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Abstracts

Main Meeting

& Symposium “Form and Function of Motion Systems”

(sorted by presenter)





Main Meeting, FG Evolutionary Biology
Poster: EVO 10

Searching for the sequence of aggression: comparative genetics of aggressive behaviour among tame and aggressive canids

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Aggression is a universal fitness trait that occurs across almost all animal taxa. Studies conducted over the last decades have shown that aggressive behaviour has a strong genetic basis, with neurogenetic studies suggesting that the molecular circuits underlying aggressive behaviour are highly evolutionary conserved. Yet, despite advances in some model organisms, most genes underpinning aggressive behaviour remain largely unknown. The rapid increase of genomic sequence information provides novel opportunities to investigate the evolution of complex polygenetic traits such as aggressive behaviour at the molecular level. Here we use genome sequences of domesticated dogs and foxes to examine the genetics of aggressive behaviour. We tested for the presence of recurrent selection in candidate genes related to aggression. We i) identified universal candidate genes linked with aggression and that are relevant in shaping the behaviour among different taxa through a comprehensive literature review; ii) developed an automated pipeline to test for selection acting on protein coding sequences; and iii) investigated sequence evolution in two organisms with discrete differences in aggressive behaviour. Our results suggest there is no major role for convergent evolution of coding sequences across both canid species to explain the observed phenotypic variation in aggression. This is in line with recent studies that suggest that complex polygenetic traits may evolve through other genetic mechanisms such as modification of gene expression. Future comparative studies should also include transcriptome data sets and investigate the role of non-coding gene expression modifiers.



Main Meeting, FG Physiology
Oral presentation

Circadian clocks determine intermediate lipid metabolism and storage lipid transport in complex interactions between nutrient-type, photic conditions, circadian clock and feeding time

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The interaction between circadian clocks and metabolism is of increasing interest, since clock dysfunction often correlates with metabolic pathologies. To study the role of circadian clock and behaviour in metabolism, metabolite profile of period01 clock mutants (per01) and Canton-S wild-type (WTCS) of *Drosophila melanogaster* were compared and revealed differing levels of glycerol(phospho)lipids, amino acids and their metabolites. Notably, diacylglycerols (DAG) and acylcarnitines showed lower levels in heads and bodies and their levels diurnally oscillated in WTCS. per01 flies showed higher locomotor activity, higher sensitivity to starvation, and shortened lifespan specifically under nutrition-depleted condition. Our results suggest that an impaired circadian clock affects mitochondrial lipid metabolism and leads to a reduced tolerance to nutrient stress.

We next asked whether clocks regulate lipid mobilisation. Levels of DAGs in the hemolymph were rhythmic in WTCS under LD, but declined in WTCS under constant darkness and in per01 under LD suggesting an impact of light and clock genes on daily DAG oscillations. Time-restricted feeding lead to comparable DAG profiles, suggesting that DAG oscillations are not exclusively entrained by feeding but rather are endogenously regulated. Bimodal oscillation of haemolymph DAGs in WTCS under LD were masked by digested fatty acids as rhythmicity of DAG levels was more robust when flies were fed a lipid-protein-free diet. Interestingly, oscillation of hemolymph DAG seems to correlate strongly with locomotor activity. Our results suggest that circulating DAGs, the major lipid transport form in insects, is influenced by complex interactions between nutrient-type, photic conditions, circadian clock and feeding time.



Main Meeting, FG Morphology
Poster: MOR 21

The role of global leg mechanics in the transition from grounded to aerial running

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It is assumed that gait changes emerge from trade-offs between optimization criteria such as locomotion stability, foraging vision, economy or speed. Animals using grounded running typically change to aerial running at dimensionless speeds u between 0.7 and 1. Some birds even exhibit grounded running far above $u=1$. In contrast, the classic inverted pendulum model predicts maximum locomotion speeds without aerial phases at $u=1$. Nevertheless, the inverted pendulum is still used as a standard model describing gait transitions in terrestrial animal locomotion. Here we show that the spring mass model (elastic leg behavior) predicts transitions between grounded and aerial running over a wide range of speeds including u greater than one. Predicted transition speeds depend on leg stiffness and angle of attack. To test model predictions, we analyzed kinematic and kinetic data from birds (Northern lapwings, oystercatchers, avocets, quail), Japanese macaques and humans during grounded running and running. Model predictions are consistent with experimental data. Minimal contact time and vertical oscillations of the center of mass seem to constrain the space of suitable transition speeds. In birds and macaques, transitions seem to be energy-driven (smooth). Thus, no or just minimal leg parameters must be tuned in order to change gait. In contrast, humans adapt leg parameters to achieve sudden gait transitions.



Main Meeting, FG Ecology
Poster: ECO 7

Giving pathogens the brush-off: the antenna cleaner of ants

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Grooming is a major part of the behaviour repertoire of insects. It is especially important to fight against and prevent diseases. In insects societies, in addition to the individual level, it is useful on a colony-scale level to ensure the good health of the group. Some insects have specific organs dedicated to grooming. This is the case of ants, with their antenna cleaner (or Strigilis), which is a modified spur on the pro-tibia. It bears a lot of combs and brushes, and functions by scrapping off infectious particles from their antennae, gather them in the mouth to later expel them as compressed pellets of antimicrobially-treated material. Whilst it is known that the different rows of hair mechanically work to remove solid particles of different sizes, it is unclear what the role of the associated gland on the tarsus is. We use an experimental approach supported by microscopy and chemical analysis to study the role of the strigilis organ in anti-pathogen defence of ants at the individual and colony level.



Main Meeting, FG Behavioural Biology
Poster: BEH 9

Discrimination and generalisation of temporal patterns of electric communication signals in the weakly electric fish, *Mormyrus rume probosciostris*

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By discharging an electric organ, the weakly electric fish *Mormyrus rume probosciostris* constantly emits series of brief electric organ discharges (EOD) used for active electrolocation and electro-communication. While EOD waveform and amplitude stay constant, the inter-discharge intervals (IDI) are highly variable between 20 and several hundred ms, depending on the behavioural context. Here we tested whether fish can recognize specific IDI-patterns and discriminate them from other patterns. Subsequently, we tested whether fish can identify specific IDI characteristics that might be linked to behavioural contexts.

We used pre-recorded IDI-patterns from individual *M. rume* while they were engaged in various behavioural contexts. Four animals were trained to discriminate between two IDI-patterns presented simultaneously from opposite ends of an aquarium. Fish were rewarded for approaching that dipole which played back an IDI-pattern pre-recorded from another fish during feeding. The negative stimuli were three IDI-patterns recorded during three other behaviours. In transfer tests following training, we tested whether fish preferred a new feeding pattern to IDI patterns recorded during various other behaviours.

All fish learned to recognize the feeding pattern and discriminated it from all other IDI-patterns. When new feeding patterns from different fish were presented, trained fish spontaneously preferred them over some patterns (resting, object inspection, exploring) but were undecided when others (foraging, chasing) were offered. We conclude that *M. rume* can identify certain, still unknown, properties of feeding patterns and thus generalizes them to some degree. However, some IDI-patterns occurring during other behaviours may be too similar to feeding for unequivocal discrimination.



Main Meeting, FG Neurobiology
Poster: NEU 3

Do you speak gibberish? Behavioural and neuronal integration time in bat vocal communication

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Vocal communication is a key feature of vertebrate behaviour, especially in birds and mammals. Vocalizations carry information that can trigger a range of vital behaviours in the receiver, e.g. in the context of mating, foraging or predation avoidance. Therefore, correct interpretation of the often very complex signals is crucial, calling for detailed auditory analysis by the receiver. Currently, it is still being debated whether such an analysis depends more on the short-term acoustic spectrum or on the slow modulation envelopes (i.e. the temporal code).

Bats often live in large communities and display a large repertoire of complex social vocalizations. Here we study the temporal integration time that may underlie species-specific communication in the bat *Phyllostomus discolor*. Combining formal psychophysics and neurophysiology, we compare behavioural thresholds to responses of single neurons in the bat auditory cortex. We use bats' vocalizations from different social contexts and manipulate the spectro-temporal information content. Inside a short window, the phase of the signal is randomized, i.e. spectral information remains while temporal information is lost (the longer the window length of the phase-randomization, the less recognisable the signal). Our study will reveal temporal integration times that underlie species-specific communication both on the behavioural and the neuronal level. From the results, we will gain novel insights into auditory processing of social communication signals under different contexts and ultimately into the evolution of mammalian vocal communication.



Main Meeting, FG Neurobiology
Oral presentation

Peeking through the foliage – Range resolution in echolocating bats

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Many echolocating bats forage close to vegetation – a chaotic arrangement of prey and foliage where multiple targets are positioned behind one another. Bats excel at determining distance: they measure target range by the delay between outgoing call and returning echo. In their auditory cortex, neurons are arranged by the specific delay they respond to, forming a topographic map. This would suggest that bats can resolve echoes of multiple targets along the range axis – a skill crucial for the forage-amongst-foliage scenario. We explicitly tested this hypothesis combining an auditory virtual reality with formal psychophysics: We simulated a prey item embedded in two foliage elements, one in front of and one behind the prey. The simulated spacing between “prey” (target) and “foliage” (maskers) was defined by the inter-masker delay (IMD). We then trained *Phyllostomus discolor* bats to detect the target in the presence of the maskers and systematically varied both loudness and spacing of the maskers. We show that target detection is considerably impaired when maskers are closely spaced ($IMD < 1$ ms), but remarkably improves with increasing spacing: the release from masking is about 5 dB for intermediate IMDs (1-3 ms) and increases to over 20 dB for large IMDs (≥ 9 ms). These results suggest that prey would enjoy considerable acoustic protection from closely spaced foliage, but also that the range resolution of bats would indeed let them “peek into gaps”. Our study puts target ranging into a meaningful context and highlights the limitations of computational topographic maps.



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

A tree of leaves: Molecular phylogeny and biogeography of leaf insects (Phylliinae: Phasmatodea)

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The order Phasmatodea is usually known for large insects having an elongated body form and masquerading as twigs or bark. Within this clade, however, we also find the oriental Phylliinae which are dorso-ventrally flattened and uniquely resemble leaves. While stick insects are part of many research projects, leaf insects have been largely neglected so far. Using a set of nuclear and mitochondrial genes, we have inferred their phylogenetic relationships and reconstructed the historical biogeography based on an impressively complete taxon sampling for this group. The huge majority of the ~80 described species pertain to the genus *Phyllium*. Whereas we corroborate the Phylliinae to be monophyletic, *Phyllium* is recovered to represent a paraphyletic assemblage with some minor genera nested among the *Phyllium* taxa. We furthermore reveal a number of undescribed leaf insect species and demonstrate that the genus *Chitoniscus*, which is distributed on New Caledonia and the Fiji Islands, is polyphyletic. Our results highlight the need for a thorough revision of this phasmatodean subgroup.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral presentation

Afrotropical biogeography and conservation using high-throughput sequencing and paleoclimate data

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Rapid developments in high-throughput sequencing technologies have increased the documentation of biodiversity in far greater detail than previously possible. Genome-wide SNP (single nucleotide polymorphism) datasets enable a wide variety of ecological and evolutionary questions to be addressed for both model and non-model organisms across multiple taxa. For many Afrotropical vertebrates, isolated forest refugia are thought to have played an important role in the diversification of spatially restricted intraspecific populations throughout Quaternary climate oscillations, which has important conservation implications. However, this hypothesis has not been tested against alternatives due to a lack of appropriate data. By explicitly testing forest refuge against alternative models (landscape barriers/ecotones/anthropogenic effects) in a demographic model-testing framework with genome-wide (RAD-seq) data and paleoclimate reconstructions, I quantitatively evaluate diversification hypotheses using novel amphibian datasets of amphibians (East Africa). Though multiple taxa show congruent biodiversity patterns (e.g. population structure, divergence times, paleoclimatic stability), mechanisms shaping these patterns across species can vary considerably, and the forest refuge hypothesis is only partly applicable, with rivers playing a particularly important role in many population divergences. Using an integrated framework which captures mechanisms of isolation, migration, secondary contact and population size changes allows powerful inference about population histories to be made, and enables a clearer mechanistic view of how biodiversity accumulates. Combined with conservation genomics approaches we can improve our understanding of the processes that shape biodiversity patterns, with multiple taxa and at varying scales, providing useful data for future conservation prioritisation.



Main Meeting, FG Behavioural Biology
Poster: BEH 18

Comparative prey-capture behaviour of some Central European rove beetles (Coleoptera, Staphylinidae: Paederinae, Staphylininae) towards three different prey types

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Despite their common occurrence and worldwide distribution, only little is known about the predatory behaviour of rove beetles of the two closely related and species-rich subfamilies Paederinae and Staphylininae. We collected beetles in Southern Germany (Tübingen, Baden-Württemberg) from debris and dung habitats, where many representatives of the two subfamilies of interest can be found. Amongst these were species of the genera *Philonthus*, *Bisnius*, *Quedius*, *Gyrohypnus* (Staphylininae), and *Rugilus* (Paederinae). We recorded their prey-capture behaviour with a highspeed camera. Each beetle was confronted with three potential prey types. Different prey-capturing methods were observed, i.e. (a) direct seizure with the mandibles, (b) predatory strike with the frontal legs, (c) pulling (i.e. direct seizure with the mandibles followed by lifting and dragging the prey backwards), and (d) formation of a catching basket (i.e. shoving the prey (with the head, the mandibles and / or the front legs) under the pronotum and between the inner side of the legs to form a cage-like structure that encloses the prey). These behavioural techniques can also be combined in various ways, which might indicate a flexible behavioural adjustment with respect to the specific prey-capture situation. For example, if the gripping performed in behaviour (a) or (b) does not lead to a proper fixation of the prey, behaviour (d) can be employed. The more complex behaviours are likely to have evolved in response to the specific prey type and might be taxon-specific. Further investigations that bring the prey-capture behaviour in correlation with mouthpart and leg morphology are planned.



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

First record of serotonin in Ctenophora contradicts their basal position in Metazoa

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The phylogenetic relations within early metazoans still remain unclear until today. With respect to two of the most basal groups, the sponges and ctenophores, there is an ongoing discussion about their specific positioning in the phylogenetic tree. Whilst morphological data see the sponges as the sister group of all other metazoans, recent molecular results place the ctenophores as the earliest lineage within Metazoa (Moroz (2014) Nature 510, 109). One major indication that supposedly supports this hypothesis is the absence of 'classical' neurotransmitters, such as serotonin. However, since serotonin is not a protein, it cannot directly be detected in any genome. Evidence for serotonin on the genomic level is always provided by the presence of 5-hydroxytryptophan-hydroxylase. If structure and/or genetic code of this enzyme are altered, serotonin may remain undetected. We therefore tested juvenile *Beroë ovata* and juvenile and adult *Mnemiopsis leidyi* for reactivity to fluorescent labelled serotonin antibodies. We found a clear signal only in early juveniles. Additional tests with immune electron microscopy are performed. Our results support a phylogenetic scenario in which sponges maintain their particular position as the sister group of all metazoans.



Main Meeting, FG Morphology
Poster: MOR 13

The evolution of photoreceptor cell types from the perspective of basally branching annelids

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Apart from shading-pigment cells (SPCs), pigmented eyes of Metazoa minimally comprise photoreceptor cells (PRCs) that perceive the optical stimuli with the help of photoreceptive pigments, the opsins, which are associated with elaborated membrane projections. Depending on the location of the membrane projections, two main types of PRCs are distinguished: (1) ciliary (c-PRCs) with membrane projections of sensory cilia and (2) rhabdomeric (r-PRCs) with microvillar projections of the non-ciliary cell surface. Commonly, c-PRCs are found in the pigmented eyes of Deuterostomia, while r-PRCs are found in the pigmented eyes of Protostomia. However, in the pigmented larval eyes of the protostomian clades Brachiopoda, Ectoprocta, Entoprocta, Gastropoda, and Nemertea c-PRCs have been found. The pigmented larval eyes of annelids on the other hand, are said to exclusively comprise r-PRCs. However, the bulk of information refers to the derived Pleistoannelida; the basally branching clades having been largely neglected until recently. To fill this gap in knowledge, we investigated the ultrastructure of the pigmented eyes of pelagic stages of *Magelona mirabilis* and recently settled stages of *Owenia fusiformis*. Unlike in the pigmented larval eyes of pleistoannelid and sipunculan species, several c-PRCs but no r-PRCs were detected. The PRCs of the first-forming pigmented eyes in *O. fusiformis* and *M. mirabilis* are thus more reminiscent of the pigmented larval eyes in several non-annelid spiralian outgroup representatives. The obtained results therefore question the hypothesis of ancestral r-PRCs in the pigmented larval eyes of Annelida and instead indicate that the first-forming pigmented eyes in Annelida originally possessed c-PRCs.



Main Meeting, FG Evolutionary Biology
Oral presentation

Sex-specific telomere dynamics in relation to age and reproductive success in a long-lived seabird

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In free-living animal populations individuals generally differ substantially in reproductive success, lifespan and other fitness-related traits. The causes of such variation with respect to the individuals' state and whether this differs between the sexes is still poorly known. Telomeres – evolutionarily conserved DNA-protein structures at chromosome ends – are a candidate biomarker as short telomeres relate to reduced health and survival in birds as well as other organisms. In the framework of a long-term project we measured telomere length in erythrocytes of Cory's shearwaters (*Calonectris borealis*), a long-lived seabird and assessed its relation to reproduction cross-sectionally and longitudinally, using a correlational as well as an experimental approach. Our results show that female telomere length changed relatively little with age, whereas male telomere length declined significantly. Telomere shortening was three times higher within than between males, suggesting a lower survival probability of males with shorter telomeres. Past long-term reproductive success was sex-specifically reflected in age-corrected telomere length. While males with high fledgling production were characterised by shorter telomeres, successful females had longer telomeres. A manipulation of reproduction in a subset of birds revealed that not the males providing parental care, but those males that experimentally failed reproduction due to egg removal experienced higher telomere loss. We discuss these results in a life-history context.



Main Meeting, FG Physiology
Oral presentation

Ca²⁺ signaling via 5-HT7 receptors in blowfly salivary glands

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Saliva secretion in the blowfly (*Calliphora vicina*) is controlled by the neurohormone serotonin (5-hydroxytryptamine, 5-HT) that acts via two different G-protein-coupled receptors, 5-HT2 α and 5-HT7. It is known that 5-HT2 α activates the InsP3/Ca²⁺ signaling cascade, whereas 5-HT7 activates the cAMP/PKA pathway (Röser et al., 2012, PLoS One 7/11). It is largely unknown whether these two 5-HT receptor types and their downstream signaling pathways act independently of each other or whether there are interactions between the two. To examine this question, cytosolic [Ca²⁺] responses were recorded in blowfly salivary glands upon selective stimulation of either 5-HT2 α , 5-HT7 or both receptors.

Selective activation of 5-HT2 α in blowfly salivary glands elicited oscillatory cytosolic [Ca²⁺] rises that were similar to the responses upon co-activation of 5-HT2 α and 5-HT7. Surprisingly, however, pharmacological agents that selectively activate 5-HT7 also led to cytosolic [Ca²⁺] oscillations. 5-HT7-mediated [Ca²⁺] responses were not the consequence of a [cAMP] rise and differed from 5-HT-induced [Ca²⁺] oscillations in several aspects. 5-HT7-mediated [Ca²⁺] oscillations 1) had lower amplitude; 2) had slower kinetics; 3) had an [agonist]-independent frequency; 4) were not sensitized by PKA activity; 5) seemed to be independent of InsP3-dependent Ca²⁺ release from the ER, but to be based on Ca²⁺ influx. It may thus be concluded that in blowfly salivary glands 5-HT7 can act in parallel via at least two signaling paths, the classical cAMP/PKA cascade and a cytosolic [Ca²⁺] rise.



