are known to function as fast and wide-ranging signals during development in several species. We, therefore, analyzed pHi and Vmem gradients in the columnar follicle-cell epithelium of *Drosophila* during the course of oogenesis and found correlations with the organization of the basal microfilament pattern (bMF) and the microtubule pattern (MT). For studying the properties of pHi and Vmem in living follicles, we used the fluorescent pH-indicator 5-CFDA,AM and the potentiometric dye DiBAC4(3). The bMF and MT patterns were analyzed in fixed follicles using labelled phalloidin and an antiserum against α -tubulin. In addition, we used the Gal4-UAS system for the follicle-cell specific expression of GFP-actin and GFP-tubulin, respectively, to investigate bMF and MT patterns in living follicles. We found that changes of pHi and Vmem correlate spatially and temporally with structural modifications of bMF and MT in the follicle-cell epithelium. Using inhibitors of several ion-transport mechanisms we modified pHi and Vmem gradients and affected the bMF pattern as well as the MT organization. Therefore, electrochemical signals can play an important role in the regulation of cell and tissue architecture by organizing elements of the cytoskeleton.



Main Meeting, FG Morphology
Poster: Morph 21

Autotomy in stick and leaf insects (Phasmatodea): comparative morphology and evolutionary implications

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Phasmatodea forms a subgroup of the diverse Polyneoptera, which also comprises well-known insects like cockroaches, grasshoppers and praying mantises. Due to their remarkable resemblance to wispy branches, bark or leaves, they are commonly referred to as stick and leaf insects. Phasmatodeans have developed numerous defence mechanisms to prevent from or to repel predators: defensive spikes spread across body and legs, striking coloured hind wings, which are disposed to startle the attacker, and defensive glands used as a chemical weapon. Also the capability to autotomize legs is generally observed among Phasmatodea. Autotomy, the self-induced limb loss, is common in many animal groups, e.g. lizards, crustaceans, and insects. Phasmatodea comprises species-rich Euphasmatodea and its sister taxon, the species-poor enigmatic genus *Timema*. Until now, autotomy has only been described for in euphasmatodeans and is thereof considered to be an apomorphy of this subgroup. Nonetheless, this knowledge is based on the examination of only a few selected taxa. Recent studies exploring the phylogeny within Euphasmatodea suggest a sister group relationship of Aschiphasmatodea and Neophasmatodea. Interestingly, autotomy in Aschiphasmatodea has not been documented so far. Here we present a comparative morphological investigation of the leg and its autotomy plane in the genus *Orthomeria*, a representative of Aschiphasmatodea and different neophasmatodeans using morphological methods such as μ CT, 3D-reconstruction and semi-thin serial sections. We demonstrate that autotomy is also present in Aschiphasmatodea, which supports the view that this feature is an apomorphic trait of Euphasmatodea, probably a key innovation leading to a major radiation of this group.



Main Meeting, FG Physiology

Poster: Phy 3

A putative steroid hormone transporter from the red flour beetle, *Tribolium castaneum*.

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ATP binding cassette (ABC) transporters in the red flour beetle, *Tribolium castaneum*, comprise eight subfamilies (TcABCA-H) encoding membrane bound proteins that are involved in the transport of a large variety of substrates. Subfamily TcABCG contains 13 genes for half-transporters that form homo- or heterodimers. We have previously shown that RNA interference (RNAi)-induced gene silencing of TcABC-G8A results in molting defects, developmental arrest and a mortality rate of about 50%. Strikingly, these effects closely resemble a phenotype that is also observed when RNAi is carried out for TcECR-A, which encodes one of two ecdysone receptors in the *T. castaneum* genome. Gene silencing of none of the other 72 ABC genes identified in the *T. castaneum* genome revealed comparable phenotypes. To test whether TcABC-G8A forms a homodimeric transporter in vivo, we expressed TcABC-G8A in yeast and Sf21 cells, and performed crosslinking- and bimolecular fluorescence complementation experiments. The results of this study demonstrate that TcABC-G8A is a homodimeric transporter involved in the transport of 20-hydroxyecysone or one of its precursors. To analyze TcABC-G8A expression, we determined transcript levels at different developmental stages and in different tissues. In line with its presumed role in development, TcABCG-8A is particularly highly expressed during pupation. Interestingly, TcABC-G8A exhibits considerable transcript levels in ectodermal tissues such as elytra but very low levels in entodermal tissues such as larval midgut. Notably, high expression is also observed in the fat body. In summary, the results of our study imply that TcABCG-8A may be involved in ecdysteroid transport across cellular membranes.