Main Meeting, FG Morphology
Poster: MOR 1

Illuminating nature's beauty – modular, scalable and affordable LED dome illumination system using 3D-printing technology

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Even 100 years after Haeckel's lifework, depicting the complexity and diversity of biological objects is still a non-trivial task. Although modern technology, like advanced scanning electron microscopy (SEM) or micro computed tomography (μ CT), enables a renaissance of morphology – photography is still inevitable. Especially, in ages of high-throughput data science – e.g. next generation sequencing – posters, talks and publications often lose the connection to the whole organism they focus on.

Proper illumination is essential to achieve detailed and compelling scientific images of an investigated object. However, necessary lighting equipment is usually very expensive, making the cost-benefit ratio disproportional. The paper dome, presented by Kawada and Buffington (2016), was a first step towards an affordable lighting system for photography. Today, due to advances in 3D-printing technology, fused deposition modeling (FDM) printers become increasingly accessible, allowing for rapid and inexpensive manufacturing. The computer assisted design process facilitates the easy scaling of components, enabling an adaption of the system to cover a wide range of sample sizes.

Here, we present a scalable, modular 3D-printed dome for micro- and macrophotography. We provide stereolithography (.stl) files and print settings, as well as a complete list of necessary components required for construction of domes in three different sizes. Furthermore, we integrated an optional iris diaphragm to maximize light harvest and a sliding table to move the specimen inside the dome. All files are ready to print – leaving you with minimized effort, costs and construction time.



Main Meeting, FG Morphology
Poster: MOR 8

Variability of male postabdomen in Mantophasmatodea (Insecta)

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The insect order Mantophasmatodea has been described by two single museum specimens collected in southern and eastern Africa (Klass et al. 2002). In the following years, a number of species have been found in the field in Southern Africa so that the knowledge about their geographical distribution increased. Morphological and behavioral data of this wingless insect order both support low dispersal abilities for all stages which is supported by the difficulty to distinguish species using external morphology. Klass et al. (2003) introduced characters of the male and female postabdomen to differentiate species, especially those from the winter rain region of South Africa. In our study, we analyzed the morphological variability of the male postabdomen in the two closely related Namibian genera *Mantophasma* and *Sclerophasma*. Within the local populations, the shape and extent of the various sclerites of the male postabdomen was constant compared to inter-population variation, although the degree of sclerotization varied. Differences in the characters of the male postabdomen were apparent between the southern populations of *Mantophasma* in Namibia. The analyses suggest that the dissection of all phallus sclerites is not necessary to reliably differentiate *Mantophasma* populations. In particular, phallus sclerite 1 appears to be a useful character for the morphological identification of closely related populations. Similar conclusions could be drawn when studying the shape of the cerci.



Main Meeting, FG Behavioural Biology
Oral presentation

(What) Do bats hear in the cocktail party nightmare?

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Every evening echolocating bats around the world fly out of their roosts in groups of tens to millions. Despite the orderly spatial appearance of such emergences, acoustically this situation was considered a 'sonar cocktail party nightmare'. In an emergence, every bat needs to constantly listen for its own echoes within a cacophony of the loud calls of other bats and their returning. Do bats use echolocation at all in such behavioural contexts? Whether bats are able to detect their own echoes in the cacophony of the cocktail party nightmare still remains unanswered.

We present sensory simulations to quantify echo detection in the sonar cocktail party nightmare for the first time. We quantified detection rates of echoes in the presence of an increasing number of loud conspecific calls. We parameterized our simulations to experimental data on bat echolocation, auditory perception, and spatial arrangement in group flight. We show that a bat detects the majority of echoes mostly within just one emitted call, and all echoes once or twice within just six or eight emitted calls, respectively (i.e., within 0.5 seconds).

Our results indicate that bats obtain regular, though partial 'glimpses' of their surroundings, even under apparently difficult sensory conditions. We thus conclude that bats may still be using echolocation even while flying in groups. Our simulation framework is also applicable to understanding group echolocation in pinnipeds, oilbirds, as well as in human-made robotic sonar systems. In sum, the so-called sonar cocktail party may be more of a 'challenge' than a nightmare.



Symposium: Form and function of motion systems: new approaches, new opportunities, new challenges

Oral presentation

Measurement of feeding-related dental microtexture using 3D surface texture analysis in Eastern Atlantic harbour seals (*Phoca vitulina*)

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Marine mammals are increasingly threatened in their habitat by various anthropogenic impacts. Understanding dietary strategies of marine mammal populations can help predict implications for their future health status. The documentation of marine mammal diets and especially ingesta quality and prey availability is essential for their conservation. In this study, we used 3D surface texture analysis (3DST, using 30 parameters according to ISO 25178) as a dietary proxy to quantify dental wear as an indicator of dietary behaviour. This method is an established approach to reconstructing diets in terrestrial mammals, but has not yet been applied to pinnipeds. We analysed skeletal material of Eastern Atlantic harbour seals (*Phoca vitulina*) from the Baltic Sea (Hesselø, Denmark) and the North Sea (Wadden Sea, Germany), curated at natural history museums of northern Europe. Our aim was to establish a workflow, opening 3DST to pinnipeds and to test 3DST for its ability in detecting dietary spectra of populations.

We detect significantly rougher texture signals in the Baltic Sea population as compared to the North Sea population and conclude that the texture signal most probably reflects the deviation in prey species. Further, we found a trend of increasing enamel texture roughness along the tooth row which we relate to prey processing biomechanics. Applying indirect dietary proxies, such as 3DST, allow to reconstruct dietary traits of pinnipeds using existing skeletal collection material. This approach opens new research avenues and could help to detect dietary shifts in marine environments of the past and the future.



Main Meeting Keynote Lectures
Oral presentation

From Hennig to genomes – the evolution of insect phylogeny

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A remarkable insect phylogeny was already presented by Carl Börner (1904), lacking a consistent methodology, but nevertheless very close to recent concepts. In the mid-20th century Willi Hennig revolutionized systematics. His “Stammesgeschichte der Insekten” (1969) was a major breakthrough. Most of what he suggested was confirmed by recent studies based on extensive morphological or molecular data. The first cladistic analysis of morphological characters, published in 2001, largely confirmed Hennig’s hypotheses. In contrast, earlier molecular studies yielded partly unorthodox and unsatisfying results. Recent phylogenomic studies (1KITE project) again largely confirm Hennig’s views, with very few exceptions, for instance the basal placement of Hymenoptera in Holometabola. The interordinal relationships are now largely resolved. Persistent problems are the relationships of the entognathous orders, the “Palaeoptera problem” (Odonata, Ephemeroptera, Neoptera), the monophyly of Paraneoptera, and Mecoptera. The impression that new insights since Hennig are limited is misleading. The methodological progress is enormous. The handling of extremely large data sets and the refinement of analytical methods are remarkable achievements. Aside from this, 1KITE yielded a robust time frame for insect evolution, with estimations of the time of origin for all major lineages. Major future challenges are exploring insect evolution in the dimension of time and documenting the rapidly declining diversity. The aims should be tackled in a close cooperation between taxonomists, morphologists, palaeontologists, and molecular systematics.



Main Meeting, FG Evolutionary Biology
Poster: EVO 4

Evolution of neuropeptide precursors in polyneopteran insects

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Neuropeptides are the most diverse group of intercellular signaling molecules in Metazoa. They are key players in information transfer in the nervous system, but also have functions as hormones and thus act as important regulators of behavior, development, and metabolism. In insects, around 50 genes code for neuropeptides. These genes encode either a single neuropeptide (single-copy neuropeptide) or multiple paralogous neuropeptides (multiple-copy neuropeptides). The latter usually target the same receptor. In our analysis, we have focused on the sequence evolution of single-copy precursors that are translated from neuropeptide genes and processed into bioactive mature neuropeptides. Sequences of single-copy neuropeptides are under a high stabilizing evolutionary pressure due to co-evolution with their respective receptor. The dataset obtained from polyneopteran insects and used herein, illustrates the sequence evolution of neuropeptide precursors over a period of 300 myr. In addition to information on lineage-specific losses of neuropeptides or neuropeptide gene duplications, we provide insights into the sequence evolution of the various parts of the neuropeptide precursors, including signal peptides, neuropeptide sequences, and additional precursor sequences. Sequence evolution of the neuropeptide precursors studied did not follow a common rule. Some precursor species evolved rather rapidly and show highly lineage-specific features, while other precursors remained highly conserved across all Polyneoptera. With that information we have generated theoretical precursor sequences of the last common ancestor of all polyneopteran lineages.



Main Meeting, FG Morphology
Poster: MOR 5

Feeding kinematics and skull morphology of the keeled box turtle, *Cuora mouhotii* Gray, 1862

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The Genus *Cuora* (Geoemydidae) originates from an aquatic ancestor (Joyce (2004), Proc.R.Soc.Lond.B, 271, pp.1) and includes aquatic, semiaquatic and terrestrial species. This ancestry indicates an inherited aquatic feeding mechanism. High speed cinematography was used to analyse terrestrial and aquatic feeding mechanisms of *Cuora mouhotii*. In addition 3D reconstructions of the head based on microCT scans were prepared. This and previous studies show only slight morphological differences within *Cuora* (Natchev (2009), Zoology, 112, pp.113). The data indicate that adaptations in hyoid morphology (Richter (2007), Amphibia-Reptilia, 28, pp. 148) and the musculus adductor mandibulae complex seem to occur due to the diet and to a lesser extent due to the medium. The palate, the basisphenoid and the supraoccipitale show adaptations for broad insertions of the prominent adductor, which is responsible for jaw closing. This thick and voluminous muscle enables the crushing of hard prey such as snails. To examine feeding kinematics peaches and snails as soft and hard food sources were compared. Results show that the feeding cycle is composed of ingestion, the manipulating phase and the transport phase. The latter is uniform for both food sources. The slow ingestion and manipulating phase displayed variability, thus indicating a prey-dependent modulation of the feeding behaviour, which is shown for the first time in *Cuora*. In contrast to all other investigated *Cuora* spp., *C. mouhotii* was not able to feed under water, which indicates an evolutionary trend towards strictly terrestrial feeding.



Main Meeting, FG Morphology
Poster: MOR 16

More than goo – a taxidermy approach on jellyfish

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Among museum collections jellyfish count to the more problematic animals to preserve and put on display. It's hardly possible to keep their color due to different aspects e.g. that they are usually put in formaldehyde. If they are thrown in alcohol it sometimes preserves the color, but it has also a shrinking effect on them. Jellyfish are about 95 percent water, which makes it almost impossible to get them on good display without any liquid. In common jellyfish are just some goo in a jar which is put in the collection. But there is more to it and a way to show their beauty even if they're not alive. To prepare these fragile animals as a taxidermist is very challenging and fascinating. Patiently you can hang them up on a thread and patch broken parts together, combined with some hidden counterweights and a good lightning can yield in magnificent results for an exhibition. New materials and a fast progress in 3D-technology allow us to produce almost perfect copies of living jellyfish, frozen in time and space. They can have all the infinitely amounts of shapes and colors as the living organism. Visitors can get a unique impression of what jellyfish really look like, next to the preserved one.



Main Meeting, FG Behavioural Biology
Poster: BEH 16

Discrimination of low frequency sounds in grey bamboo sharks (*Chiloscyllium griseum*)

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Sound is likely to provide ecologically relevant information for many fish species including sharks. The acoustic abilities of elasmobranchs have not been well studied and the little data available for only five of the approximately 1200 extant species indicates that their hearing ranges seem limited to low frequency sounds up to about 1000 Hz. This study investigated if adult grey bamboo sharks (*Chiloscyllium griseum*) can discriminate between different low frequency sounds ranging from 140 Hz to 280 Hz, while amplitude was kept constant. For this purpose, Go/No-Go experiments were used in which individuals had to learn to swim to and touch a loudspeaker when a 200 Hz tone was given but refrain from doing so when no sound was provided or at frequencies of 140 Hz or 280 Hz. All seven individuals learned to touch the speaker within 19-31 sessions and learned to not touch it in the absence of a sound or when a new frequency was used within 21-108 trials (within one super-session). In transfer tests, 200 Hertz was also successfully distinguished from 150 Hz and 160 Hz, while 170-190 Hz elicited mixed responses or were not discriminated. Accordingly, the behavioural threshold for grey bamboo sharks to discriminate between two low frequency sounds at, appears to be around a 20-30 Hz difference. Considering that sharks are not known to make any sounds (which otherwise would have certainly influenced shark hearing spectra), it can be expected that hearing abilities have been shaped by ecologically relevant sounds encountered in the shark's environment.



Main Meeting, FG Ecology
Poster: ECO 4

Comparison of two tropical ant species (*Camponotus* spp.) as a mobile task force against herbivores of the rattan palm *Korthalsia robusta*

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Mutualistic ant plant interactions where ants protect their host plants against herbivores in return for shelter are widespread in tropical ecosystems. Such interactions may involve several partner species that usually vary in magnitude of delivered benefits. The rattan palm *Korthalsia robusta* is commonly inhabited and defended by colonies of one of two *Camponotus* spp. (A or B). In a first approach to investigate this mutualistic system, we quantified the ants' ability to recruit conspecifics as a proxy for their defensibility by conducting a behavioural field experiment. Therefore, we placed a model intruder on plants inhabited by *Camponotus* species A or B, that was either moved actively to simulate a moving intruder or left there without further movements. Both ant species reacted to the stimuli delivered by the model and significantly increased the number of individuals present. More individuals were recruited immediately after intruder attachment by species B, though numbers of recruited individuals converged after two minutes between both species. Furthermore, we collected leaflets of *K. robusta* to score the amount of herbivore damage on palms settled by species A, B or on unsettled ones. Herbivore damage was significantly lower for palms settled by ants compared to unsettled ones. Interestingly, levels of herbivory did not vary significantly between plants settled by species A or B, suggesting the detected differences in the recruitment behaviour not to be relevant for herbivore defence in the investigated context.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral presentation

The first comprehensive study of insect body mass for a complete elevational gradient in the tropics reveals a striking pattern

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The body size of an animal may well be its most important functional trait. For arthropods, geographical patterns and environmental drivers of body size variation are still poorly documented and poorly understood, especially in the tropics. Along a complete tropical elevational gradient in Costa Rica, we studied two species-rich, phylogenetically independent moth taxa (794 species of Geometridae, 308 species of Arctiinae; 19,214 individuals, total) to assess the following hypotheses: 1) body size increases with decreasing ambient temperature (a Bergmann pattern), as predicted by the temperature–size rule (temperature-dependent discordance between growth and reproductive maturation rates); 2) body size increases with increasing rainfall and primary productivity, as predicted from considerations of starvation resistance; and 3) body size scales allometrically with wing area, as elevation increases, such that wing loading (the ratio of body size to wing area) decreases with increasing elevation to compensate for decreasing air density. We analyzed mean forewing length (a proven proxy for body mass) along the elevational gradient within species, among species means, and for assemblage means.

Body size consistently increased with elevation in both taxa—for individuals within species, species means, and assemblage means. Temperature was the best predictor for these patterns, whereas body size was poorly correlated with rainfall and enhanced vegetation index. Wing loading increased with elevation, counter to hypothesis. Our results support the temperature–size rule as an important mechanism for body size variation in arthropods along largely aseasonal tropical elevational gradients, whereas starvation resistance and optimization of flight mechanics seem to be of minor importance.



Main Meeting Keynote Lectures
Oral presentation

Unravelling the evolution of animal coloniality: a case study in tunicates of a solitary to a colonial transitions

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Coloniality – a higher level of biological organization with modular and coordinated growth – has evolved multiple times independently in the tunicates, the sister group of vertebrates. What ecological, genomic, and cellular factors have influenced the evolution of solitary and colonial life histories? Ecological factors: by documenting patterns of dominance and growth of solitary and colonial species in artificial substrata of a subtropical community, we determined that predation acts as an evolutionary force driving developmental changes favoring coloniality. Genomic factors: by comparing the ncRNA repertoire of *de novo* colonial ascidian genome assemblies to publicly available solitary tunicate genomes, we find overall losses in the Tunicata of many classes (families) of ncRNA types analyzed. Cellular factors: to understand the evolutionary origins of circulating putative stem cells (CPSCs) of budding and regeneration in colonial botryllid ascidians, we searched and found presence of CPSCs in the hemolymph of closely related solitary species, and identified a putative niche of CPSCs in the intestinal submucosa of solitary species. These results support the hypothesis that CPSCs were already present in the solitary styelid ancestor possibly involved in tissue/organ regeneration, and that CPSCs diverged functionally to acquire new functions in asexual reproduction or whole body regeneration in the colonial styelids. We are only beginning to identify selective factors acting at different levels of biological organization that influence solitary-colonial transitions in the tunicates. A highly dynamic nature of adult cell signaling, migration and homing affect adult developmental mechanisms adaptively to withstand environmental perturbations, and facilitate evolutionary transitions to coloniality.



Main Meeting, FG Evolutionary Biology
Oral presentation

Evolution of the gene regulatory network underlying eye and head development in closely related *Drosophila* species

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Insect compound eyes are highly complex organs, which are composed of individual subunits, so called ommatidia. We have recently shown that closely related *Drosophila* species show remarkable differences in eye size and head shape. The eye size differences between *D. melanogaster* and *D. mauritiana* are a result of differences in the number of ommatidia. We use this model to identify the molecular changes underlying the observed morphological variation in adult structures and try to understand how gene regulatory networks (GRN) in closely related species evolve.

A comparative developmental transcriptome dataset combined with a transcription factor binding site analysis showed that the GATA factor Pannier (Pnr) regulates many genes that are differentially expressed between *D. melanogaster* and *D. mauritiana*. We found that the transcript of *pnr* itself is differentially expressed in the two species during eye development. To test, if the regulatory module composed of Pnr and its co-factor Ush may represent a flexible node in the eye and head developmental GRN, we overexpressed *pnr* and *ush*, respectively in the eye-antennal disc in *D. melanogaster*. We indeed were able to phenocopy aspects of the differences observed between *D. melanogaster* and *D. mauritiana*, showing that higher levels of Pnr lead to a bigger eye area due to a higher number of ommatidia and a narrower, interstitial face cuticle. In summary, our data suggests that differences in the expression of *pnr* and *ush* explain part of the variation observed between the head shapes of *D. melanogaster* and *D. mauritiana*.



Main Meeting, FG Neurobiology
Oral presentation

Heterochronic development of the central complex: Using genome editing to follow the development of homologous neurons in different species

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The insect brain is built by a conserved set of neuropils. However, size, shape and developmental timing of neuropils differ, reflecting evolutionary adaptations. The central complex (CX) provides an intriguing example of a heterochronic shift of development: Ancestrally, the CX develops during embryogenesis but in *D. melanogaster* it emerges post-embryonically during metamorphosis. In the red flour beetle *Tribolium castaneum*, a partial CX is found at the end of embryogenesis. We want to understand the cellular and the genetic bases of heterochronic development of CX by comparing these two genetic model systems.

In both species, we marked neurons that express the transcription factor retinal homeobox (*rx*). In *T. castaneum* we used an enhancer trap while in *D. melanogaster*, we generated a bicistronic line where EGFP is translated from the endogenous *rx* locus by CRISPR/Cas9 mediated homology directed repair. Indeed, *rx* positive cells showed similar cell body location and projection patterns.

Next, we compared the development of these homologous neurons from embryo to the adult. Indeed, *rx* positive cells develop in a similar way but enter certain steps at different times. A protocerebral bridge emerges in the beetle embryo but in the pupa of *Drosophila*. Intriguingly, a developmentally immature form of the central body forms synapses at the end of beetle embryogenesis, while in the fly this stage remains non-functional. We discuss the relevance of our results for the mechanism of heterochronic brain development and in how far they change our view on CX development in holometabolous insects.



Main Meeting, FG Evolutionary Biology
Oral presentation

From ants to wasps: Evolutionary conserved cuticular hydrocarbon functionalities over a large phylogenetic distance in eusocial and solitary Hymenoptera

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Cuticular hydrocarbons (CHC) form the basis for a wide array of chemical communication systems in insects while primarily functioning as desiccation barrier. Conserved signaling properties in CHC profiles can range from nestmate recognition in eusocial insects to sex pheromones in solitary insects. Simultaneously, CHC profiles have been postulated to display considerable flexibility to allow insects to adapt to a wide range of different climatic conditions. However, preservation of species-specific signaling functions might constrain the adaptive flexibility postulated to be crucial for insect survival and desiccation prevention in different environments. To shed light on these seemingly contradictory selective pressures, we analyzed CHC profiles in representative eusocial and solitary Hymenopteran species and isolated the particular CHC compound classes correlating with environmental factors most closely associated with humidity and desiccation. In the invasive Argentine ant *Linepithema humile*, huge super colonies partially transcending continents retain the capability of widely expanded nestmate recognition while adapting to vastly different micro-climates, whereas in the cosmopolitan parasitoid jewel wasp *Nasonia vitripennis*, CHC function as universally recognized female-specific sex pheromones. By unraveling the compounds with the most potential for adaptive flexibility in both species, we were also able to narrow down the CHC compounds most likely encoding and conveying the conserved signaling function, revealing interesting similarities despite the actual communicated information varying so widely between both species. This suggests that the main signaling properties in CHC profiles can be evolutionary conserved traversing vast phylogenetic boundaries, delivering the first hints at elements of a unified, common “chemical language”.



Main Meeting, FG Evolutionary Biology
Oral presentation

Genomics of hybridization, speciation, and parallel phenotypic evolution in a color-polymorphic songbird radiation

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Species with a high incidence of hybridization in which various phenotypes exhibit discordant patterns of divergence offer unique opportunities to study genetic basis and evolutionary origin of species and phenotypic diversity. In this presentation, I introduce a new songbird system characterized by pervasive introgression and genus-wide parallel evolution of plumage color-phenotypes – wheatears (genus *Oenanthe*). Species tree reconstruction based on RADseq data confirm patterns of parallel plumage color evolution across the genus, and uncover parallel evolution also at a recent time scale in the *O. hispanica-pleschanka-melanoleuca-cypriaca* complex. The presence of the entire admixture spectrum in the hybrid zone of pervasively hybridizing *O. melanoleuca* and *O. pleschanka* in Iran, and the detection of footprints of introgression from *O. pleschanka* into *O. melanoleuca* suggest a potential role for introgression in parallel plumage colour evolution. Furthermore, the analysis of seven de novo genome assemblies uncover intriguing patterns of differentiation that in other systems have been interpreted as consequences of chromosomal inversions. Together with an ongoing range-wide whole-genome resequencing effort, these results contribute to uncovering the molecular bases and evolutionary histories of species and parallel phenotypic evolution in wheatears and related species.



Main Meeting, FG Morphology
Oral presentation

Morphology and synergistic action of complementary attachment pads in stick insects (Phasmatodea)

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Stick insects (Phasmatodea) are distributed in a wide range of habitats worldwide and cope with several different surfaces and topographies in their environments. The tarsus consists of two different devices: pad-like structures (arolium and euplantulae) and claws. The functional properties of single pads were shown in the past to be different for arolia and euplantulae. While arolia are rather adhesive pads, euplantulae are characterised as friction pads. Euplantulae, additionally, reveal different surface microstructures as adaptations to different degrees of surface roughness. Surprisingly, neither the whole attachment apparatus nor the contribution of its parts to the overall performance have been subject of experimental investigations. We therefore analysed the usage of different attachment pad types and the performance of the entire attachment system in two stick insect species with different euplantular microstructures: *Medauroidea extradentata* (smooth) and *Sungaya inexpectata* (nubby). Insects were filmed in different posture situations (upright, vertical, ceiling) and the videos were analysed to assess the usage of different attachment structures. Furthermore, we measured attachment forces of the whole attachment system at different levels of surface roughness in pull-off and shear directions. As a general result, we revealed that the combination of claws, arolia and euplantulae (1) provides mechanical interlocking on corrugated surfaces, (2) generates adhesion and friction on smooth surfaces and (3) facilitates attachment on a broad range of surface roughnesses, with the least performance at 0.3 - 1.0 μm . The overall attachment forces on smooth surfaces are higher for *M. extradentata* and on rough surfaces for *S. inexpectata*.



Main Meeting, FG Morphology
Oral presentation

Multifunctional feet: How webspinners (Insecta: Embioptera) can walk and spin with the same tools

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Using the legs for multiple functions next to walking, potentially imposes constraints and compromises. Within this context, webspinners show a unique morphological adaptation: they use their front feet to produce silk for building a shelter. They spin with stereotypical spin-steps releasing silk with each step. The morphology of the so-called spinning-tarsus is well studied; however, the actual process of silk ejection, is addressed only vaguely. The spinning apparatus, located within the prothoracic basitarsus, is composed of: i) multinucleated silk glands enclose a reservoir used for silk storage; ii) the ejection duct with canal cage; iii) hollow, cuticular hair-like tubes (silk-ejectors) located on the ventral surface of the spinning tarsus.

We here present morphological and experimental evidence for a “passive” pressure-induced spinning mechanism induced by external mechanical stimuli. Material distribution of the tarsal cuticle and anatomy of the spinning apparatus provide both deformability of the basitarsus and mechanical resistance for proper pressure generation; resulting in ejection of the silk, when the silk-ejectors contact the surface. When the first contact between single threads and substrate is established, it is sufficient to pulling off the substrate to continue silk generation. Furthermore, we experimentally induced silk production in anaesthetised individuals by applying a mechanical stimulus to the spinning-tarsus. As silk spinning is induced by likely any mechanical contact of the ventral surface of the spinning-tarsus, the proposed mechanism results in a complex behaviour for both, application of the silk, as well as for contact avoidance of the spinning apparatus with the substrate during locomotion.



Main Meeting, FG Morphology
Oral presentation

Confused chondrocytes: Are the cells in stingray mineralized cartilage performing the roles of bone cells?

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In most vertebrates the embryonic cartilaginous skeleton is replaced by bone during development. During this process, cartilage cells (chondrocytes) mineralize the matrix and die, giving way to bone cells (osteocytes). However, sharks and rays (elasmobranchs) have cartilaginous skeletons throughout life, where only the surface mineralizes, forming a layer of tiles (tesserae). Elasmobranch chondrocytes, unlike those of other vertebrates, survive cartilage mineralization and are maintained alive in cell-rich layers in tesserae. However, the roles of the chondrocytes and the reasons for housing them alive in the mineralized tissue remain unknown. Applying a custom analysis workflow to high-resolution synchrotron microCT scans of tesserae, we characterize how stingray chondrocyte morphology and arrangement vary, comparing with other vertebrates. We show that even when cells have been incorporated into tesserae, they maintain the same volume indicating they do not hypertrophy during mineralization, as in other taxa. Cells, however, show distinct zonal variation—being flatter further from the cartilage matrix and spherical in the center of tesserae—which may indicate local variation in function. The cell density is higher near canals passing the tesserae, suggesting this is a nutrients source. Cells are linked by small passages in the matrix, arranged in series and oriented toward neighboring tesserae, illustrating connectivity and perhaps communication between tesserae. This network arrangement and the shape variation of chondrocytes in tesserae indicates that these cells may interact and manage mineralization differently from chondrocytes in other vertebrates, perhaps performing analogous roles to osteocytes in bone.



Main Meeting, FG Developmental Biology
Poster: DEV 2

Development in stand-by: (sub)cellular changes in *Daphnia* embryos during diapause

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Diapause is a form of dormancy, predetermined by the genotype allowing animals to overcome harsh environmental conditions. During the phase of apparent death, development, growth and metabolic activity are depressed until distinctive environmental cues signal favorable living conditions. Metabolic depression during the ontogenetic interruption is challenging for cell viability, cells must maintain their viability at reduced energy flows. However, the mechanisms allowing cells to sustain such long periods of suspended animation remain elusive.

We investigated diapause related changes on the cellular level in diapausing and non-diapausing *Daphnia* embryos. Using (immuno-)fluorescent labeling, we observed the expressions of cell cycle associated proteins, nucleolar proteins and cytoskeletal proteins at different developmental stages.

We found that the cytoskeleton is gradually reduced to a minimum, rendering diapausing cells compact and condensed. Accompanied by a downregulation of the proliferating cell nuclear antigen (PCNA), the mitotic activity is brought to a halt during diapause. At the same time, we observed that cells in 35-year-old diapausing *D. galeata* embryos still maintain their nucleoli structure, which may indicate ongoing RNA translation. We here provide first insights into the cellular changes in *Daphnia* embryos during diapause. Our results suggest that cells in diapause have evolved some unique strategies that allow long-term suspended animation maintaining the capacity of resurrection.



Main Meeting, FG Behavioural Biology
Poster: BEH 4

Influence of males' morphology and mating position on paternity share in a polyandrous tree frog

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In the theory of sexual selection, male-male competition and female choice for mates contribute to the variance in organisms' reproductive successes and to the evolution of the mating strategy. Since males' reproductive success is associated with the number of females they mate with, males should adopt the reproductive tactic which can increase their chance of mating (i.e. pre-mating sexual selection). However, in some species, sexual selection does not end at mating; sperm competition and cryptic female choice are two main forces in post-mating selection. In the anurans the operational sex ratio of which is male biased, the males' opportunities for mating successes are limited. Unpaired males may gather around the mating pair and release sperm in order to obtain reproductive success (polyandrous mating). Polyandrous mating behavior has been observed in the emerald tree frog (*Rhacophorus prasinatus*), a lek-chorus anuran, in the field. However, evidence of multiple paternity and the relationships between males' traits and paternity share are still lacking. In this study, we monitored reproductive behavior in a wild population of the emerald tree frog for two breeding season peaks, and conducted parentage analysis of clutches resulting from polyandrous mating. Then we examined the relationships among males' body size, body mass, mating positions and offspring number. The results showed that (1) the proportion of polyandry is around 42% in the wild population, (2) multiple paternity was detected in polyandrous clutches, (3) in polyandrous clutches, the number of a male's offspring was correlated with its mating position but not its morphology.



Symposium: Form and function of motion systems: new approaches, new opportunities, new challenges

Oral presentation

The muscle as a wobbling mass: Impact responses in key experiments

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For any type of terrestrial locomotion, the common working condition is active contraction of skeletal muscles that generates skeletal movement through space. For mammalian locomotion, propulsion requires repulsion from a surrounding solid that in turn induces shock-wave-like accelerations (impact) to the system via bones muscles and joints.

In order to emulate shock waves that propagate through a muscle in response to impacts in Wistar rat m. gastrocnemius medialis and lateralis (GAS), we dropped fully stimulated specimens of isolated rat (*Rattus norvegicus*, Wistar) muscle (m. gastrocnemius medialis and lateralis) clamped ex vivo into a custom-made C-shaped frame on the ground. In order to capture muscle kinematics as a result of impact the muscle belly was patterned with sphere markers and recorded with high speed cameras. Also all experiments were conducted at optimal length and with an impact force corresponding to a rat running at 0.5 ms^{-1} .

In the low intensity conditions we determined the properties of the fibre material across the whole isometric force range, we calculated mechanical work loops of the MTC centre of mass during one damped oscillation period and the damping coefficients. This talk will focus on the experimental part of our work from the design development to our first results and conclusion.



Main Meeting, FG Behavioural Biology
Poster: BEH 14

Do echolocating bats adapt their calls to weather-induced variations in sound attenuation to maintain constant detection range?

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Echolocation is the use of self-generated ultrasonic emissions to probe the surrounding environment. It is based on the auditory analysis of the temporal and spectral properties of the returning echoes. However, ultrasound is strongly attenuated by the atmosphere, thus severely limiting the maximum object detection range in echolocating animals. Importantly, this atmospheric attenuation varies with sound frequency and ambient temperature and humidity. In temperate areas, bats face a broad range of temperatures and humidities throughout the year, causing seasonal and daily variations in their prey detection range. Echolocating bats constantly adapt the frequency, duration, and amplitude of their calls to the behavioural and spatial context. Given this extreme and fast plasticity, we hypothesized that echolocating bats also adapt their call to the local weather conditions to optimize detection range. We recorded the echolocation calls of different species of wild, free-flying bats with a microphone array, along with ambient temperature and humidity. Using the time-of-arrival differences of each call at the different microphones, we reconstructed their 3D flight trajectories, which allowed us to correct for distance-, frequency- and weather-dependent attenuation to reconstruct the call as emitted by the bat. We then measured emitted call frequency, duration, and amplitude, calculated maximum prey detection ranges for calls of those properties, and correlated these data to the local atmospheric attenuation. We predict that bats keep detection range constant by increasing call duration and amplitude with increasing atmospheric attenuation (to counteract the increased attenuation), and by decreasing call frequency (to lower atmospheric attenuation).



Main Meeting, FG Morphology
Poster: MOR 18

Multiscale structural reinforcement strategies in the tiled cartilage of sharks and rays

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Shark and ray skeletons are predominantly (~80%) unmineralized cartilage, a counterintuitive material design compared with the stiff, bony skeletons of other vertebrates. Through synthesizing our group's studies of materials and performance of these skeletons, however, we illustrate that this distinct cartilage type exhibits structural features at multiple scales to facilitate management of mechanical loads. In whole skeletal elements, for example, the densest material—the mineralized tiles (tesserae) covering the skeleton—are confined to regions of high stress (i.e. farthest from the skeleton's neutral axis of bending). Skeletal cross-sections are typically subcircular, with most material in-line with the primary axis of loading. In the surface tiling (tessellation), the arrangements of the tesserae and the soft joints between them allow mechanical asymmetry in tension and compression and a regulated response to bending loads. This is combined with local level control of interactions between tesserae, where joint surface topology creates a subtle locking behavior. The shape and size of individual tesserae reflects particular loading orientations, with some morphologies being also more tunable for particular emergent material properties. Finally, at the tissue level, high mineral density features are spatially organized according to the highest stresses, with the growth fronts at tesserae margins allowing local tuning of structure and mechanical properties in response to changing skeletal stresses. Adjustments at all of these structural levels will affect skeletal mechanical properties at larger size scales, making tessellated cartilage a mechanically-efficient, low density skeletal material, where the most "expensive" materials are employed sparingly and effectively.



Main Meeting, FG Morphology
Poster: MOR 4

Evolutionary morphology of sperm transfer forms in cryptic daddy long-leg spiders (Araneae: Pholcidae: Ninetinae)

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Ninetinae is the smallest of all pholcid subfamilies, consisting of only 34 described extant species. Ninetinae are tiny ground dwelling spiders with a cryptic lifestyle mainly in arid habitats. Preliminary data indicate that Ninetinae hold an early branching position within the pholcid phylogeny [1], making them a key taxon for studies on pholcid systematics and evolution. It was already suggested that Ninetinae are exceptional in terms of sperm morphology and sperm transfer form. In contrast to all other scrutinized pholcid groups, the single Ninetinae species previously studied retained synspermia – an aggregation of fused spermatozoa [2]. Here, we investigate the evolutionary morphology of sperm and sperm transfer forms in two further Ninetinae genera using Transmission Electron Microscopy (TEM). Our data reveal the presence of complex synspermia in all studied Ninetinae species, strengthening our hypothesis that this subfamily is generally characterized by plesiomorphic synspermia. These findings suggest that cleistospermia (i.e. individualized sperm for transfer) may have evolved once in Pholcidae as that transfer form may be a synapomorphy uniting all subfamilies other than Ninetinae [2].

[1] Huber et al. (2018) *ZooKeys* 789: 51.

[2] Michalik and Ramírez (2014) *Arthropod Struct Dev* 43: 291.



Main Meeting, FG Evolutionary Biology Keynote Lectures
Oral presentation

The evolution of infectivity in parasitoid wasps

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Parasitoid wasps are a diverse group of insects that reproduce by fatally infecting their hosts. This lifestyle requires specific adaptations and has generated high species diversity and often tight host specializations. Parasitoids that specialize in attacking aphids are a diverse group with the potential for biocontrol. Aphid defenses against parasitoids come largely from a suite of heritable bacterial endosymbionts that produce toxins to halt egg development. In the wild, diversity in both aphid genotypes and their endosymbionts creates a mosaic of potential hosts to which parasitoids must adapt. We have used experimental evolution to examine the basis of infectivity in the parasitoid *Lysiphlebus fabarum*. Rearing parasitoids in aphids housing different endosymbionts has rapidly generated populations with different infective phenotypes. Using comparative transcriptomics of adult and larval wasps, we have identified a suite of putative detoxifying and venom components that likely enable them to parasitize varying aphid hosts. Variation across experimental populations appears to be largely genetically based, rather than a plastic trait. We hypothesize that these diverse infective phenotypes are maintained in the wild by negative frequency dependent selection. These fascinating and interconnected systems illustrate the potential for rapid genetic shifts in wild populations, depending on their hosts.



Main Meeting, FG Physiology
Oral presentation

Acclimation of intestinal morphology and function in Djungarian hamsters (*Phodopus sungorus*) related to seasonal and acute energy balance

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Many small mammalian species exhibit seasonal changes in intestinal morphology and function to increase energy yield from food resources during winter. These changes mostly occur as increased intestinal size and absorptive surface or enhanced mucosal nutrient transport capacity. We investigated whether seasonal Djungarian hamsters also profit from an increase in nutrient absorption in addition to their numerous energy saving winter acclimatizations in response to short photoperiod. As spontaneous daily torpor in the hamsters represents one of these energy saving mechanisms related to food quality and quantity, we hypothesized that the variable torpor expression patterns in this species might be influenced by an individual nutrient uptake capacity. A comparison of small intestinal histology and physiology between long and short photoperiod- acclimated hamsters did neither indicate seasonal changes in nutrient uptake capacity nor any relation to torpor expression. However, a short photoperiod-induced increase in relative intestinal length and dry weight led to the assumption of an increased intestinal absorptive surface as result of seasonal body mass reduction. However, this rather indirect effect appeared to be of minor importance for maintaining energy balance during winter. In food-restricted hamsters under long photoperiod that showed non-seasonal fasting-induced torpor, we measured a higher electrogenic transport capacity for glucose, which showed a trend towards a negative correlation with torpor incidence. Reduced food availability did not induce intestinal atrophies or malfunction, but led to fasting-induced torpor as acute response towards the lack of energy, which seemed to become more important when individual nutrient uptake capacity was low.



Main Meeting, FG Neurobiology
Oral presentation

Orcokinins in primary olfactory and other sensory neurons, interneurons and neurosecretory neurons in the CNS of the crayfish *Orconectes limosus*

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Native orcokinins (OKs) were discovered as hindgut-activating peptides of the crayfish *Orconectes limosus* (Asn13-OK: NFDEIDRSGFGFN; Val13 OK). Furthermore, Ser9-OK, Val13-OK, Ala13 OK analogues, Thr8-His13-OK occur on prepro-orcokinins as now cloned by us from several parts of the CNS.