Main Meeting, FG Ecology

Poster: Ecol 2

Increased strandings of dead grey seals (*Halichoerus grypus*) in fall 2017 in Mecklenburg – Western Pomerania: Pathological investigation, legal situation and consequences

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Twenty-three dead grey seals were found in the southeast of the island Rügen (Germany) from 10th September to 4th December 2017. In the same period from 1997 to 2016, a combined number of only 30 grey seals were found in Mecklenburg- Western Pomerania. Most carcasses, mostly juvenile males, are usually found in May and June and not in autumn. Although grey seal numbers in this area have increased, the strandings exceed expected numbers by far. In the same area, the maximum count of live grey seals was below 100 animals in October 2017, which would suggest that around 25 % of the local seals died within that period. Maximum distance between the stranding localities was less than 15 km. Both major resting sites, the Stubber Bank (~10 km) and the island Greifswalder Oie (~20 km), in the German Baltic Sea are located close-by. In summary 19 of the carcasses were recovered and 15 were pathologically investigated until now. All individuals were subadult or adult males, above 2 m length, in good nutritional status and showed no or few signs of decomposition in contrast to regular strandings that typically show advanced decay. All investigated animals died of acute cardiovascular failure and did not show any unusual physical trauma. Virological and bacteriological investigations did not reveal clear pathogens causing the deaths. Parasite infections were unremarkable. Toxicological investigations were negative. As diagnose of exclusion drowning, most likely in a closed fish trap, is the only possible remaining cause of death.



Main Meeting, FG Physiology
Oral Presentation

Different mechanisms of organic osmolyte accumulation in subgroups of *Theodoxus fluviatilis* under hyperosmotic stress

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When faced with hyperosmotic stress, aquatic animals with water-permeable integuments are forced to activate physiological or biochemical mechanisms to avoid detrimental shrinkage of their cell and body volume. Most animals accumulate organic and inorganic osmolytes to adjust their internal osmolality according to the degree of the environmental stress. In molluscs, the majority of osmolytes are composed of various combinations of amino acids and amino acid derivatives (Shumway et al. (1977), J EXP MAR BIOL ECOL 29(2):131-150). The euryhaline snail *Theodoxus fluviatilis* (Linnaeus, 1758), a gastropoda belonging to the family of Neritidae, can be found in freshwater, but also in brackish waters along the coast of the Baltic Sea. Individuals from the brackish waters have been observed to tolerate and survive high salinities better than individuals from freshwaters (Wiesenthal et al. (2018), HYDROBIOLOGIA 811(1):339-350). The results of this study, however, showed that the reason for a higher tolerance does not lie within a superior ability of brackish water snails to mobilise free amino acids. Despite both groups pursuing different metabolic pathways when accumulating osmolytes, they showed equal abilities to accumulate amino acid compositions when acclimated to their respective maximum tolerable salinity in a stepwise manner. Though several amino acids were accumulated, alanine, proline and urea seem to be of special importance for osmoregulation and body volume stabilisation under hyperosmotic stress. The data indicates that the source for the broad mass of amino acids in *Theodoxus fluviatilis* is hydrolysis of storage proteins, while synthesis contributes to the accumulation of alanine and proline.



Symposium: Phenotypic Plasticity - RESPONSES of Animals to
Environmental Change
Oral Presentation

Phenotypic plasticity allows the euryhaline snail *Theodoxus fluviatilis* to cope with hyperosmotic stress