Hundreds of novel OK-immunoreactive (OKir) neurones densely innervate almost all neuropils of the eyestalk, brain, suboesophageal ganglion (SOG), thoracic (TG) and abdominal ganglia (AG). Moreover, several large projection interneurons as well in the brain as well as many distinct neurons within the stomatogastric nervous system exist. We found strong OKir in nearly all primary olfactory sensory neurons of the aesthetascs that enter the olfactory lobe of the brain via the antennular nerves; the occurrence of Asn13-OK has been confirmed by mass spectroscopic determination and precursor cloning from antennules. OKir fibres in several nerves of each ventral nerve cord ganglion lead to dense neuropile innervation. A large group of OKir neurons in the terminal abdominal ganglion is responsible for an extensive innervation of the entire hindgut musculature. Furthermore, mainly from a group of neurosecretory OKir neurones in anterior lateral SOG, fibres give rise to abundant neurohaemal terminals in the SOG perineurium and in the pericardial organs. These localisations are corroborated by the cloning of several different OK-precursors for the OK-family peptides from different parts of the CNS. Altogether this distribution suggests many more physiological functions of OKs than the known hindgut-myotropic actions, meaning several novel functions as sensory, modulatory and neurohormonal neuropeptides, which merit further exploration.



Main Meeting, FG Developmental Biology Keynote Lectures
Oral presentation

Phylogeny-ontogeny correlations: lessons from microbial biofilms

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Many bacteria species form biofilms. These multicellular communities display organised behaviours that resemble to some extent developmental processes in truly multicellular organisms like animals and plants. Ontogenies in multicellular eukaryotes were recently studied by phylo-transcriptomic approaches that uncover phylogeny-ontogeny correlations during development. Underlying causes of these correlation patterns are still debated; however, they readily demonstrate that true developmental processes harbour phylogenetic (macroevolutionary) imprints that could be found at the molecular level. To test if similar phylogeny-ontogeny correlations exist during the formation of bacterial biofilms we performed RNAseq of a fine-grained series of biofilm stages in the common biofilm model *Bacillus subtilis*. After obtaining a phylostratigraphic map for *B. subtilis* genome we calculated transcriptome age index which revealed a clear correlation between the biofilm stage and phylogenetic age of the transcriptome. This result suggests that biofilm development has a built-in macroevolutionary logic that is also found in more complex eukaryotic multicellularity. We discuss these findings in relation to the origin of life, development and major macroevolutionary transitions.



Main Meeting, FG Morphology
Poster: MOR 9

Towards a formalised basis of biomimetics

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An engineering design approach is introduced to better understand the processes operating during biomimetic research projects. Thereby different levels are distinguished: task, function, working principle [Wirkprinzip], construction and overarching system. Function and working principle are identified as the core elements in the biomimetic knowledge transfer. An organism can be considered as a web of functions (a functional whole), with some general functions that always have to be fulfilled, such as “to sustain organisation”. Attached to them are particular functions that directly relate to working principles. The engineering design schema can be used for various biological entities, as shown by some examples. Thereby it can help to clarify concepts that are also relevant for morphology and evolutionary biology.



Symposium: Form and function of motion systems: new approaches, new opportunities, new challenges; Keynote
Oral presentation

Limb proportions and motor flexibility in insects

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Insects have been used as model systems in the study of locomotion for decades, and research has accumulated knowledge on species of very different body structure, size, habitat preferences and behaviour. Although several fundamental aspects of the insect locomotor system are very similar, the functional use of limbs in insects may differ tremendously among species. Generally, this different functional use of limbs is reflected by morphological characteristics, sometimes with obvious functional specialisation of a particular limb pair. On the other hand, every insect species uses its limbs in different functional contexts, including locomotion, manipulation or exploration. In order to assess the effect of a particular morphological factor on motor behaviour, it should be advantageous to compare multiple behaviours in a group of species with little variation in other morphological features. In an attempt to do so, I will discuss the relevance of differences in body-limb-proportions in the flexible use of limbs in terrestrial motor behaviours such as walking, climbing and searching. Apart from some considerations on differences between insect orders, I will focus on the comparison of the stick insect species *Carausius morosus*, *Medauroidea extradentata* and *Aretaon asperimus*. The main idea of this intra-order comparison is to avoid strong differences in body plan, habitat or ecological niche, and to focus on the role of different limb proportions instead. I will show how differences in limb proportions affect the spatial coordination and the transfer of contact information among limbs, and will discuss the significance for different contexts of motor behaviour.



Main Meeting, Rathmayer Prize
Oral presentation

Artbestimmung von Heuschrecken mittels Analyse des Rufspektrogramms

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Verschiedene Heuschreckenarten auf einer Wiese zu erfassen ist schwer, da sich die Spezies mitunter, rein durch optische Merkmale, sehr ähneln. Es wurde daher in dem Projekt ein System entwickelt, welches eine eindeutige Unterscheidung der Tiere anhand ihrer Laute ermöglicht. Dabei wurden Aufnahmen mit dem Gerät „Batlogger M“ der Firma Elekon getätigt, das Ultraschall-Laute aufzeichnet. Um artspezifische Laute der Tiere zu verifizieren, erfolgte nach der Erfassung des Gesangs noch eine Bestimmung anhand von optischen Merkmalen. Als Bestimmungsliteratur wurde hier [Bellmann, H.] (1993). Heuschrecken beobachten, bestimmen. Augsburg: Weltbild Verlag GmbH. verwendet. Bei der Vermessung am Computer, welche mittels des Programmes Batsound von Elekon erfolgte, wurden Parameter wie Hauptfrequenz, Impulsanzahl, Impulsdauer und Pulsdauer bestimmt. Die Abgrenzung der Parameter erfolgte nach den Definitionen aus [Roesti, C., & Keist, B.] (2009). Die Stimmen der Heuschrecken. Bern: Haupt-Verlag. Besonders nützlich ist diese Methode für den Einstieg in die Bestimmung von Arten in der Ordnung Orthoptera. Selbst mit wenig Kenntnissen kann eine fehlerfreie Laut-Vermessung und somit Artbestimmung durchgeführt werden; denn mit Hilfe weniger Parameter ist eine sichere Bestimmung jeder singenden Heuschreckenart möglich. Die entwickelte Methode erlaubt, mehr Kenntnis über die Heuschreckenfauna, z.B. Deutschlands, zu gewinnen und somit kann zu einem besseren Schutz der Tiere beigetragen werden.



Main Meeting, FG Morphology
Oral presentation

Ovipositor bending movements of a chalcidoid wasp

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Most chalcidoid wasps are minute sized parasitoids of other insects. In order to reach their hosts and permit greater control over egg placement, several species are able to actively bend and rotate their terebra (= ovipositor shaft) in various directions despite the lack of intrinsic musculature.

We investigated the oviposition process and the musculoskeletal ovipositor system of *Lariophagus distinguendus* (Förster, 1841) (Pteromalidae), a solitary, idiobiont larval ectoparasitoid of several coleopteran species that exhibits extensive terebra movements in both the lateral and dorso–ventral direction during oviposition. We discuss the actuation of the different ovipositor movements, the underlying mechanisms of the terebra movements (lateral/dorso–ventral bending, rotation), and their potential eco-evolutionary significance.

In hard substrates, a movable terebra increases the chance of making contact with the host within a concealed cavity, since the position of the terebra is ‘fixed’ at the puncture site. The evolution of the ability to actively bend the terebra might be considered to be a key innovation that has largely contributed to the acquisition of new hosts to a parasitoid’s host range. Such shifts in host exploitation, followed by rapid radiations, have likely enabled the evolutionary success of Chalcidoidea (> 500,000 estimated chalcidoid species).



Main Meeting, FG Neurobiology
Poster: NEU 6

The projection pattern of the mechanosensory lateral line nerves of the zebrafish, *Danio rerio*

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The zebrafish mechanosensory lateral line is a model system for the investigation of neuronal mechanisms like axon-guidance and the formation of topographic maps. The lateral line consists of peripheral sensory organs, the neuromasts, and afferent and efferent fibres. The projection of these afferents into the hindbrain displays a topographic ordering, i.e., the relative position of afferent axons in the hindbrain represent that of the neuromasts they innervate (Alexandre, 1999, PNAS, 96(13), 7558). Whether this topography extends to the synaptic projections of these axons in the hindbrain has not been investigated thus far. In fact, the projections of the afferents to the hindbrain medial octavolateral nucleus (MON), have been shown to be very broad (Metcalf, 1985, J Comp Neurol 233:377), raising the question, if the peripheral topography indeed is maintained in the MON.

To investigate this, we performed double and triple staining of defined neuromasts on the trunk and head of the adult zebrafish, using fluorescent BDA and biocytin. To further investigate, if the two sub-systems of the mechanosensory lateral line (canal and superficial neuromasts) differ in their projections, we also stained a single neuromast in the supraorbital canal.

The projections of individually stained afferents were traced and reconstructed from transverse sections and cleared whole-brain scans. We confirm that while the axons of the head and trunk differ in their arrangement within the MON, both project and synapse broadly within the whole MON. This includes the projection of canal neuromasts, indicating a lack of difference in the neuronal representation of this sub-modality.



Main Meeting, FG Evolutionary Biology
Oral presentation

One, two, many – honeybee queen pheromones are manifold and redundant in function

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Queens of social insect (e.g. ants, bees, termites, wasps) signal their presence and fertility to workers using pheromones. Workers usually decide to react altruistically and forego their own reproduction. In honeybees, pheromones from mandibular glands suppressing worker reproduction had been identified 60 years ago (queen mandibular pheromone, QMP, a blend of carboxylic acids and aromatics). Only recently, queen pheromones have also been identified in other social insects. In ants, wasps, and bumblebees, these queen pheromones are long-chained hydrocarbons and often conserved across species. We tested whether queen hydrocarbons could also induce sterility in workers of the honeybee, *Apis mellifera*. By offering different compound mixes to queen-less workers, we show that not only QMP, but also alkenes, carboxylic acids, and esters typically found on a queen's cuticle, act as queen pheromones (Princen et al., 2019). There was not always synergy between different compounds, not even within the QMP blend. This suggests a surprising redundancy in signalling compounds. How such a redundant system could have evolved is not obvious, and I will discuss several suggestions. The complex set of honeybee pheromones serves several functions, which might explain part of the redundancy.

Princen et al. (2019) ProcRSocB, 286, 20190517



Main Meeting, FG Systematics, Biogeography and Diversity
Oral presentation

Reconstructing two hundred years of faunal change in North and Baltic Sea – what museum records can tell us

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Human action is increasingly distorting the distribution and abundance of species. Confirming and quantifying this new paradigm, however, is inherently difficult, as it requires to look back in time, comparing past and present species assemblages. Museum collections represent a physical record of past species occurrences, and are therefore an irreplaceable resource in understanding faunal change. In contrast to literature records for example, museum specimens can be re-identified, counted and measured. Unfortunately, collections may also be riddled with biases associated with unsystematic sampling efforts and the loss of older records. So what can museum collections tell us? In an attempt to answer this question, we focus on the North and Baltic Sea as regions heavily impacted by humans. We compiled a database of ca 25,000 museum records for three dominant invertebrate taxa, Crustacea, Echinodermata and Mollusca, from museums of the NORe association and the Senckenberg Research Institute and Museum of Natural History in Frankfurt. We discuss statistical approaches that might be able to account for collection-specific biases. Lastly, we present first results of the analyses, peeking into the past to ultimately characterise faunal change at a large scale.



Main Meeting, FG Neurobiology Keynote Lectures
Oral presentation

The neural basis of parental care in poison frogs

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Parental care has evolved repeatedly and independently across animals. Yet while the ecological and evolutionary importance of parental behavior is well recognized, underlying mechanisms remain poorly understood. We took advantage of behavioral diversity within and across closely related species of South American poison frogs (Family Dendrobatidae) to identify core neuroendocrine correlates of parental behavior shared across sexes and species. Dendrobatid poison frogs show remarkable diversity in parental care. Both male and female care occur with and without pair bonding in this clade, and a number of species exhibit behavioral flexibility, wherein the typically non-parenting sex will occasionally perform parental duties. Taking a multi-level approach, we characterized differences in hormone levels, neural induction, and gene expression in active neurons in three species with distinct parental care patterns: male uniparental, female uniparental, and biparental. We identified the medial pallium and preoptic area as core brain regions associated with parental care, independent of sex and species. Identification of neurons active during parental care confirms a role for hormones and neuropeptides associated with parental care in other vertebrates. Our work highlights the potential for comparative, mechanistic studies to build a more complete understanding of how shared principles and species-specific diversity govern parental care and other social behaviors in amphibians, among vertebrates, and across animals.



Main Meeting, FG Morphology
Poster: MOR 3

Rapid evaluation of ultrastructural features in epoxy resin embedded samples using serial- and re-sectioning techniques

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Ultra-thin sectioning of epoxy resin embedded samples can be a quite lengthy process, especially if specific singular target structures have to be located by slowly approaching the region of interest using semi-thin sections. Staining of the sections, followed by visual control at the light microscope, over and over again, makes it a very time-consuming procedure. Furthermore it is always accompanied by the risk of over-sectioning the area of interest, especially when new samples are sectioned for the first time. It is much more time efficient and comfortable to define the area of interest on basis of an initially sectioned series of semi-thin sections at the light microscope and to proceed with a re-sectioning of specific semi-thin sections into ultra-thin sections for subsequent ultrastructural investigations. The presented re-sectioning methodology allows for a secure uptake and subsequent ultra-thin sectioning of single sections and section ribbons as well as to prepare proper ultra-thin sections of samples that have been incompletely infiltrated with resin in first place. Applying this approach, ultrastructural information of structures of unknown position in the samples can be gained within a time frame of about twelve hours (starting with an embedded sample until finished ultra-thin sectioning). Besides the use for regular transmission electron microscopical investigations, the gained results from the re-sectioning are suitable for rapid evaluation of traced and segmented structures in 3D reconstructions (based on the previously collected semi-thin sections), as they reveal ultrastructural information of the sample, beyond the resolution limit of light microscopy.



Main Meeting, FG Physiology
Poster: PHY 6

Prey or foe? – characterization of two different venom types from assassin bugs

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The suborder Heteroptera comprises more than 40.000 species and represents a highly diverse group regarding the different habitats and food sources they have exploited. From the ancestral phytophagous Heteropterans, several groups of hematophagous and predacious species have evolved. The ability to feed on animal prey can be mainly traced back to the transformation of salivary glands into venom glands and the functions of these venom compounds not only include prey killing but also immobilization and extra-oral digestion. In this project, we used an integrated transcriptomic and proteomic approach in order to unravel the protein composition of venom from two terrestrial predatory Heteropterans, *Platymeris biguttatus* L. and *Psytalla horrida* Stål. In both species, the two main gland types, posterior main gland (PMG) and anterior main gland (AMG), secrete different sets of proteins. PMG venom mainly consists of S1 proteases, redulyisin-like proteins, and several venom proteins known from other assassin bug species. In AMG venom, hemolysin-like proteins and cystatin-like proteins are predominant aside from different venom protein families. The differences between the two gland parts can be attributed to the differential use of AMG venom for defense and PMG venom for subduing prey, and therefore the adaptation to different target groups. The comparison between venom gland and gut transcriptome revealed that some venom protein families are not venom-specific but also highly expressed in the gut. This indicates a probable digestive function of these protein families. The study demonstrates the importance of venom composition for prey killing and defense in predatory Heteroptera.



Main Meeting, FG Morphology
Oral presentation

Dogs in motion

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No other species has experienced a higher selection of body mass, body shape, size or skull shape than dogs. Studying effects of domestication is a key to the understanding of character variation and character combination ever since Darwin. In the last 15 years we (many students and coworkers) have studied locomotion and postcranial morphology of more than 400 dogs of 35 different breeds. The presentation will give a summary of these studies. While sagittal plane locomotion is not affected by any of the foregoing mentioned parameters and simply rules by the principle of limbs as inverted, zigzag-shaped pendulum with matched motion of the first and third limb element moving in the highest possible pivot, body shape has a crucial influence on 3D-kinematics. This cannot be analyzed using skin markers but solely with high-speed, biplanar fluoroscopy followed by scientific roscoping (see Gatesy et al. 2010, JEZ). For example, French bulldogs translate extensive femoral long axis rotation ($>30^\circ$) into a strong lateral displacement and rotations about the craniocaudal (roll) and the distal-proximal (yaw) axes of the pelvis in order to compensate for a highly abducted hindlimb position from the beginning of stance. 3D kinematics absolutely reflect the differences in body shape and limb position. Speed types and strength types (according to Chase et al. 2002, PNAS) differ in skull and pelvis shape and in the transverse profile of their long bones (elliptical vs. round), and a difference in ribcage shape (either slim or round in cross-section).



Main Meeting, FG Behavioural Biology
Poster: BEH 3

Mollies playing tiddlywinks: social learning in a visual color discrimination task – do sexes differ?

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Fish and many other animal species are able to adapt their behavior to better cope with the environment by observing others, that is through social learning. Several studies show that social learning in fish occurs in different contexts like foraging, mate choice, anti-predator behaviour, migration or short-range orientation. Following poeciliids playing tiddlywinks in a visual serial reversal learning task using private information (Fuss and Witte (2019), *Current Zoology*, in press, <https://doi.org/10.1093/cz/zoz029>), we investigated the ability of experimentally naive Atlantic molly 'observers' (*Poecilia mexicana*, 10 males, 10 females) to learn a color discrimination task by mere observation of male 'demonstrators'. First, we trained five demonstrators to discriminate between green and yellow winks, one of which was rewarded with food until they reached a learning criterion of 75% correct responses in five out of six consecutive training sessions. Afterwards, we tested the observers' performance in test sessions, each consisting of a series of demonstrator trials accompanied by six observer trials. To succeed in their task, observer had to learn (a) to associate a specific wink color with the hole-board and food reward, (b) which wink to choose and (c) how to access the food reward. Because this was too complex, observers were pre-trained to dislodge red and blue winks and then tested in a second test session. First results showed that (a) all observers (males, females) impressively improved their performance compared to the first test sessions and (b) males clearly excelled their female conspecifics.



Main Meeting, FG Morphology
Oral presentation

Comparative analysis of the size and shape of the middle ear cavity of turtles

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The middle ear of turtles differs from other reptiles in being separated into two distinct compartments. Several ideas have been proposed as to why the middle ear is compartmentalized in turtles, of which most suggest an adaptation to underwater hearing. Due to differences in fluid properties of water and air, ecomorphological hypotheses of turtle hearing predict that habitat preferences (aquatic/terrestrial) should correlate with the morphology of the middle ear. To test for this correlation, we studied the shape and size of the air-filled middle ear cavity of 56 extant turtles using 3D data and phylogenetic comparative analysis. The turtle middle ear cavity exhibits high shape diversity among species, but no relationship between shape variation and ecology is present. Surprisingly, the estimated acoustic transformer ratio, a key functional parameter of impedance-matching ears in vertebrates, also shows no relation to ecology. Weak correlations are only detected between middle ear cavity size and habitat preferences, with aquatic taxa having proportionally smaller cavity volumes. We suggest that middle ear cavity shape is constrained by factors unrelated to hearing, such as the spatial demands of surrounding cranial structures. A review of the fossil record indicates that the modern turtle ear evolved during the Early to Middle Jurassic in stem turtles broadly adapted to both terrestrial and freshwater environments. This, combined with our finding that evolutionary habitat shifts caused only minor evolutionary changes in the middle ear structure, suggests that tympanic hearing in turtles evolved as a compromise between subaerial and underwater hearing.



Main Meeting, FG Developmental Biology
Oral presentation

Evolution and functionality of closely related Wnt genes in *Drosophila melanogaster*

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Wnt signalling regulates many biological processes during animal development. There are thirteen subfamilies of Wnt ligands in metazoans, seven of which are represented in *Drosophila melanogaster*. Although some Wnt genes appear to have unique roles in *Drosophila*, it is thought that they can act cooperatively in some contexts. The molecular basis for the functional diversification of Wnt proteins and their individual interactions with receptors and other proteins remains unknown. Using CRISPR/Cas9, we modified Wnt loci endogenously to analyse and compare functions of Wnt ligands and test if they can substitute each other in different developmental contexts. Focusing on the closely related Wnt genes wingless (wg) and Wnt6, and Wnt9 and Wnt10, we are currently testing if Wnt6 and chimeric Wnt6-wg ligands can rescue the wg-knockout phenotype to identify domains responsible for the diversification of these two Wnt ligands. Additionally, we study the effects of coding sequence variation exemplified by the wg locus and replaced it with another arthropod homologue. Furthermore, we studied the function of Wnt10, which is, in contrast to most *Drosophila* Wnt genes, unknown. Expression is observed in the mesoderm, gut and central nervous system during embryogenesis. Our knock-out flies appear to be fully viable and fertile. We have therefore measured body and wing size, and performed fecundity, immune and lifespan assays on Wnt10KO flies to analyse the function of this ambiguous *Drosophila* Wnt gene. Identifying the molecular basis of functional differences among these Wnt ligands will help to understand how this important signalling system regulates developmental processes.



Main Meeting, FG Evolutionary Biology
Oral presentation

Dissecting the transcriptomic basis of phenotypic evolution in an aquatic keystone grazer

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Knowledge of the molecular basis of phenotypic responses to environmental cues is key to understanding the process of adaptation. Insights to adaptation at an evolutionary time scale can be gained by observing organismal responses before and after a shift in environmental conditions, but such observations can rarely be made. Here, we combined paleogenomics with a network approach linking transcriptional and phenotypic responses of resurrected ancestral isolates (~600 years old) of the aquatic keystone herbivore *Daphnia*, and of their modern descendants. We discovered highly preserved gene networks shared between ancient genotypes and their modern descendants, but also detected clear evidence of transcriptional divergence between these evolutionarily separated genotypes. Together, the employed analyses allowed us, for the first time in an ecological keystone species, to decipher genetic key drivers of phenotypic evolution. Our study highlights that phenotypic evolution is a result of molecular fine-tuning on different layers ranging from basic cellular responses to higher order phenotypes. In a broader context, these findings advance our understanding how populations are able to persist throughout major environmental shifts.



Main Meeting, FG Behavioural Biology
Oral presentation

Direct and indirect fitness benefits as drivers of complex group structure

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Cooperative breeding, i.e. individuals helping others in their brood care, is among the most derived social behaviors. It can be explained by helpers gaining indirect fitness benefits through increasing the survival of related individuals. However, indirect fitness benefits cannot explain why unrelated individuals help others in raising offspring. Here, direct benefits are of importance. Protection from predators is such direct benefit and has been acknowledged as a major driving force of sociality. Still, how such risk related direct benefits interact with indirect fitness benefits in driving the evolution of complex cooperative societies is limited. We investigated this interplay in the cooperatively breeding cichlid *Neolamprologus pulcher*. We measured group structure, helping behavior, relatedness and reproductive success in eight populations, differing in predation risk. Group structure related to predation risk, with groups in high risk populations containing more large helpers that engage most in predator defense. In these populations the number of large helpers had a strong effect on the breeder's chance to reproduce. Microsatellite analyses revealed that the degree of within-group relatedness was generally low. Notably, smaller helpers, which invest least in defense, were more related to breeders in high risk populations. These results indicate that direct fitness benefits play a crucial role in the cooperative system of *N. pulcher*, which can be further modified by indirect fitness gains depending on the predatory environment. Our work highlights the importance to understand the interplay of direct and indirect benefits when aiming to comprehend the evolution of complex animal societies.



Main Meeting, FG Behavioural Biology
Poster: BEH 2

Poeciliids playing tiddlywinks 2.0: personal learning versus social learning in a visual serial reversal task – do sexes differ?

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The capability to learn enables individuals to alter or retire no longer viable strategies and to develop new ones when environmental demands change. Mammals, birds or fish can gather private information about the environment by personal learning via repeated trial and error. Alternatively, they can learn to adapt their behavior by observing the behavioral responses of others to guide their own future actions, thus via social learning. Here, we investigated sex differences in visual serial reversal learning in two molly species (*Poecilia latipinna*, *P. mexicana*) and the guppy *P. reticulata* in two different learning regimes: personal learning and social learning. Fish were first trained in color discrimination using green and yellow tiddlywinks, which was quickly learned by all females (guppies, mollies) and all molly males alike. Surprisingly, once the reward contingency was serially reversed, molly males performed considerably better by inhibiting their previous response and reached the learning criterion significantly faster than their respective conspecific females. Atlantic molly males clearly outperformed all other individuals. We tested naive Atlantic molly observers (males, females) for their ability to learn the visual serial reversal task by mere observation of male conspecifics (demonstrators). After demonstrators were successfully trained to find food in a well of a wellplate covered by a green or a yellow tiddlywink, we recorded the success of the observers' foraging skills in 2x6 test sessions. Will observers reach a comparably high performance level as their experienced demonstrators? Will the accuracy level differ between female and male observers?



Main Meeting, FG Physiology
Oral presentation

The adipokinetic hormone/corazonin-related peptide (ACP) system in the mosquito, *Aedes aegypti*: ligand-receptor analyses

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Three neuropeptide systems (i.e. the mature peptides and their cognate G protein-coupled receptors (GPCRs)) are structurally similar in invertebrates, and are related to the vertebrate gonadotropin releasing hormone system. The neuropeptide systems are the adipokinetic hormone/red pigment-concentrating hormone, corazonin, and the adipokinetic hormone/corazonin-related peptide (ACP) family. All three receptors in the mosquito, *Aedes aegypti*, have been characterized, and found individually to exhibit high specificity for their native ligands.

A. aegypti is a disease vector for pathogens, such as Yellow and Dengue fever, chikungunya and Zika arboviruses, all of which summarily are responsible for affecting approximately 50-100 million people annually. In the current study, we designed a series of Ala replacement analogs based on the native ACP sequence of *A. aegypti* (pGlu-Val-Thr-Phe-Ser-Arg-Asp-Trp-Asn-Ala amide) and screened them against the ACP receptor using a heterologous system that reports receptor activation. We identified critical residues of the ACP neuropeptide required for activity via its receptor. Specifically, free acid and analogs replacing aromatic residues abolished all activity, whereas replacement of charged residues did not have a serious detrimental effect. Truncated peptides had much less activity (C-terminal truncation) or none at all (N-terminal). In conclusion, determining indispensable amino acid residues of ACP for activation of its receptor will help clarify how the three evolutionary related systems uphold specific signalling networks and avoid cross activation to be functionally distinct. Funding: NRF and UCT Research Council (GG); NSERC Discovery Grant and Ontario Ministry of Research & Innovation Early Researcher Award (JPP).



Main Meeting, FG Physiology
Oral presentation

All you need is love? No, it is oxygen: detecting positive selection in deep-diving mammals

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Upon their return to the sea, marine mammals have undergone fascinating evolutionary changes to adapt to the aquatic environment. However, they have never acquired the ability to use the oxygen present in the water. Instead, diving mammals have evolved a series of adaptations to store and conserve oxygen in order to undertake dives of extended periods to forage in great depth. In spite of their adaptations, marine mammals frequently experience very low levels of arterial oxygen tension that would lead to unconsciousness and neuronal damage in the brain of most terrestrial mammals and humans. Hippocampal neurons of the deep-diving hooded seal (*Cystophora cristata*) survive up to 3 hours of low oxygen levels (hypoxia). To date, little is known about the mechanisms that confer this remarkable cerebral hypoxia tolerance. In this study, we analysed the transcriptomes of deep-diving whales and seals, such as the sperm whale and the hooded seal, and short-diving as well as terrestrial mammals in order to detect positive selection in genes that might play a role in the neuronal hypoxia tolerance. Across all 15 analysed species, we identified 3011 orthologous genes and, after correcting for multiple testing, detected positive selection in 69 genes. To estimate the functional relevance of these genes, we additionally consider the position of the positively selected sites in the gene, their cerebral expression levels and we discuss relevant pathways these genes are involved in.



Main Meeting, FG Systematics, Biogeography and Diversity
Poster: SYS 1

News from the freshwater jellyfish *Craspedacusta sowerbii* – multiple invasions and secrets from the polyp stage

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A worldwide successful invasive species is the freshwater jellyfish *Craspedacusta sowerbii* (Lankester 1880) originating from the Yangtze River System in China. Its complex life cycle enables fast response to changing environmental demands by switching between sessile polyp, mobile and resting stages promoting long-term colonization success. The asexually reproducing polyps allow for rapid establishment in newly invaded habitats. They are tiny predators present in the benthos all over the year and sometimes bud off medusae which are sexually reproducing predators in the pelagial food web. Regarding the genetic population structure, the focus was thus far on jellyfish blooms, with sporadic evidence for cryptic species invasion. We wanted to know if the genetic lineages reported from jellyfish reflect the spread of haplotypes in polyp founder populations. By screening 16S and COI polymorphisms among 481 *C. sowerbii* individuals (polyps and medusae) from 53 European lakes, we found one new haplotype line which dominated the polyp stage. Medusae were fixed for one sex-specific haplotype within most lakes, in contrast to haplotype coexistence among polyps. Because in one lake medusae from different species and both gender were detected, bisexual reproduction is likely and hybridization may occur known as stimulator for invasiveness.



Main Meeting, FG Developmental Biology
Poster: DEV 1

Development of intraspecific size variation in black coucals, white-browed coucals and ruffs

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Studies on the evolution of sexual size dimorphism (SSD) often focus on adults, neglecting the fact that SSD usually develops during ontogeny. Here we examined when and how SSD in body mass and tarsus length developed in three bird species with striking differences in adult SSD: black coucals (adult females 71% heavier than males), white-browed coucals (females 13% heavier than males) and ruffs (males 69% heavier than females). In ruffs, we additionally examined the development of intrasexual size variation, as ruffs exhibit three morphs (Independents, Satellites and Faeders) that contribute to further adult size variation. We took repeated measurements from hatching until leaving the nest in wild coucals and until fledging in captive ruffs and analyzed growth with a generalized additive model framework. Only black coucals and ruffs developed clear SSD. In black coucals, body mass differed between the sexes from day 7 onwards and in ruffs from day 6 onwards. By the end of data collection, they had developed 25% and 76% of their adult SSD respectively. In tarsus length, only ruffs developed significant SSD from day 9 on. Morph-specific size variation was significant starting on day 11 in females and from day 15 in males. In general, the larger sex/morph grew faster and reached maximal growth rates later than the smaller sex/morph. These results highlight the importance of early ontogeny in the development of intraspecific size variation and provide a basis for future studies to relate selective pressures and proximate mechanisms with growth variation in these three species.



Main Meeting, FG Behavioural Biology
Oral presentation

Anti-predator strategies in singing and non-singing insects against echolocating bats

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Predator avoidance is a key component of survival, often composed of different strategies adapted to different predator types and threat levels. In contrast to the defence strategies of visually guided animals, we know comparatively little about the defence strategies guided by other sensory modalities. Echolocating insectivorous bats drove the multiple independent evolution of hearing and auditory-guided anti-predator strategies in many insects.

Many male insects sing to attract females, thereby also attracting eavesdropping predators. Males thus trade-off singing (mate attraction) with song cessation (predator avoidance). We hypothesized that males prioritize predator avoidance over mate attraction early in the mating season, yet accept higher predation risk towards the end of their life span, to optimize reproductive success. Male great green bushcrickets (*Tettigonia viridissima*) indeed stopped singing in response to acoustically simulated bat attacks. Notably, song cessation occurred less for low simulated predation threat and old males. Singing male bushcrickets thus optimize reproductive success by adapting decision making to predation threat and remaining life span.

Silent flying moths rely on erratic evasive flight to escape attacking bats. The escape-tactic diversity hypothesis postulates that the overall unpredictability of evasive movements increases if species with different evasion strategies mix, resulting in enhanced predator protection for all. We recorded tethered flight of eight moth species under acoustically simulated bat attacks. Moth escape flight was species-specific, size-independent and (in some species) individual-specific, by differing in overall flight strength and temporal reaction pattern, thus confirming for the first time the escape-tactic diversity hypothesis for eared moths.



Main Meeting, FG Evolutionary Biology
Poster: EVO 11

Unravelling of the body surface microbiome and its effects on cuticular hydrocarbon variation in parasitoid wasps

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Cuticular hydrocarbons (CHCs) play a major role in many different aspects of an insect's life. They can be found in various chemical communication systems as key components and are known to have an impact on the resistance against desiccation. However, some mechanisms governing CHC variation are not well understood, for instance how CHCs can be affected by the surface microbiome. To better understand CHC diversity in general, it is crucial to understand how the chemical profile of an insect develops and responds to the presence of the different microorganisms colonizing the cuticle. We are planning on testing the influence of the cuticular microbiome on CHC profiles in the parasitoid jewel wasp *Nasonia*, an established model organism for genetics, ecology and evolution. The gut microbiome of *Nasonia* has already been investigated, showing variation between species, sexes and even individuals, but detailed studies on the cuticular microbiome have not been attempted so far. Since CHCs can function as species-specific sexual cues in *Nasonia* and thus have a role in mate choice, any factors influencing their variation and diversity may have an impact on assortative mating, prezygotic reproductive isolation and ultimately, speciation. The findings from this study have the potential to considerably advance our understanding of biotic factors influencing CHC variation in particular and the influence of microbial communities on phenotypic traits of their respective hosts in general.



Symposium: Form and function of motion systems: new approaches, new opportunities, new challenges

Oral presentation

Swimming with the mountain shrimps – locomotion in “ancient” crustaceans (Malacostraca, Anaspidacea)

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In malacostracan crustaceans, the dominant mode of locomotion is swimming. However, in different taxa different swimming mechanisms have evolved. In the well-known decapod shrimps, swimming propulsion is generated by an adlocomotory metachronal beating pattern of the pleopods. In other shrimp-like malacostracans, pleopodal swimming activity is either assisted by thoracopodal exopods (e.g. Lophogastrida) or even totally replaced by those (e.g. Mysida).

We analyzed the locomotion in several species of the “living fossil” Anaspides (Anaspidacea) endemic to Tasmania in comparison to other malacostracan shrimps. Various aspects of these shrimps locomotion were captured and documented with different recording technics (including in-habitat underwater filming and macro high-speed recording), while μ CT reconstructions of muscles and cuticle add the morphological background. In *Anaspides*, swimming is realized only by the exopods of thoracopods 2-6 as well as of all pleopods where the endopods are vestigial. All exopods are unified in a monoplanar metachronal beat, with the left and right sides being in phase. Our observations further revealed a surprising congruence of the locomotive kinematics in swimming and walking. In total, our findings suggest for the shrimp-like malacostracans (Caridoida) the combined use of pleopods and thoracopodal exopods in locomotion as ancestral condition.



Main Meeting, FG Morphology
Oral presentation

Skinny eaters – structure and function of a digestive epidermis in an animal-microbe symbiosis

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Gutless oligochaetes are marine interstitial worms that have reduced both their intestinal tracts and excretory organs. Their nutrition comes from extracellular chemosynthetic bacterial symbionts, which reside in the worm's body wall (between epidermis and cuticle) and use the energy gained from reduced inorganic compounds present in the environment to fix carbon dioxide into biomass. How exactly this biomass is then transferred to the host is, however, not fully understood. Our analysis of the host-symbiont interface of the gutless oligochaete *Olavius algarvensis* by serial section transmission electron microscopy, visualisation of symbionts by fluorescence in-situ hybridisation (FISH) in combination with staining of lysosomal organelles and the cytoskeleton reveals phagocytosis of entire symbionts by the epidermal cells as the predominant mode of carbon transfer. Engulfment of symbionts as well as all stages of the phagolysosomal pathway occur abundantly in epidermal cells of *O. algarvensis*. Lysosome and symbiont abundances are correlated and combined FISH and lysosomal staining clearly attests presence of symbiont 16S rRNA inside phagolysosomes. Rate estimations render phagolysosomal digestion a significant and continuous process that can equilibrate symbiont proliferation. Hybridisation chain reaction mRNA FISH of digestive enzymes suggests that digestion is primarily intracellular. Lysosomal degradation genes are expressed at high levels in the epidermis, whereas secreted extracellular digestive enzymes and those of dual digestive and antimicrobial function, for example lysozyme, are expressed in tissues connected to coelomic cavities and the circulatory system suggesting their exclusive immune defense role in *O. algarvensis*.



Main Meeting, FG Ecology
Poster: ECO 11

Variation in ecologically important traits – latitude reflects altitude

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Understanding how organisms adapt to complex environments lies at the very heart of evolutionary biology and ecology, and is of special concern in the current era of anthropogenic global change. Variation in ecologically important traits associated with environmental gradients is considered to be a strong evidence for adaptive responses, which may result from either genetic adaptation or phenotypic plasticity. Here, we study phenotypic variation along a latitudinal and an altitudinal cline in 968 field-collected males of the widespread European butterfly *Pieris napi*. In contrast to our expectations, body size decreased with increasing latitude and altitude, suggesting that warmer rather than cooler conditions may be more beneficial for individual development in this species. Higher altitudes but not latitudes seemed to be associated with increased flight performance (as indicated by e.g. a higher wing aspect ratio), suggesting stronger challenges for flight activity in high-altitude environments, e.g. due to strong wind. Moreover, wing melanisation increased while yellow reflectance decreased towards colder environments in both clines. Thus, increased melanisation under thermally challenging conditions seem to compromise investment into a sexually selected trait, resulting in a trade-off. Our study, although exclusively based on field-collected males, revealed indications of adaptive patterns along geographical clines. It documents the usefulness of field-collected specimens, and the strength of comparing latitudinal and altitudinal clines to identify traits being potentially under thermal selection.



Symposium: Form and function of motion systems: new approaches, new opportunities, new challenges

Oral presentation

The characteristic time of a muscle accelerating itself, and its scaling with size

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I will show in this presentation that delayed responses of muscle displacement to changed force demand, which are due to the interaction of a muscle's force-velocity relation with its own mass inertia, do have impact beyond impact loading situations in which 'wobbling mass' dynamics of e.g. leg muscles is enforced. In particular, it is very likely that muscle inertia also imposes an insurmountable restriction to legged, terrestrial locomotion: maximum running speed in terrestrial environment has an absolute upper limit which strikes if an animal's body exceeds a critical size. The reason is that the characteristic time to accelerate an actively contracting muscle from the isometric condition around midstance up to such concentric contraction velocities that are required for doing work until the leg's lift-off increases steeper with muscle mass than the leg's stance duration. Hence, I dare to predict for over-critically big animals that their 'last muscle standing' is prematurely interrupted in its doing work. At this, 'prematurely' refers to the muscle not reaching any more the very contraction velocity that corresponds to a force equilibrium with air drag, due to the characteristic acceleration time becoming longer than the leg's stance duration. Across all conceivable running species, due to basic mechanics, the capability of the crucial muscles to still do work at late stance, and therewith compensate energy losses by air drag and body-internal material deformations, does insurmountably decrease with body (thus muscle) mass beyond a critical body size which thus corresponds to an absolute maximum in running speed.



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

Comparison of the diversity of the Coleoptera between the understory and the canopy in the floodplain forest of Leipzig

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Our study is part of the Leipzig Canopy Crane (LCC) project and investigates the diversity and ecology of the Coleoptera in the nature reserve “Burgaue”. It facilitates the investigation of different forest strata and of conceivable changes in the number of individuals and species composition in the understory and canopy. During a period of 26 weeks, more than 270,000 arthropods were captured (with 44 window-flight traps), from which 19,906 individuals belonged to the Coleoptera. Among them Scolytidae and Cantharidae were identified as the most abundant families, *Sericoderus lateralis* (Corylophidae) and *Rhagonycha fulva* (Cantharidae) as the most abundant species in the understory and canopy, respectively. In addition, several faunistic peculiarities were found, which underline the outstanding value of the floodplain forest in Leipzig. Special attention was paid to the comparison of the understory and the canopy, which was investigated in parallel studies. We detected pronounced differences both in the number of individuals and in the family composition. The data evaluated in this study serves as a basis for further long-term investigation of the Coleoptera and their spatial and temporal distribution pattern. Beyond, we are extending our determination towards DNA-barcoding and will establish a reference database, the “Leipzig Barcode of Coleoptera – LBoC”.