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The euryhaline snail *Theodoxus fluviatilis* (Linnaeus, 1758), a gastropoda belonging to the family of Neritidae, can be found in freshwater, as well as in brackish waters along the coast of the Baltic Sea. These two groups are closely related, yet have been observed to have different tolerances in coping with hyperosmotic stress, with brackish water snails being more tolerant to high salinities than freshwater snails (Wiesenthal et al. (2018), *HYDROBIOLOGIA* 811(1):339-350). Despite genetic differences causing brackish water snails to be more tolerant towards hyperosmotic stress, individuals of both groups demonstrated the ability for phenotypic plasticity leading to a shifted tolerance range. Since these animals have water-permeable integuments, hyperosmotic stress would lead to detrimental shrinkage of cell and body volumes, if they did not activate physiological or biochemical mechanisms to avoid this osmotically caused damage. While most animals accumulate organic and inorganic osmolytes to adjust their internal osmolality depending on the environmental stress, molluscs mainly accumulate various compositions of amino acids and amino acid derivatives (Shumway et al. (1977), *J EXP MAR BIOL ECOL* 29(2):131-150). Despite both groups showing equal abilities to accumulate amino acid compositions, they pursued different metabolic pathways when accumulating these osmolytes when acclimated to their respective maximum tolerable salinity in a stepwise manner. The different underlying mechanisms to cope with hyperosmotic stress reveal both phenotypic plasticity as well as genetic responses to the changing environmental condition.



Main Meeting, FG Evolutionary Biology
Oral Presentation

Protein-coding gene repertoires – Annotation, characterization and dynamics in non-model insects

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The rapidly filling treasure trove of available genomes from diverse organisms provides the means to approach a central goal: explaining the evolution of biodiversity in the context of changed hereditary makeups. To this end, we are witnessing a shift from the analysis of individual genes towards the investigation of the genome and its components as a whole. Yet, evolutionary mechanisms and processes shaping the composition of protein-coding gene repertoires have been barely explored. Additionally, the data deluge poses unprecedented problems, mostly related to handling, quality assurance, and efficient analysis of these extensive quantities. Standardization is lagging behind, especially concerning the tools and terminology to describe not one but all genes of a species. The presented work focuses on the gene repertoires of Hymenoptera in comparison to other holometabolous as well as hemimetabolous insects. Holometabola, insects that undergo pupal development and metamorphosis, are a tremendously diverse and species-rich group given their phylogenetic age. The genomes of insects in general appear to be highly dynamic. To date, it is open whether and how these factors interact in genome evolution. The description of repertoire structures provides a first, necessary gauge to assess insect genomes. Suggestions for the standardization of repertoire characterization regarding methods, terms, and publication were formulated. Turning to data quality, it was shown that gene models derived from automated annotation procedures are suitable to study structural features of gene repertoires. Finally, the commonalities and differences between hymenopteran genomes were explored to both calibrate expectations and identify potential drivers of repertoire change.



Main Meeting, FG Evolutionary Biology

Poster: EvoBio 9

Functional roles and differences between the Na,K-ATPase α/β -subunit combinations in the large milkweed bug

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The well-studied transmembrane enzyme Na,K-ATPase is essential for the maintenance of membrane potentials and the functionality of cells. Plant toxins like cardenolides inhibit the enzyme resulting in harmful or even lethal effects. *Oncopeltus fasciatus* is one of few insect species that is able to cope with these toxins. Two rounds of gene duplications of the Na,K-ATPase α -subunit resulted in three paralogs (A, B, C) differing in number and identity of amino acid substitutions. Additionally, four different copies of the β -subunit exist that are expected to modulate the Na,K-ATPase's behavior. We found that nine different α/β -subunit combinations expressed in cell culture show different insensitivities against the two cardenolides ouabain and calotropin, differing in polarity, structure, steric conformation and inhibitory potential. But so far, nothing is known about the tissue specific α/β -subunit combinations in *O. fasciatus* and their functional differentiation. The already detected expression patterns hint to different functions that trade-off ion transport, cardenolide insensitivity and morphogenetic potential of the β -subunit in a tissue specific manner. Therefore, we suggest that the evolution of three α -subunit paralogs combined with one of the four β -subunits enables *O. fasciatus* to adjust the Na,K-ATPases performance to fulfill particular tissue specific functional roles. To fill the gap of knowledge, we are currently elucidating the protein abundances of the α/β -subunit combinations in nerves, ovaries, muscles, hindgut and Malpighian tubules followed by targeted gene-knockdowns to analyze the functional roles and differences between the Na,K-ATPase α/β -subunit combinations.