Main Meeting, FG Morphology
Poster: MOR 17

A new imaging approach to study the tracheal system in insects

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The tracheal system in insects can generally be understood as a complex three dimensional branching network of tubes, being the central respiratory organ. Just like many other branching biological transport systems the tracheal system is not a simple hierarchical branching tree. It is a highly anastomosing three dimensional network and every stigma can be understood as a root in a network topological point of view. Even though the high species richness of insects and them being a group studied in great detail with respect to morphology, the knowledge about the tracheal system in detail is still limited. The increasing availability of laboratory-based CT system has stimulated a number of studies in the tracheal system in insects. However, in many cases the resolution is quite limited due to different factors and therefore misses great parts of this organ system.

Here we present a new workflow combining the imaging of freshly killed specimens with fast μ CT acquisition times at the synchrotron and propagation based phase contrast imaging. This allows for a fast and high contrast acquisition of cm sized specimens at a resolution to about 2 μ m. The obtained 3D models of the studied specimens are comprised of almost all air filled sections of the tracheal system down to the actual resolution limit. We present results for different species and developmental stages and some quantitative and qualitative results to further characterize the tracheal system in insects.



Main Meeting, FG Evolutionary Biology
Poster: EVO 9

Too late to mate? Timing of mating activity drives species diversification in a moth

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Little is known on how changes in circadian rhythms evolve. The noctuid moth *Spodoptera frugiperda* occurs as two strains that show differentiation in circadian timing of mating activity: The corn-strain mates early and the rice-strain mates late at night, which acts as a premating isolation barrier between the strains. We investigated the genetic basis of the strain-specific timing differences to identify the molecular mechanism of differentiation in these circadian rhythms. Through QTL analyses we identified one major Quantitative trait chromosome (QTC) underlying the timing differentiation on which the clock gene *vriille* is located. *Vriille* showed strain-specific polymorphisms as well as strain-specific expression differences, with the rice-strain showing higher expression levels than the corn-strain. Our results indicate that the differentiation in daily mating rhythms in *S. frugiperda* is associated with differential transcription of *vriille* or a cis-acting gene close to *vriille* (Hänniger et al. 2017, BMC Evolutionary Biology, 17:68)

To verify the contribution of *vriille* and other clock genes to the evolution of prezygotic isolation in natural *S. frugiperda* populations, we are conducting a broad scale investigation of field populations from the Americas and the recently invaded Africa. Freshly collected field samples of both strains are observed for their timing of mating activity and sequenced for differences in the clock genes. By investigating the natural variation in timing of mating behavior and its genetic basis, we will determine how much impact this isolation barrier has on the divergence of the two *S. frugiperda* strains.



Main Meeting, FG Ecology
Poster: ECO 1

Conservation genetics of a threatened amphibian, *Bombina variegata*, in northern Rhineland-Palatinate, Germany

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In Germany, the yellow-bellied toad, *Bombina variegata*, is threatened and strictly protected. We studied the genetic population structure and diversity of this amphibian species inhabiting a low mountain range, the Westerwald in northern Rhineland-Palatinate. This is one of the northernmost regions where *Bombina variegata* is widely distributed, thus serving as an important reservoir for (re)colonisation. Population connectivity and genetic diversity of 200 specimens belonging to seven sites (200-450 m a.s.l.) were investigated using ten molecular markers (microsatellites). The analysis of genetic sub-structuring identified at least two differentiated groups of populations inhabiting the southern and northern region of the Westerwald. We found low overall genetic diversity, but partially large genetic differences among populations. Fragmentation of populations inhabiting nearby locations (< 500 m distance in between) indicates a low dispersal capacity. Thus, conservation measures should focus on the connectivity of neighbouring populations through stepping stone ponds. Further analyses will give more precise insights concerning genetic relatedness to nearby populations in western Hesse.



Main Meeting, FG Evolutionary Biology
Poster: EVO 5

Eat me or not – Deciphering the molecular signals of diploid drone removal in the honey bee *Apis mellifera*

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Social insects have evolved many novel morphological, physiological and behavioral traits relative to their solitary ancestors. One remarkable behavior of the western honey bee *Apis mellifera* is the detection and cannibalism of diploid drone larvae at early developmental stages. Diploid drones differ in their homozygous genotype for the gene complementary sex determiner (*csd*) compared to diploid females (heterozygous) and haploid drones (hemizygous) and would produce diploid sperm. We will test the hypothesis that the sex determination pathway affects the synthesis of signaling substances in honey bee larvae differently, leading to the removal of diploid males. These signaling substances are unknown, whereas quantitative differences of larval cuticular substances were proposed in the past to be recognized by worker bees. We expect to detect differences in gene expression and e.g. cuticular substances among developmental stages in diploid females, haploid males and diploid males. Sex specific cuticular extracts of honey bee larvae have been detected in preliminary Bioassays. Analysis of cuticular extracts via mass spectrometry showed differences between the sexes of interest. Finally, the results of transcriptome analysis using RNA-seq of diploid females and diploid males provide striking gene expression differences in these early larval stages of the honey bee. Consequently, our study combine for the first time molecular and biochemical analysis to investigate the differences between the sexes in young larvae to elucidate the molecular network and evolution underlying the cannibalism behavior in *Apis mellifera*.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral presentation

Overcoming the Taxonomic Impediment in “Dark Taxa” by DNA-Barcoding

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DNA-barcoding has become a widely accepted and generally available tool for reliable and fast determination of all life-cycle stages or tissue remainings of taxa. Next Generation Sequencing as well as progress in the field of bioinformatics have provided the methodological basis to apply DNA-barcoding not only for single specimens but also for environmental or bulk samples. However, whereas the inference “the same species” can easily be reached by non-named MOTUs or BINs (Barcode Index Numbers), the correlation of BINs with a Linnean taxon remains crucial for many further and far-reaching applications of environmental or meta-barcoding studies

Since 2009 the Zoological State Collection München (ZSM) together with a number of other German natural history museums (namely the Zoologisches Forschungsmuseum A. König in Bonn) has “barcoded” (i.e. correlated BINs and Linnean names) about 65% of all (38-40.000) German metazoan species in the scope of Bavarian (Barcoding Fauna Bavaria) or German-wide (GBOL I + II) projects. Despite this success, large gaps remain in Diptera, parasitic wasps (Hymenoptera), all kinds of “lice”, Acari, and soil fauna in general. In these “dark taxa” with still thousands of species only a few taxonomic specialists are able to determine species, and many subtaxa lack expertise at all. GBOL III “Dark Taxa” (currently applied at BMBF) shows a way to overcome the “taxonomic impediment” in the dark taxa mentioned by means of so-called reverse taxonomy (first the BIN, later the name) and also by training a next generation of integrative taxonomists.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral presentation

An old story – The European flat oyster in the North Sea in the 19th century

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Ostrea edulis Linnaeus, 1758 or the European flat oyster has been used as food source by humans for centuries (Lüttschwager (1954) Schriften des Naturwissenschaftlichen Vereins für Schleswig-Holstein, 27; Yonge (1960) Oysters, London, Collins; Neudecker (1990) Deutsche Hydrografische Zeitschrift, Ergänzungsheft Reihe B, 22, pp. 518; Thüry (1990) Helbing & Lichtenhahn; Lotze (2007) Fisheries Research, 87, pp. 208; Gercken (2014) Bundesamt für Naturschutz). However, due to the constant fishing of adult oysters in the past, the populations of *O. edulis* have declined dramatically in the North Sea and are now threatened by extinction. The concomitant invasion of the common limpet slipper *Crepidula fornicata* Linnaeus, 1758 in the North Sea has been implicated to have negative effects on *O. edulis*. In order to reconstruct the change in distribution and diversity in both species in the North Sea over the past 200 years, we combined the temporal and spatial information contained in several European natural history collections (NORe museums, the Natural History Museum London, the Naturalis Biodiversity Centre Leiden and the Muséum national d'Histoire naturelle Paris). Our data recovers the decline of *O. edulis* in the North Sea from the 19th century to the present and the process of invasion of *C. fornicata*.



Main Meeting, FG Morphology
Oral presentation

The evolution of swimming crabs – homologous or convergent?

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Swimming crabs within the taxon Portunoidea (Brachyura, Decapoda) are well known for their ability to swim using their 5th pereopods (P5) that are developed as a specialized swimming leg. However, morphological modifications of swimming crabs do not only concern the 5th pereopod itself, but also the axial skeleton. The axial skeleton involves a complex system of cuticular infoldings serving as attachment sites for the enlarged extrinsic swimming leg musculature. However, the morphology of only a few species had been examined so far and little is known about the evolution of the swimming capacity. We here present new 3-dimensional reconstructions of the axial skeleton and extrinsic musculature together with data from the swimming legs of several swimming crab species including representatives of the genera *Liocarcinus*, *Portumnus*, *Callinectes* and *Ashtoret*. A comparison of morphological features between species permits statements on the question if swimming adaptations are to be considered as homologous or convergent. Our results are further discussed in the light of current phylogenetic data.



Symposium: Form and function of motion systems: new approaches, new opportunities, new challenges; Keynote
Oral presentation

Structure from motion with insects – a novel approach for 3D-modelling and its potential applications for functional and comparative morphology

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Most interactions of animals with their environment (biotic/abiotic) occur in a three-dimensional space and include three-dimensional morphological structures. Hence, 3D imaging techniques have become important tools not only in morphological sciences, but also in ecology, where three-dimensional trait measurements are more and more included to understand species interactions and environmental filtering processes. However, the reconstruction of a specimens' 3D geometry is not a simple task and usually requires expensive equipment (μ CT) and/or translucent objects (CLSM, light sheet microscopy). If objects are larger than ~5 cm and only the crude external morphology is of interest, inexpensive and easy-to-use techniques such as structured light scanning (SLS) or 3D-laserscanning are well suited. Their resolution, however, is insufficient for small and complex objects such as insects. Structure from motion (Sfm) is a photogrammetric method to reconstruct point clouds from matching feature points among images of an object taken from different viewing angles. While Sfm is well established for 3D reconstructions of landscapes, buildings, archeological sites and larger animals or animal parts (e.g. skulls), it has hardly been used in combination with insect macro photography due to the narrow depth of field that inevitably occurs in this size range. To overcome this limitation, we combined two techniques: focus stacking (extended depth of field imaging, EDOF) and multi-angle imaging in a single setup (Darmstadt Insect Scanner, DISC3D). EDOF-images obtained by DISC3D fulfil the pinhole camera model (a precondition for Sfm) and can be used to reconstruct 3D models. DISC3D is a relatively low-cost (~10k €) open source project and is constantly improved regarding speed and quality of image acquisition. Resulting 3D-models could be used for parallax-error free measurements of 2D and 3D traits and for geometric morphometry. They can additionally be textured and serve as archivable "digital twins" for unique objects such as holotypes. Finally, results from motion analyses of living specimens can be applied to the virtual model.



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

Phylogenomic relationships of Australian *Amitermes*

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The Australian *Amitermes* Group (AAG; Blattodea: Termitidae) currently consists of 5 genera and 100 described species. These termites are considered to be ecosystem engineers altering their environment substantially via nutrient cycling and soil enrichment. In addition, they provide food and habitat for many other species and have evolved traits that are highly unusual in the termite world, including unique foraging behaviours and nest parasitism. However, almost nothing is known about the relationships between the species or how their ecological niches may have shaped and been shaped by their unique characteristics. As a first step, mitochondrial genomes of *Amitermes* and *Drepanotermes* species were used to calculate Bayesian inference and maximum likelihood trees. The results suggest that *Amitermes* and *Drepanotermes* constitute a single clade rather than sister genera, whereby *Drepanotermes* are the most derived *Amitermes*. In addition, divergence time estimation with my current mitochondrial genome data set finds that *Drepanotermes* diverged from *Amitermes* at 9.1 ± 2 Mya, coinciding with the 'Hill' gap, an interval of aridification in the late Miocene. I have estimated the divergence time of the AAG from the rest of *Amitermes* at around 17.7 ± 4 Mya, which is within the range estimated by previous family-level phylogenies.



Main Meeting, FG Behavioural Biology
Poster: BEH 11

Searchlights in the dark. Multiple functions of subocular light organs in the bioluminescent flashlight fish *Photoblepharon palpebratum*

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The flashlight fish *P. steinitzi*, lives in the Red Sea and can be found in fringing reefs with crevices and caves. After sunset the fish can be observed alone or in pairs at the entrance area of reef caves. *Photoblepharon steinitzi* is characterized by sub-ocular light organs with symbiotic bioluminescent bacteria emitting a blue greenish light. *Photoblepharon steinitzi* use an eyelid like shutter to interrupt light emission and to produce blink patterns. We studied the behavior of *P. steinitzi* in its native environment to gain an understanding of how bioluminescent signals are used during territorial behavior, aggression behavior, social interaction and feeding. Undisturbed pairs of *P. steinitzi* and single specimens show open light organs and low blink frequencies. A similar behavior was observed during feeding zooplankton. We found that *P. steinitzi* increases its blinking frequency, while attacking intraspecific intruders or different light organ and fish dummies stimuli simulating intraspecific intruders. Four different types of attack modes could be observed, which are elicited to different degrees by different stimuli all associated with high blinking frequencies. These attack modes can be described as darting movement, repeated swimming with or without turn and ram and bite reactions. The fish attacks occur from the entrance of the cave, where *P. steinitzi* mainly resides during the night. Thus our data suggest that *P. steinitzi* use bioluminescence for feeding and changes its blinking patterns, from open light organs to fast blinking, during different modes of territorial aggression depending on the light stimulus of the intruder.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral presentation

New insights into the evolution of the Charlie Chaplin worms (Annelida, Histiobdellidae)

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Histiobdellidae – the so-called Charlie Chaplin worms – are an enigmatic group of minute commensal annelids associated with marine and freshwater decapods. They lack external segmentation and bear a complex jaw apparatus in the ventral muscular pharynx. Although histiobdellids were always thought to be a part of the jaw-bearing Eunicida, an ultimate placement within the annelid tree is still pending due to their highly derived external morphology and lack of comparative molecular and morphological investigations. In order to gain new insights into phylogeny and evolution of Histiobdellidae, we studied adults and different developmental stages of *Histiobdella homari* Beneden, 1858, a commensal of the European lobster, and *Stratiodrilus aeglaphilus* Vila & Bahamonde, 1985, a commensal of several South American freshwater crayfish. Using an integrative approach including molecular analyses of nuclear and mitochondrial genes as well as immunohistochemistry with standard neuronal and muscular markers, subsequent confocal laser scanning microscopy (clsm), and scanning electron microscopic (SEM) examinations of the jaw apparatus and external body features, we provide important details to comment on the phylogenetic position of histiobdellids. Our study reveals the presence of prionognath-like maxillae and neuronal and muscular features highly comparable to other well-investigated families within Eunicida. Consequently, our results represent an important basis to unveil the evolution of the Charlie Chaplin worms and to finally place them into the annelid radiation.



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

More leaves on the phylogenetic tree of Scaphopoda (Bronn, 1862)

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Despite the global marine distribution, the taxon of Scaphopoda is notoriously understudied. The evolutionary position of this infaunal group within the molluscs is as disputed as the internal systematics. The greatest diversity of scaphopod species is recorded from depths below 200 m and tropical shallow water habitats. Diagnoses of the 576 recent species are mostly based on shell characters. Only in some cases the description is supplemented by radula features (Steiner (2004), *Zoosystema*, 26, 549). Scaphopod systematics was investigated in several morphological studies based on softbody characters. Although the major subtaxa are well defined, the validity of many family and genus-rank taxa remains unresolved (Reynolds (2002), *Advances in marine biology*, 42, 137). Molecular phylogenetic studies suffered from limited taxon sampling and agreed with the morphological studies on a robust support for the subtaxa Dentaliida and Gadilida only (Steiner (2003), *Zoologica Scripta*, 32, 343). The present study is mostly based on Indo-Pacific dentaliid specimens from the National Museum of Natural History, Paris. Nuclear marker sequences of the 18S rRNA and 28S rRNA genes as well as mitochondrial markers, i.e., 16S rRNA gene and cytochrome c oxidase subunit 1 gene (CO1) were analysed. The study will improve our knowledge on the phylogenetic signal of these markers, which, once established, will allow to considerably increase taxon sampling. We will test the monophyly of some of the doubtful genus-level taxa and the questionable shell characters they are based on and eventually obtain new insights into the poorly studied phylogeny of this group.



Symposium: Form and function of motion systems: new approaches, new opportunities, new challenges; Keynote

Oral presentation

The evolution of locomotion capacity in frogs: a functional approach using invasive *Xenopus* frogs as a model system

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Xenopus laevis is generally considered as one of the worst invasive amphibians worldwide. It has colonized many countries on at least four continents and new invasions being reported on a regular basis. Despite the negative impact of this species on native amphibians and freshwater invertebrates, these invasive populations provide an excellent model system to explore how dispersal evolves. Moreover, invasive populations allow us to investigate the anatomical and functional trade-offs associated with investment in dispersal. Finally, these invasive populations allow us to test for adaptive differences to new habitats and climatic conditions. Here we compare external morphology, organ size and limb muscle mass in invasive populations characterized by different habitats as well across populations at the centre and the range front of the invasive population in France. We further explore how the temperature~performance relationships have changed by comparing animals from the native range to those established in France. Our results show significant differences between populations in external morphology as well as in organ and muscle size. Furthermore, animals at the range edge had better developed muscles, longer limbs and smaller gonads indicating an allocation trade-off. Finally, we detected significant shifts in the optimal temperature for performance and the 80% optimal performance range. These results show that frogs have adapted to the specific constraints of the different habitats and have rapidly evolved dispersal phenotypes.



Main Meeting, FG Behavioural Biology
Oral presentation

Generation of Gellermann sequences and evaluation of learning success in two-alternative force choice experiments

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Behavioral experiments based on two-alternative force choice paradigms often use pseudo-random stimulus sequences, e.g. those suggested by Gellermann (1933). The success of training is commonly evaluated by a pre-defined learning criterion, e.g. at least X successful trials within a session and Y successive sessions in a row. Two scripts were programmed in Python software for 1) creating stimulus sequences of various lengths and 2) choosing a learning criterion of suitably low probability of occurrence by random choices of the animal. Re-evaluation of former study's methodology using these scripts revealed that 1) Gellermann's (1933) extensively used exemplary sequences do not stand their own standards and that 2) learning criteria used in some previous studies failed to ensure a random "learning success" with $P < 0.05$.



Main Meeting, FG Behavioural Biology
Poster: BEH 12

Size matters – Territoriality and shelter selection in a scorpion

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Behavioural studies on Chelicerata in general, and scorpions in particular, are only scarcely available. In this context, the choice of an appropriate shelter is a pivotal task, but information how scorpions solve this challenge is nearly uninvestigated. *Euscorpis italicus* is often found in old walls built of natural stone, where many individuals are living closely next to each other. Due to the considerable population density, we ask if individuals do have a fixed refuge to which they return regularly, or do they select their hiding place rather randomly? To answer this question, we constructed the following setup: A circular test arena, 150 cm in diameter, was filled approx. 2 cm with soil. 30 pottery shards of different size have been randomly distributed in this arena as shelters. The experiment started with a group of 20 animals. Checking the shelters twice a day confirmed that these scorpions do not change their shelter during daytime. There are indications that individuals change at night between a couple of different shelters over several days. After five weeks, only 14 individuals were left due to cannibalism. However, scorpions were fed regularly. Therefore, we suggest rivalry around attractive shelters as the main source for cannibalism. After analysing the attractiveness of the shelters, only 14 out of 30 shards were seen as appropriate. This was supported by a more stable system after the population diminished to the number of attractive shelters. The size of the shelter seems to be an important factor of attractiveness.