Symposium: 5th Meeting of the Arthropod Neuroscience Network
Oral Presentation

High speed locomotion in the Saharan silver ant *Cataglyphis bombycina*

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The thermophilic Saharan silver ant, *Cataglyphis bombycina*, is the fastest of the North African *Cataglyphis* desert ant species. It is probably also one of the fastest running animals on the planet with respect to body size (i.e. body lengths per second). These highly mobile ants challenge the extreme temperatures of their sand dune environment with outstanding behavioural and morphological adaptations. Surprisingly, *C. bombycina* has comparatively shorter legs than its well-studied sister species, *Cataglyphis fortis* from salt pan habitats. This holds despite the somewhat hotter surface temperatures and the more yielding sand substrate. We report that *C. bombycina* employs a different strategy in reaching high running speeds, outperforming the fastest known runs of *C. fortis* ants, despite its relatively shorter legs. Video analysis across a broad range of locomotor speeds revealed several differences to *C. fortis*. Stride frequency levels off at a remarkably high maximum of about 40 Hz. With increasing walking speed, the duty factor decreases below 0.5, even before reaching the frequency plateau. Above speeds of 120 mm s⁻¹, the stance phase is reduced to a minimum of 7 ms and the ants exhibit aerial phases. All three legs of one tripod are lifted in synchrony and show a consistent tripod coordination. Tripod coordination strength (TCS) ranges around 0.8 over the entire walking speed range. This synchrony in leg touch-down and lift-off may facilitate movement across the yielding sand dune substrate.



Main Meeting, FG Neurobiology

Poster: NB 14

Weakly electric fish as models for electric imaging of objects under water

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Underwater object detection is a difficult task in turbid or dark surroundings. Aquatic animals living in such environments have developed various sensory adaptations to cope with these challenges. One solution is active electrolocation, which has evolved independently in two groups of tropical freshwater fish, the African Mormyriiforms and the South American Gymnotiforms. These fish emit electric signals by an electric organ (electric organ discharges, EODs) to generate an electric field surrounding the fish. Cutaneous electroreceptor organs distributed over almost the entire body surface perceive this field. Nearby objects are detected and analysed by local modulations of the self-emitted signal, i.e. electric field distortion. Fish can thus perceive various properties of an object such as size, distance, shape and material. We devised a biomimetic, multi-electrode, active sensor system that is, like the fish, capable of recording and analysing electric images of nearby objects. It was used to measure objects varying in shape (cube, sphere, and pyramid), size, and material (plastic, aluminium) at various distances. We found strong similarities between the electric images captured with this biomimetic device and those recorded in real fish: images increased in blur with higher distances, metal objects elicited central increase and peripheral decrease of metering signals (Mexican head profile), and plastic objects showed an opposite pattern. In conclusion, our sensor platform can detect and evaluate underwater objects even when vision or other sensory systems cannot work and thus may be used for nautical navigation and material testing applications.



Main Meeting Keynote Lectures
Oral Presentation

Seminal contributions: how male-derived proteins regulate reproduction

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Mating profoundly changes the physiology of female animals, impacting their reproductive success and their progeny. Males' seminal fluid molecules induce these changes - but how do they do so? We have been dissecting these proteins' mechanisms in the genetic model, *Drosophila*, whose post-mating changes are dramatic (increased egg production, sperm storage, modulated behaviors, physiology, and transcriptome/proteome). Genome editing, CT-scanning, genome comparisons, and molecular assays have uncovered how seminal proteins regulate *Drosophila* reproductive physiology at different timescales (immediate vs. long-term) and, even longer-term, affect the evolution of these seminal proteins. For example, some seminal proteins act rapidly via the nervous system to cause relaxation or contraction of reproductive tract organs, mediating release or movement of eggs through the reproductive tract. In contrast, other seminal proteins act in sequence to bind a critical molecule to sperm so this molecule can be stored long-term in female and influence her physiology for many days. I will discuss these findings and then relate them to seminal protein action in other organisms, including mammals and insect vectors of disease.



Main Meeting, FG Evolutionary Biology

Poster: EvoBio 10

Latitudinal differences in life history traits of a rapidly range-expanding spider

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Global climate change can result in poleward range expansions. A well-established model species for studying rapid range expansion is the orb-weaving spider *Argiope bruennichi*, which spread from the Mediterranean region into continental climates and up to Baltic countries in less than 100 years. Consequently, individuals have to cope with very different climates and environments. We collected mated females from the northern range limit (Estonia) and from within its original range (Southern France). After oviposition, the spiderlings overwintered in egg sacs that were allocated to a common garden experiment, mimicking the winter conditions from both sites of origin. We investigated the effect of origin on morphology and reproductive investment of females. Aiming to illuminate the effects of winter treatment and origin we explored hatching success, survival probability and body weight of the spiderlings. Overall, we found significant effects of origin on all traits inspected in females. In particular, females from the northern range are smaller but show similar reproductive investment to females from the original range, indicating adaptations to local environmental factors. Effects of both origin and winter treatment on the traits of spiderlings suggest an interplay between genetic adaptation and phenotypic plasticity. In conclusion, our results highlight latitudinal variation in life history traits in a range expanding spider.



Main Meeting, FG Behavioural Biology
Oral Presentation

Species-specific functions of male genital titillators in bushcrickets

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Males of many bushcricket species bear sclerotized genitalia, which show wide-ranging interspecific morphological variation that may reflect different pressures of sexual selection. As the exact function of these titillators is still disputed, we comparatively analyzed their role during mating in species with stepwise phylogenetic relationship from *Metrioptera roeselii* followed by *Pholidoptera littoralis* to *Tettigonia viridissima*, and *Letana inflata* as an out-group-species. In *M. roeselii*, synchrotron-based in vivo X-ray-cineradiography was used to visualize titillator movement and spermatophore attachment within the female (Wulff et al. 2017, Sci Rep 7). Neurophysiological recordings demonstrated that females can sense the titillator stimulation at their genital fold. In mating experiments, females expressed resistance behaviours towards males with asymmetrically shortened titillators. Pharmacologically or mechanically blocking of the mechanoreceptors at the female's genital fold largely reduced the resistance behaviour. In *M. roeselii* the titillators apparently act as mechanical stimulators to promote female acceptance of copulation and sperm transfer. In *T. viridissima* and *Ph. littoralis*, however, titillator manipulation had no effect on female's behavior, suggesting a different function than mechanical stimulation. In *Ph. littoralis*, titillators seem to be morphologically adopted as mechanical anchors, as manipulated males failed to maintain themselves in the mating position. In the out-group species *L. inflata* manipulation of the single titillator resulted in increased female resistance and mating failures. Bushcricket titillators may have different species-specific functions ranging from mechanical stimulation, suppressing female resistance to mechanical facilitation of male fixation and spermatophore attachment. Phylogeny does not explain titillator function, sexual selection could be an unifying theory.



Main Meeting, FG Physiology
Oral Presentation

Adjustments of protein digestion to temperature changes in *Daphnia pulex*

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In poikilothermic animals, rising temperatures affect metabolic rates and the dynamics of many physiological processes. In the planktonic species *Daphnia pulex*, the rates of somatic growth as well as the production of offspring are increased under warm conditions, thus the demand for protein resources is raised considerably. Protein digestion in *Daphnia* is mainly accomplished by the intestinal enzymes trypsin and chymotrypsin. Sixteen chymotrypsin and 40 trypsin isoforms were classified as potentially functional in the genome of *D. pulex*. The expression and activity of these serine proteases was studied in *D. pulex* acclimated to 10°C, 20°C or 24°C. On the transcript level, both enzymes were induced by increased temperatures. On the protein level, the activity was studied in photometrical assays and with gel electrophoresis followed by activity staining (zymogels). Here, the chymotrypsin activity was increased by elevated temperatures to a higher extent than it was determined for trypsin. The contribution of the different isoforms to protein digestion indicated differential protein expression to adjust the set of active proteases to the altered needs of protein metabolism. This temperature-induced phenotypic plasticity contributes to optimizing protein digestion for the temperature conditions experienced in the habitat.