Main Meeting, FG Neurobiology
Oral presentation

Impact of correlated neural variability on the encoding of natural stimuli at the population level in the electrosensory hindbrain

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It is generally accepted that perception and behavior are mediated by the concerted activity of neural populations rather than single neuron activity. Understanding such population codes is however complicated because neuronal activities are often correlated both in their average responses (signal correlations) and/or in their trial-to-trial variabilities (noise correlations). This can create synergy or redundancy in the neural code, i.e. from case to case the presence of correlations can be either beneficial or detrimental for information transmission in the brain (Averbeck et al. (2006) *Nat. Rev. Neurosci.*, 7, 358).

While noise correlations were generally thought to originate from shared neuronal input, we show, for the first time, that they can also arise from the complex spatiotemporal structure of natural stimuli. Across all sensory modalities (visual, acoustic, somatosensory) naturalistic stimuli consist of 1st and 2nd order stimulus attributes that vary independent of one another (Clarke et al (2015) *Nat. Rev. Neurosci.*, 16, 733).

We use the weakly electric fish *Apteronotus leptorhynchus*, to investigate the implications of this novel type of noise correlations towards population coding of electrosensory stimuli. We found that in the medulla correlations were unexpectedly reduced in opposite-type neural pairs (On-Off) relative to those found in same-type pairs (On-On or Off-Off). Investigating the population information using physiological realistic decoders showed that this increased the transmitted amount of information. Thus, our data reveals a novel function for On- and Off-type neurons towards improving information transmission of natural stimuli with complex spatiotemporal structure.



Main Meeting, FG Evolutionary Biology
Poster: EVO 13

Genetic architecture and evolution of candidate genes for CHC biosynthesis in parasitoid wasps

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Cuticular hydrocarbons (CHC) play an important role in desiccation prevention and inter- and intraspecific communication in insects. Most research on the biosynthesis and genetics of CHC has been conducted in the fruit fly *Drosophila melanogaster*. However, how exactly this knowledge can be transferred to other insect taxa, for instance the economically and ecologically important Hymenoptera, remains poorly understood. In the closely related parasitoid wasp genera *Muscidifurax*, *Trichomalopsis* and *Nasonia* (Hymenoptera: Pteromalidae) differences in the reliance on CHC as species-specific female sexual signals have been found. Their haplo-diploid sex determination, sequenced genomes and long research history render them particularly suited to greatly expand upon the knowledge gained from *Drosophila* on the genetic architecture and evolution of CHC variation. A list of 38 *D. melanogaster* genes involved in CHC biosynthesis or intraspecific variation was checked for orthologs in the model organism *Nasonia vitripennis*. In addition, the positions of the *Nasonia* orthologs were mapped onto a linkage map that also contained quantitative trait loci (QTL) for species differences in CHC profiles of *Nasonia* males. A co-localization of candidate gene and QTL would support the validity of a candidate gene. Furthermore, we calculated dN/dS ratios for our candidate genes between *Muscidifurax*, *Trichomalopsis* and *Nasonia* to see whether one of our candidates was under positive selection in *Nasonia*. This study contributes to unraveling the genetic and evolutionary mechanisms that lead to the divergence in function and composition of CHC profiles within parasitoid wasps in particular and within the Hymenoptera in general.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral presentation

Glacial influence on the phylogeographic pattern in Tasmanian mountain shrimps (*Anaspides*, Anaspidacea, Malacostraca)

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During the Pleistocene, not only large parts of Europe, Northern Asia and North America were glaciated but also parts of Australia, especially Tasmania. At least 10 glaciation events have been shown, with the last one ending 17000 years ago. Especially mountain ranges and plateaus were glaciated, which are nowadays typical alpine areas showing low vegetation and numerous small tarns and streams. These tarns and streams are inhabited by Tasmanian mountain shrimps (*Anaspides* spp.) and a few larger lakes by the closely related lake shrimps (*Paranaspides* spp.). These freshwater crustaceans are not real decapod shrimps but belong to a separate group within Malacostraca, the Anaspidacea. Anaspidacea are endemic to Tasmania and their phylogenetic affinities are uncertain. The few so far described species show a remarkable geographical and vertical distribution. We studied the genetic differentiation within species and populations by analyzing COI and partial 28S rRNA sequences of about 311 specimens with particular emphasis on the phylogeographic pattern. Special focus is laid on the multiple separations of populations and species through glaciation and the recolonization of mountain ranges and plateaus, previously completely covered with ice. It is suggested that temperature is the main trigger for habitat shift. Furthermore, we studied the multiple events of immigration of *Anaspides* into the subterranean habitat, probably used as glacial refuge. Immigration is known to have happened at least three times independently across Tasmania but our data suggest that this number could actually be higher. Remarkably, surface and cave forms sometimes share the same COI-haplotypes.



Main Meeting, FG Ecology
Oral presentation

Facing the green threat: A waterflea's defences against a carnivorous plant

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Waterfleas of the family Daphniidae are keystone species in many lentic ecosystems. As the most abundant filter feeders in these systems they link the primary production to higher trophic levels. Being a key species in freshwater foodwebs and especially due to their ability to develop predator induced defences, Daphniidae are regarded as models for ecological research. Inducible defences are a form of phenotypic plasticity that decrease an organism's vulnerability to specific predators. Until now, only animals were shown to induce defensive strategies, however in freshwater ecosystems Daphniidae are also preyed by carnivorous plants. For example, the southern bladderwort *Utricularia australis* is known to pose strong predation pressures on prey species like Daphniidae. We here investigated whether *U. australis* induces defences in the coexisting freshwater crustacean *Ceriodaphnia dubia*. *U. australis*-exposed *C. dubia* form changes in behaviour, morphology and life-history. We show that these changes render *C. dubia* less susceptible to *U. australis* predation. To our knowledge this is the first plant induced morphological defence described. The comprehensive response of *C. dubia* to the presence of *U. australis* suggests that carnivorous water plants may be an underestimated threat to zooplankton.



Main Meeting, FG Physiology Keynote Lectures
Oral presentation

pH regulation in marine calcifying systems

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To generate CaCO₃ skeletons organisms need to acquire calcification substrates (e.g. Ca²⁺, HCO₃⁻/CO₃²⁻), and at the same time remove protons from the calcification front. Thus, biological calcification and pH regulation are intrinsically linked processes that remain relatively unexplored.

The sea urchin embryo develops an elaborate calcitic endoskeleton produced by the primary mesenchyme cells (PMCs). One of my research foci is dedicated to the cellular pH regulatory mechanisms that are critical for the intracellular precipitation of CaCO₃ by PMCs.

Using a wide range of techniques ranging from life cell imaging and intracellular pH recordings over protein-biochemical methods to molecular technologies our experiments demonstrated that provision of HCO₃⁻ as a substrate and removal of protons is mediated by a set of PMC specific ion transporters. During skeleton regeneration pH_i and intracellular HCO₃⁻ levels are increased accompanied by a dramatic downregulation of pH_i regulatory capacities of PMCs. Life cell imaging techniques suggest that this loss of pH regulatory capacities is compensated by another cell type. Large filopodial cells containing acidic vesicles connect to the PMC syncytium to locally support pH regulatory capacities. The process of skeleton rebuild and vesicular acidification in PMC associated cells is sensitive to bafilomycin suggesting a central role of the V-type H⁺-ATPase in place. We propose that PMCs utilize so far undescribed vesicular mechanisms to eliminate protons from the calcification front. These results highlight the importance to better understand pH regulatory processes in calcifying systems including cell-cell interactions and acid-base transport on the cellular and sub-cellular level.



Main Meeting, FG Developmental Biology Keynote Lectures
Oral presentation

Haeckel's recapitulation theory refuted by the hourglass model?

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First inspired by Ernst Haeckel's recapitulation theory, it has long been assumed that earliest developmental stages retain the most ancestral features, and should be conserved the most. Given that up-stream, earlier signals are required for later developmental processes, the early-conservation model sounded reasonable. However, recent comparative transcriptomic studies did not support this idea, showing that that mid-embryonic stages (especially organogenesis stages) are the most conserved stages during development (the developmental hourglass model), and this has been reported in variety of animal groups.

The question however, is why did animal embryos follow this kind of rule? In addition, did recapitulation tendency fully refuted by the hourglass model? In my talk, I would like to discuss over our recent findings, including unpublished data toward these questions. In short, we found possible contributions of pleiotropic constraints on the mid-embryonic conservation, together with recapitulative tendency of gene regulations during latter part of the embryogenesis.

Uesaka et al. *bioRxiv* 481309 (2019) [Recapitulative tendency found in gene regulation during development]

Uchida et al. *EvoDevo* 9:7 (2018) [Embryonic lethality does not explain mid-embryonic conservation]

Hu et al. *Nature Eco & Evo* (2017) [Pleiotropic constraint could be contributing to the hourglass-like conservation]



Main Meeting, FG Behavioural Biology
Poster: BEH 15

Social signaling in the bioluminescent flashlight fish *Anomalops katoptron*

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The splitfin flashlight fish *Anomalops katoptron* appears during moonless nights in large schools in shallow waters of coral reefs. Sub-ocular light organs densely packed with luminous, symbiotic bacteria characterize *A. katoptron*. The symbionts show a bluish light emission at 500 nm wavelengths. Light organs can be occluded via an inward rotation leading to fascinating blink patterns during schooling. The usage of light organs in active food localization was recently shown. During feeding *A. katoptron* increases light organ exposures associated with a decreased blink frequency. The role in social communication remained unclear.

Here we used a dummy with artificial light organs to investigate interaction within conspecifics, analyzed differences in blink frequencies and nearest neighbour distance during several conditions.

Isolated specimen show increased swimming speed and blink frequency. The activation of a static playback (1 Hz; LED timing: 0,5s on + 0,5s off; 500 nm) could trigger an orientation towards the artificial light organs and a decreased blink frequency. Changes in blink frequency of *A. katoptron* are the result of a modification in light organ occlusion while light organ exposure is consistent. A further experiment with changed off-times in LED timing revealed a correlation in distances towards the dummy.

Furthermore we compared our laboratory data to stress reactions in the field (Banda Islands, Indonesia).

Our results demonstrate that flashlight fish interact with artificial light organs based on different playback signals. We reveal a communicative purpose in light organ occlusion, leading to differences in nearest neighbour distance and higher group cohesion during stress.



Main Meeting, FG Ecology
Oral presentation

Diversity and trait patterns of moths at the edge of an Amazonian rainforest

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From the forest edge to the forest interior, a small-scale gradient in the microclimate exists. Little is known about its influence on the abundance, diversity and morphological traits of insects in Amazonian forests, a major component of global terrestrial diversity. We focused on these traits in Arctiinae and Geometridae moths, two taxa that differ in life history, habitat preferences and body architecture, at the interior and the edge of the Peruvian lowland rainforest. A total of 1286 Arctiinae and 2012 Geometridae specimens were collected, sorted according to DNA barcodes and identified using relevant type material. Moths' assemblages at the forest edge differed significantly in their composition. At short distance from the forest edge, small-sized taxa (Lithosiini, Sterrhinae, Geometrinae) were already less abundant whereas larger-sized Arctiini were more abundant. Moths were significantly larger at the forest edge than inside the forest, and these differences hold at subfamily and tribal level, possibly reflecting moth mobility, and abiotic conditions of habitats: larger moths might better tolerate desiccating conditions than smaller moths. A larger proportion of females was found at the forest edge, probably due to differences in the dispersal activity among sexes and/or in the tolerance to desiccation due to size. Our results revealed the edge effect on two rich herbivorous taxa in the Amazon basin. We provide a fully illustrated catalogue of all species as a baseline for further study.



Main Meeting, FG Morphology
Poster: MOR 12

How to feed on sponges – The larval morphology of the spongefly *Sisyra nigra* (Neuroptera: Sisyridae)

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Larval stages of spongeflies, which belong to the small order of Neuroptera, use sponges and bryozoans as their hosts (Aspöck, Aspöck & Hölzel 1980; Weißmaier 1994, 1999). Due to this fact several special morphological features like elongated sucking mouthparts are found in the head region. The morphology of mature larvae of *Sisyra nigra* was studied and documented with a broad spectrum of techniques with a large emphasis on modern 3D- reconstruction. Other established methods like SEM, cross sections and microphotography were also used. Special focus lies on the cephalic anatomy and on the digestive tract. These two complexes are highly connected to the feeding habits and are modified for ingestion, manipulation, transport and digestion of the food resource. Cephalic structures are highly modified, with numerous autapomorphic conditions, including a globular head capsule, an extended area with very large cornea lenses, a massive tentorium, a very strongly developed prepharyngeal pumping apparatus with an unusual arrangement of dilators, a sharp flexure between the prepharynx and pharynx, and an unusual filter apparatus at the entrance of the very large crop. Also other body regions are formed by the aquatic habitat, such as zigzag shaped abdominal tracheal gills. With the help of the morphological data a new scenario for the evolution of larval features in Neuroptera is suggested.



Main Meeting Keynote Lectures
Oral presentation

Serial homology, novelty and the evolution of panarthropod body plans

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The extraordinary diversity of panarthropods is built on an ancient body plan that incorporated a large number of morphologically similar segments. Diversification involved multiple processes including changes in segment number and divergence of serially homologous structures along the body axis. In this talk, I will illustrate the developmental basis for this morphological divergence using examples from tardigrades, *Tribolium* and treehoppers. The tardigrade example highlights one route to a novel body plan via evolutionary changes in segment number. The *Tribolium* (beetle) example illustrates how differentiated appendage types are patterned within a conserved regulatory network, highlighting the mixture of developmental independence and dependence characteristic of serial homologues. I will conclude by describing how divergence of serial homologues led to an evolutionarily recent novelty in the hemipteran family Membracidae (treehoppers). This lineage is characterized by an enlarged, elaborate body wall projection called the helmet, which enabled radiation into a new morphospace. The helmet has subsequently been molded into a wide (and bizarre) array of shapes thought to contribute to defense. Morphologically, this transformation came about by transforming an ancestrally flat part of the dorsal body wall into a three-dimensional cuticular sculpture. Developmentally, and in line with how diversification of serially homologous appendages has occurred, we would predict that the helmet originated by tinkering with the ancestral body wall patterning network. However, our comparative transcriptomic analyses instead suggest a new mechanism for the divergence of serial homologues, in which divergence occurs through large-scale replacement of, rather than mere tinkering with, the ancestrally shared patterning network.



Main Meeting, FG Morphology
Oral presentation

Functional morphology of the mouthparts in adult *Anax imperator* (Odonata: Anisoptera) and their role in the feeding process

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Insects have developed different types of specialized mouthparts, which show various adaptations to their respective type of feeding. Adult dragonflies are predators, catching their prey in flight and process it while they are still airborne or on a safe perch. To gain insights into the feeding biomechanics of the biting-chewing mouthparts of adult *Anax imperator*, we combine results from micro computed tomography (μ CT), confocal laser scanning microscopy (CLSM), maximum working angle measurements and high-speed videography. Living specimens of *A. imperator* were filmed during the feeding process using high-speed videography to determine the in vivo angles of movement for each mouthpart. For comparison, the maximum angles of movement were measured using an angle measuring microscope. These results were combined with μ CT-data, delivering a comprehensive visualization of the 3D-geometry of each mouthpart as well as quantitative description of the attachment points of the corresponding musculature. The CLSM-data allows us to determine the material composition of the cuticle of the different mouthparts. The combination of the obtained results allows us to compare the quantitative morphology data with the in vivo movements of the mouthparts. This furthers our understanding of the role of individual mouthparts in the feeding process. In the future, we aim to create a foundation for biomechanical comparisons between dragonfly species belonging to different eco-types according to their food preferences and feeding habits.



Symposium: Form and function of motion systems: new approaches, new opportunities, new challenges

Oral presentation

Geckos racing across the water's surface and biorobotic fish undulating with soft actuator co-contraction

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Undulatory body motion is the dominant locomotion mode in fish, amphibians, and many reptiles. Laboratory and field experiments allowed observations of geckos' ability to race quadrupedally along the water's surface with little loss in speed compared to terrestrial running. To do this, the lizards combine several mechanisms: Surface slapping with feet (fluid inertia), body and tail undulation (hydrodynamic thrust), superhydrophobic skin structures (surface tension), and aquaplaning. Geckos occupy a size range directly between the surface locomotion of aquatic insects (surface tension dominated) and aquatic birds (drag and inertia dominated). By combining multiple mechanisms at once, geckos are able to move with astonishing rapidity over water, barely breaking stride.

Building on these insights, we have developed undulatory locomotion abilities in aquatic soft robots, using physical models made of soft fluidic actuators made of silicon elastomers. This enabled body stiffness modulation via lateral co-contraction, elucidating the neuromechanics of live fish swimming. Numerous studies of body kinematics and muscle activity have provided insights into swimming mechanics, yet have not been sufficient to understand how certain parameters (e.g. bilateral muscle activation extent) affect propulsion, due to the inability to manipulate muscle activation in live swimming fish. Using active soft bending actuators for body stiffness control in flow tank we varied undulation frequency and actuator phasing at different flow speeds. Experiments revealed that maximum thrust is generated with a small amount of antagonistic co-contraction over ~3% to 5% of the cycle period. Integrating soft sensors to the fish-like physical model successfully produced measurements of body curvature, paving the way for closing the loop with sensory feedback.



Main Meeting, FG Ecology
Oral presentation

Species diversity and ecology of Aculeata in the understory of the Leipzig floodplain forest

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Despite growing interest in bee diversity and ecology, only few studies focus on habitats, such as wetlands and forests, which are not the main nevertheless important habitats for bees and their relatives. Especially when populations in the main distribution areas are declining, these habitats may serve as reservoirs. In this study, which is part of the Leipzig Auwald Kran (LAK) project, we recorded the Aculeata species diversity in the understory of the Leipzig floodplain forest, using flight-interception traps between March and September in 2017 and 2018.

The sampling accumulated ca. 1000 individuals from at least eight Aculeata families, whereby the majority belonged to the Andrenidae (Anthophila).

Results from that investigation will include temporal abundance and species diversity distribution of the Aculeata as well as ecological factors such as host / parasite-interactions, available food resources and abiotic factors surrounding the trap locations.

Aim of the study is not only to inventory the rarely studied habitat of floodplain forests regarding Aculeata, but also to identify factors that possibly lead to differences in abundance and diversity among the trap locations. Ideally, factors that potentially facilitate Aculeata abundance and diversity are identified and will be of use to future conservation management.



Main Meeting, FG Morphology
Oral presentation

Morphology and innervation of head appendages in the ampharetid annelid *Hypania invalida*

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Annelid head appendages such as the prominent antennae, palps and tentacular cirri play a key role in annelid systematics and are important features for our understanding of annelid evolution. They can show an impressive range of morphologies, such as feather-like crowns in Sabellidae and Owenidae, slender feeding-palps in Spionidae and Magelonidae or numerous cirrus-like tentacles in Terebellidae. Nevertheless, these putative sensory and feeding organs are still scarcely investigated and homology of the various types of head appendages in different annelid groups is still under discussion. *Hypania invalida*, a freshwater polychaete of the sedentary family Ampharetidae, also bears several head appendages behind the first segment and in the buccal region, and in both cases a definite homology statement is still pending. Notably, detailed anatomical investigations dealing with these morphological features are lacking for these enigmatic annelids. For that reason we used immunohistochemical stainings and subsequent clsm analyses, serial azan sections as well as μ -CT data to analyse the morphology and innervation patterns of the anterior appendages in *H. invalida*. Our data give an overview of muscular and neuroanatomical characteristics of the appendages of interest, and provide new insights for our understanding of the evolution of annelid head appendages and the evolution of Annelida in general.