Main Meeting, FG Neurobiology

Poster: NB 15

Topographical relationship between the optic tectum and lateral nucleus of the torus semicircularis of the midbrain in the weakly electric fish, *Gnathonemus petersii*

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The African weakly electric fish *Gnathonemus petersii* is capable of cross-modal object recognition and uses its electric sense and vision for object recognition. Thus, object features stored in the brain are accessed by multiple senses, either through connections between mono-sensory brain regions or because of multimodal representations in multisensory areas. Primary electrosensory information is processed in the medullary electrosensory lateral line lobe (ELL) which projects topographically to the lateral nucleus of the torus semicircularis (NL). Visual information reaches the optic tectum (OT), which projects to various other brain regions. We investigated the neuroanatomical connections of visual and electrosensory brain areas, concentrating on the topographical relationship of interconnections between OT and NL. The neural tracer Dil was injected systematically into different tectal quadrants, as well as into the NL. Tectal injections revealed topographically organized retrograde and anterograde label in the NL. Rostral and caudal tectal parts were interconnected with rostral and caudal areas of the NL, respectively, whereas tectal dorsal and ventral parts were represented in a roughly inverted fashion in NL, because dorsal tectal injections labeled ventral areas in NL and vice versa. In addition, tectal injections labeled ipsilateral basel cells in the valvula cerebelli, neurons in the central zone of the dorsal telencephalon, the torus longitudinalis, the nucleus isthmi, in various tegmental, thalamic and pretectal nuclei, as well as in other nuclei of the torus semicircularis. The dorsal preglomerular and dorsal posterior thalamic nuclei were anterogradely labeled as were some nuclei in the torus semicircularis and the nucleus isthmi.



Main Meeting, FG Developmental Biology
Oral Presentation

Comparative assessment of Sox gene involvement in molluscan neural development

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Mollusca is a large animal phylum that includes simple-built worm-like representatives and chitons as well as bivalves, gastropods and cephalopods. Consistent with this striking body plan diversity, mollusks show very different degrees of nervous system centralization and morphological organization. True ganglia are mostly absent in polyplacophorans, while conchiferans possess multiple pairs that can be more or less fused in some representatives and, especially in cephalopods, may even form highly complex brains. Our focus is on the comparative assessment of molluscan neurogenesis via morphological, immunohistochemical and gene expression analyses in the polyplacophoran *Acanthochitona crinita*, the bivalve *Dreissena polymorpha* and the cephalopod *Idiosepius notoides*. We are particularly interested in Sox genes that are known to play conserved roles during bilaterian neural progenitor specification, proliferation and differentiation (i.e. SoxB1, SoxB2, SoxC). In order to assess the expression of these genes in relation to the developing molluscan nervous system, we further use EdU labeling of cell proliferation as well as custom antibodies against selected molluscan neuropeptides (e.g. cerebrin, whitnin, insulin) and neuronal markers. The data obtained in this study should allow us to elucidate key aspects of nervous system formation in mollusks and provide new insights into the evolution of diverse neuronal architectures.



Main Meeting, FG Physiology

Poster: Phy 12

***Staphylococcus aureus* α -toxin induces defects in cell layer integrity by actin filament remodeling via cofilin activation in human airway epithelial cells**

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Staphylococcus aureus (*S. aureus*) is a commensal bacterium in humans. It may, however, become a pathogen under certain conditions and may cause severe infections like pneumonia (Lowy 1998, N Engl J Med 339, 520). One of the most important virulence factors of *S. aureus* is α -toxin (hemolysin A, Hla) which forms transmembrane pores in eukaryotic host cells (Bhakdi and Tranum-Jensen 1991, Microbiol Rev 55, 733). Because epithelia in the respiratory tract are major barriers between inhaled air that may contain microorganisms like *S. aureus* and the internal space of the body (Evans et al. 2010, Annu Rev Physiol 72, 413), we investigate the effects of recombinant Hla (rHla) on human airway epithelial cells (16HBE14o- cells). Exposure of cultured 16HBE14o-cells to rHla induced changes in cell morphology and cell layer integrity resulting in formations of paracellular gaps. As detected by confocal microscopy, Hla induced a loss of focal contacts and a loss of cell stabilizing actin stress fibers resulting in an accumulation of short actin filaments in the cellular periphery. Actin remodeling was associated with rHla-mediated hypo-phosphorylation of the actin-depolymerizing protein cofilin, a response that was dependent on the attenuation of the activities of PAK (p21-activated protein kinase) and LIM kinase. The rHla-mediated loss of focal contacts and degradation of actin stress fibers induced by hypo-phosphorylation of cofilin cause the formation of gaps in the cell layer which may, in the natural situation, compromise epithelial barrier function and allow bacteria to access the internal space of the body.



Main Meeting, FG Neurobiology*

Poster: NB 8

Receptive-field tuning to celestial polarization patterns is topographically organized in the locust central complex

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The desert locust *Schistocerca gregaria* is able to perceive the polarization pattern of the sky, which is characterized by electric field vectors, E-vectors, arranged tangentially along concentric circles around the sun. This pattern depends directly on the solar position in the sky and may be used to determine geographic directions. The central complex plays a key role in the processing of E-vector information: The protocerebral bridge is innervated such that the preferred E-vector orientation of single neurons is represented topographically, mapping a range of 360° of E-vector orientations across the bridge. While the tuning of central-complex neurons to E-vectors presented from the zenith is relatively well known, their receptive fields regarding the whole visual field have not been determined yet. In order to map these receptive fields, we recorded intracellularly from polarized-light sensitive central-complex neurons while presenting blue light stimuli polarized by a rotating polarizer from different positions in the locust's dorsal visual field. Neurobiotin tracer injection allowed for identification of neuron types and reconstruction of anatomical relationships. We found that central-complex neurons show E-vector-tuning patterns matching the sky-polarization pattern of a distinct solar position. This matched-filter property theoretically allows the cells to unambiguously determine the solar azimuth from the sky-polarization pattern alone. The solar azimuth corresponding to the best-matching polarization-pattern is topographically encoded in the protocerebral bridge, covering the full range of azimuthal directions. This supports the hypothesis that the central complex is a hub for spatial navigation that incorporates a sun compass. Funded by DFG grant HO 950/24-1.

* Contribution also presented in: Symposium: 5th Meeting of the Arthropod Neuroscience Network (Oral Presentation)



Main Meeting, FG Behavioural Biology

Poster: Behav 10

Are harbour porpoises displaced or quiet during construction work of offshore windparks?

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Harbour porpoises (*Phocoena phocoena*) face a wide variety of stressors with potentially harmful effects. In this study the impact of pile driving during construction of the offshore wind farm DanTysk was analyzed using behavioural information in click activity recorded by C-PODs (Chelonia Ltd.). Harbour porpoise echolocation activity, landmark orientation and foraging were analyzed in 14 of 80 pile drivings. For each driving swim speeds and distances travelled were compared for the periods before (24 h), during and after pile driving (24 h). This was done based on a visual screening for feeding events and landmark orientation. The results show a distinct decrease in echolocation activity within 12 km radius during the construction of DanTysk. In addition results show that within a distance of 6 km harbour porpoises swam faster, traveled further and showed an increase in foraging activity in the 24 h after pile driving in comparison to before pile driving. Porpoises were recorded in close vicinity already below 20 minutes after cease of pile driving, indicating that not all porpoises evacuated the area of concern, but remained silent. This study is therefore a first indication that behavioural responses of harbour porpoises to pile driving are more complex than previously assumed. A moderately increased travel velocity after pile-driving may be an indication, that porpoises return to the pile driving site. Increased foraging activity on the other hand can be interpreted as a sign of reduced energy intake during pile driving and therefore increased food demands after cease of noisy activities.



Main Meeting, FG Systematics, Biogeography and Diversity
Poster: Syst 5

**Phylogenetic exploration on the genetic diversity of
Maindronia neotropicalis (Thysanura: Maindroniidae) - an
enigmatic Gondwanean relict from the Atacama Desert**

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The genus *Maindronia* currently consists of only three described species from desert biomes in Sudan, Arabian Peninsula and Chile. The distribution range of these bizarre insects is unique for closely related arthropods and suggests the presence of a Gondwanean relict group. In Chile, *Maindronia neotropicalis* inhabits only the Atacama Desert. Previously published collecting data indicated that *M. neotropicalis* is a silverfish adapted to live in hyperarid areas but the distribution and genetic diversity of this taxon is poorly studied. Extensive sampling in the Atacama Desert revealed a considerable number of populations of *Maindronia* which are, however, entirely restricted to the coastal Atacama. Analyses of COI sequences allowed for the first time insights into the evolutionary history of *M. neotropicalis*. In fact, the data suggest the presence of two well-separated lineages in the Chilean Atacama Desert. The deep divergence of the two extremophile lineages suggests a rather old origin of these clades. This genetic differentiation is corroborated by distinct morphological features each.