Main Meeting, FG Evolutionary Biology
Oral presentation

The role of the fruitless (*fru*) gene in specifying evolved male behaviours in the honeybee colony

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The transcription factor fruitless (*fru*) mediates the hardwiring of male brains in different insect species. In *Drosophila melanogaster* the transcript of the most distal promoter (P1) is sex-specifically spliced which leads to dimorphic expression of *fru* protein in the brain. The *fru* protein directs the male-specific hardwiring of the brain that leads to male behaviours. The honeybee *fru* gene has the same P1 derived male-specifically spliced transcript that translates a *fru* protein only in the male neuronal tissue suggesting functional conservation. However, male behaviours further evolved in honeybees as they were adapted to the life in the social environment of a colony. This new adaptation for males raises the question if the conserved *fru* gene also hardwires the evolutionary derived social behaviours in the brain. In order to answer this question, I produced *fru* minus mutants using the CRISPR/Cas9 system and studied male behaviours in the social environment of a small colony and petri dish experiments. Behavioural studies in colonies were conducted with computer-based tracking of *fru* minus mutant males using the Bee Behavioural Annotation System (BBAS) (Blut (2018), Scientific Reports, 2017; 7: 17663). My preliminary results suggest that at least some evolutionary derived behaviours are hardwired in the brain by the conserved *fru* gene.



Main Meeting, FG Systematics, Diversity and Biogeography Keynote Lectures
Oral presentation

The A's and B's of animal phylogeny

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Over the past twenty years our understanding of the relationships between animal phyla has changed dramatically as the result of advances in sequencing technologies, development of more realistic evolutionary models and improved efficiency of inference software. Using genome and transcriptome datasets, the community has reached a consensus on previously ambiguous relationships and has gained valuable insights into evolution of phenotype. There are, nevertheless, a few key relationships in the animal tree that remain controversial. Two of the most puzzling are whether the Xenacoelomorpha (a phylum of simple marine worms) is sister to Ambulacraria or to all other bilaterians, and, whether Porifera or Ctenophora is the sister clade to all other animals. The placement of both Porifera and Xenacoelomorpha has important impacts for our interpretation of the evolution of the animals. In both cases, one topology implies progressive evolution from simpler to more complicated phenotypes and the other implies substantial secondary character loss. So far, studies have worked on the two phylogenomic problems using independent datasets and pipelines. We use empirical and simulated sequence data to show the effects of model violations and data problems on the inference of the position of both Xenacoelomorpha and Porifera.



Main Meeting, FG Developmental Biology
Oral presentation

Is the breakdown of posterior segmentation irreversible?

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The red flour beetle, *Tribolium castaneum*, undergoes short germ embryogenesis, where anterior segments are patterned during the blastoderm stage, while posterior segments are progressively added from a Segment Addition Zone (SAZ) analogous to vertebrate segmentation.

The SAZ is set up during early blastoderm stages by Wnt and torso signaling. Segmentation is governed by three primary pair rule genes, even-skipped (*eve*), runt (*run*), and odd-skipped (*odd*), which oscillate to specify segments. RNAi-mediated knock-down of any of these genes leads to severe posterior truncations, indicating a breakdown of the segmentation machinery. However, it remained unknown whether the machinery can re-establish itself if the knocked-down components are brought back into the system.

We developed a novel genetic tool, hsVSR, whereby a Viral Suppressor of RNAi (VSR) is expressed via heat-shock, inhibiting RNAi. I knocked down a number of segmentation genes by RNAi and rescued their expression by hsVSR to ask for rescue of segmentation.

hsVSR was not able to rescue abdominal segments in Wnt pathway RNAi, indicating the importance for continuous Wnt signaling. Rescuing *eve*RNAi during early germ band elongation rescued abdominal segment formation, showing that the SAZ can re-establish its function even after a complete breakdown.

Further expression analysis of segmentation genes in RNAi and RNAi/rescued embryos by hybridization chain reaction (HCR) will give more insights into the mechanisms of re-establishment of posterior segmentation. The VSR technique has the potential to open new technical opportunities like temporal or spatial restriction of RNAi.



Main Meeting, FG Developmental Biology
Oral presentation

Diploblastic sea anemones have distinct cell types with signatures reminiscent of bilaterian muscle

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The evolution of a third germ layer, the mesoderm, was a key event for the triploblastic Bilateria that led to the acquisition of a number of new tissues, including three distinct muscle cell types. Although contractile cells are also present in non-bilaterians, evolutionary relationships to bilaterian muscle cells are unclear. Using a combination of anatomical, transgenic, and transcriptomic approaches we demonstrate that longitudinal muscles in *N. vectensis* show nervous stimulation and appear to have distinct neuromuscular junctions. Similar to vertebrates, these anthozoan muscles express acetylcholine and GABA receptors. Analysis of transcriptomic data, from both bulk RNA-seq of FACS-sorted cells from a transgenic muscle-reporter line and single cell sequencing data from sub-adult tissues, detects no evidence of functional glutamate receptors. Furthermore, these transcriptomic data demonstrate that molecular signatures for two effector modules similar to bilaterian muscle cells are already present in the diploblastic anthozoan *Nematostella vectensis*, constituting slow- (body wall) and fast- (retractor) contracting muscle modules. Moreover, we find four distinct transcriptomic profiles associated with each of the morphologically defined muscle cell populations. Transcription factor usage across these muscle populations reveals both pan-muscle elements as well as putative cell-type specific selector genes, including bHLH and T-box genes. Mutants of the pan-muscle bHLH binding partner e-protein support the idea that bHLH transcription factors are essential for the development of anthozoan muscles. Interestingly, all four muscle cell type profiles display various degrees of overlap with bilaterian muscle signatures.



Main Meeting, FG Morphology
Poster: MOR 6

The morphology of the feeding apparatus in *Aphanius mento*

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Aphanius is a genus of pupfishes belonging to the family Cyprinodontidae within ray-finned fish. They feed on insect larvae, crustaceans and algae, using suction feeding as a mechanism of prey capture. This led to some adaptations like a special mechanism of jaw protrusion.

The objective of this thesis is to reconstruct the morphology of the feeding apparatus in *Aphanius mento*, for comparison with related groups, as well as to prepare a detailed foundation for further kinematic studies.

To investigate the skeletal elements, as well as the appertaining musculature, microCT scans in combination with 3D reconstructions were used. Furthermore, the specimens' skeletons were prepared via clearing and staining.

Due to the structure of the skeletal elements and the associated musculature in *A. mento* it is reasonable to conclude that within this species the maxilla is pulled forward as the lower jaw is depressed, resulting in the Type B mechanism of jaw protrusion, also known as "twisting maxilla model" (Motta (1984) Copeia, No.1, pp.1). A similar type of jaw arrangement and therefore a similar mechanism of jaw protrusion is present in *Poecilia sphenops*, *Fundulus* sp. and *Mugil* sp. (Motta (1984) Copeia, No.1, pp.1).

Furthermore, *A. mento*'s mouth region shows a beak-like appearance, well-suited for the mechanism of suction feeding, as well as picking prey from the surface of the water or the ground (Alexander (1967a) Zoology, Vol.151, pp.43). This beak-like appearance can also be seen in *Gambusia affinis* and *Kryptolebias marmoratus* (Ferry-Graham (2008) Zoology, Vol.111(6), pp.455).



Main Meeting, FG Developmental Biology
Oral presentation

Role of taxon-restricted genes in cell type evolution: Insights from the cnidarian *Hydra*

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Understanding the molecular events that underlie the evolution of morphological diversity remains a major challenge in biology. In every animal species, highly-conserved genes make up the functional core of their genomes, essential for their development. Yet, a substantial portion of each genome is represented by taxon-restricted genes (TRGs) that show no detectable homology to other genes outside a certain taxon. The lack of homology confounds attempts to determine the putative function of the proteins coded by TRGs and impedes their systematic analysis.

Recently, we uncovered (Klimovich et al., in prep.) that TRGs dominate among the genes differentially expressed in the neurons of freshwater cnidarian *Hydra*. They comprise the molecular signature of each of seven neuronal. By combining genomic, transcriptomic and proteomic dataset analysis, in silico peptide analysis and machine learning with in vitro assays, we systematically analyze the complexity and function of the TRGs in *Hydra* neurons. We classify these TRGs into families and reveal common principle of their expression and structure. Using transgenesis, we investigate the function of neuron-specific TRGs in *Hydra*. Our study uncovers the previously underappreciated role of the TRGs in generating the cell-type diversity. It reveals that TRGs may drive the emergence of novelties and radiation of major animal clades.

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.



Main Meeting, FG Morphology
Oral presentation

Influence factors on the performance of the predatory strike in dragonfly larvae

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The labium in Odonata larvae is a highly modified prey capturing device. The mouthpart is modified into a prehensile mask, allowing them to ambush prey up to their own body size. The prehensile labial mask is capable of rapid accelerations of up to 114.5m/s^2 (11.7g), but also to stop at prey items with high precision to grasp them with their hook-like labial palps. To drive the rapid extension, the system is powered by a versatile dual catapult mechanism. The performance is remarkable considering the challenges of high-speed movement in a dense fluid, which is, due to the size of the specimens, dominated by viscous forces. Using a series of feeding experiments analysed with a combination of underwater force measurement techniques and high-speed videography, we identified several factors influencing strike performance. We assessed the influence of prey distance and temperature on the performance of the predatory strike, as well as the impact of differently shaped labial masks in *Sympetrum* and *Anax*. We provide evidence that the predatory strike adjusts to prey distance and that the performance is dependent on ambient temperature. The latter contradicts previous assumptions that catapult mechanisms are generally insensitive to temperature. Once the complex hydrodynamics have been understood, these results might foster our understanding of the ecomorphological adaptations within the aquatic habitat.



Main Meeting, FG Neurobiology
Poster: NEU 2

A close look to the bilateral collision detection in locusts – inspiration for a bionic solution

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Locusts exhibit a transition from the solitary to the gregarious phase when the population density increases due to specific environmental influences. As behavioral repulsion among solitary insects declines, they become social and form flying swarms as adults. Visual and acoustic cues contribute to swarm cohesion. Importantly, the collision detecting system of the insects responds very sensitive to approaching neighbors. Approaching objects lead to an increase of object size over the ommatidia (looming). A major component of the collision detecting system in locusts constitutes the DCMD-neuron (descending contralateral movement detector) that forwards the visual information from the brain to the thorax that houses the flight muscles. We recorded and analyzed the response of both DCMD-neurons to various looming paradigms by means of a pair of hook electrodes placed at the neck connectives. The stimuli were displayed by two curved monitors covering a field of view of 180 degrees. The results provided insights into specific response properties and the directionality of the collision detection system. Furthermore, we analyzed the responses of DCMD neurons to various near-crash scenarios recorded by two cameras attached to drones. Based on the activity of DCMD neurons we developed a bionic algorithm for collision detection that works in the absence of any distance estimation and object recognition algorithm. In a further project, we aim to implement this algorithm on a hardware for real time collision risk estimation and the computation of an evasive vector.



Main Meeting, FG Evolutionary Biology
Poster: EVO 6

Venom collection and analysis in the pseudoscorpion *Chelifer cancroides*

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Pseudoscorpions are tiny arachnids adapted to crevice habitats. Some pseudoscorpions possess pedipalps equipped with a unique venom apparatus for paralyzing prey. The venom of these animals is poorly known. We performed a proteomic analysis of the pseudoscorpion venom, which identified the first genuine venom compounds of these animals. To this end, we have developed a non-invasive approach for extracting minute amounts of venom, enabling the collection of pure venom samples from pseudoscorpions with minimal contamination and high reproducibility. To our knowledge, pseudoscorpions are the smallest venomous animals that have ever been milked individually. Venom release needed to be triggered by a combined mechanical and electrical stimulation, indicating the presence of a mechanism that prevents the wasteful release of venom. High-resolution scanning electron micrographs of the venom delivery system confirmed the presence of a modified seta (lamina defensor) at the base of all venom teeth, which might be involved in the venom release. Extracted venom was used for top down proteomics, which, in combination with transcriptomic data, enabled the identification of venom compounds that show sequence similarity to Megicin, an antimicrobial peptide known from the venom of the scorpion *Mesobuthus gibbosus*.



Main Meeting, FG Behavioural Biology
Oral presentation

The influence of the early environment on behavioural and physiological traits in cavies (*Cavia aperea*)

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Animal personality, i.e. behavioural differences between individuals that are consistent across time and contexts, are common across taxa but our knowledge about mechanisms generating and maintaining individual differences is still rather limited. Hence, there is an increasing interest in investigating the contribution of the early social environment in shaping the behaviour and physiology of the developing phenotype of an individual.

In cavies, the size rank in the litter (i.e. being the largest, middle or smallest pup) predicted the personality type a juvenile develops. The aim of this study is to investigate the influence of the early social environment on the stability of personality. To disentangle pre- and postnatal influences, we cross-fostered pups after birth to either maintain their original size rank, obtained a higher or a lower size rank. We expect pups that changed their size rank to develop either the personality that belonged to the new size rank or to develop the personality of their original size rank.

All animals were tested twice in an open field test, a novel object test and a struggle test. Moreover, physiological parameters like heart rate, resting metabolic rate and basal cortisol were measured.

First results suggest that the cross-fostering into a different size rank influenced the development of the behavioural type. Consequently, personality is not fixed directly after birth, even in the highly precocial cavy, but the early social environment exerts a strong and potentially long-lasting influence on the developing phenotype.



Main Meeting, FG Physiology
Oral presentation

Physiological effects, toxicity and detoxification of gossypol, a cotton secondary metabolite in Heliothine moths

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The agricultural pests *Helicoverpa armigera* and *Heliothis virescens* (Lepidoptera: Noctuidae) are generalist insects, confronted with a large variety of plant secondary metabolites. The major defence compound of one of their host plants, cotton, is gossypol, a secondary metabolite toxic to most organisms. Here, we investigated physiological effects and toxicity of gossypol, as well as the detoxification strategies of *H. armigera* and *H. virescens*, which allow them to feed successfully on cotton plants. Analysis of feces revealed several glycosylated gossypol isomers when larvae fed on gossypol-supplemented diet. Based on gossypol-inducible expression patterns, we selected *H. armigera* candidate UGT genes and functionally expressed the respective proteins in insect cells. In enzymatic assays, we showed that UGT41B3 and UGT40D1 are glycosylating gossypol mainly to a diglycosylated gossypol isomer, a potential strategy of *H. armigera* to detoxify gossypol.

Further, we identified high concentrations of fatty acid-amino acid conjugates (FACs) in the feces of gossypol fed larvae, when compared to control larvae. FACs are present in the oral secretions of lepidopteran larvae and are elicitors of the indirect plant defense system. Despite this fitness cost, the physiological role of FACs in lepidopteran larvae is largely unexplored. We heterologously expressed insect aminoacylase, which hydrolyzes FACs into fatty acid and amino acid in the insect gut. In enzymatic assays we showed that gossypol inhibits the aminoacylase activity in vitro. Interference of the FAC metabolism by gossypol ingestion might reduce larval fitness and by that enhance negative and more direct effects caused by gossypol.



Main Meeting, FG Ecology
Poster: ECO 2

Nectar supply for pollinators – a case study in extremely long-proboscid flies (Nemestrinidae)

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Diptera of the genus *Prosoeca* (Nemestrinidae) belong to the long-proboscid fly pollination system in the Greater Cape Floristic Region of Southern Africa. These nectar-feeding insects have a morphologically complex proboscis which reaches up to 40 mm in length. These particularly long-proboscid flies are the sole pollinators of a plant guild with very long-tubed flowers. We studied the proboscis morphology, the flower-visiting behaviour and nectar uptake capabilities of the local endemic species *P. marinus* in a small, isolated area of natural vegetation which is surrounded by transformed landscapes in the Northern Cape Province of South Africa. At this isolated patch, the nemestrinid fly *Prosoeca marinus* was the only legitimate nectar feeder of the long-tubed irid *Babiana vanzijliae*. This particular one-to-one insect-flower interaction provided the opportunity to estimate the mean quantity of nectar ingested per flower visit by *P. marinus* and the total daily nectar supply available to the population of pollinating flies. This is the first assessment to estimate the total nectar availability that fuels the activities of specialist pollinating insects under natural conditions in the field.



Main Meeting, FG Evolutionary Biology
Oral presentation

Tracing evolution tooth by tooth: Convergent trophic specialization of a paludomid species flock in an “ancient” African lake

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“Ancient” Lake Tanganyika is a hotspot of freshwater biodiversity because of the high number of endemic species. Its paludomid gastropods represent a spectacular example of closely related taxa with an extraordinarily interspecific diversity of radular tooth morphologies. In order to understand, whether this can be explained by trophic specialization, we correlated, against the background of a molecular phylogeny, the radular tooth morphologies and its most characteristic features with the specific feeding substrate (solid or soft). We evaluated not only the radula tooth morphology, but also its mechanical properties by nanoindentation, a test measuring hardness and elasticity modulus of materials. We incorporated these properties in a Finite Element Analysis (FEA) model. FEA is a method that allows to model behavior of structures under mechanical loads and to visualize the stress and strain distribution within structures. FEA combines tooth material properties with its exact 3D form and therefore helps in understanding functional significance of different radular teeth. Together these results shed light on adaptations of gastropods to their specific feeding substrates. Finally, we are able to support the hypothesis of independent colonialization events of Lake Tanganyika from surrounding rivers. Adaptations in the radular teeth to soft substrates are ancestral and teeth enabling foraging algae from solid substrates have evolved at least four times convergent.



Main Meeting, FG Physiology
Oral presentation

Molecular mechanisms of hypoxia tolerance in the whale brain

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Low oxygen conditions (hypoxia) have immediate effects on the oxidative metabolism of mammals and thus on brain function. While in most mammals, hypoxia causes severe brain damage, whales and seals must have developed strategies of hypoxia tolerance that allows them to dive for up to 2 h without surfacing.

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

For a better understanding of the molecular adaptations in the cetacean brain, we compared Illumina-generated transcriptomes of the deep-diving pilot whale (*Globicephala melas*) and the killer whale (*Orcinus orca*) with a terrestrial relative, the cattle (*Bos taurus*). We analyzed the abundances of transcripts in the visual cortex and the cerebellum as well as mRNA expression levels of enzymes of the energy metabolism and typical stress-related genes. Our data suggest a divergent evolutionary strategy in whales and seals to sustain the demands for metabolic energy during cerebral hypoxia.



Main Meeting, FG Morphology
Oral presentation

Uncovering the hidden dynamics in the development of ciliary bands in *Platynereis dumerilii* and *Thalassema thalassema* (Polychaeta)

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The spiralian phylum Annelida, together with Mollusca and possibly Entoprocta, belongs to Trochozoa, a clade that is characterized by a typical larva, the trochophora. The eponymous organ of the trochophora is the prototroch, a pre-oral circumferential belt of ciliated cells. Confined to the larval stage, it is used for swimming and feeding in the majority of polychaete species. Due to its stereotypic cell lineage and transitory fate, the prototroch has been considered homologous across Trochozoa. However, a survey of the available literature shows that the numbers of cells constituting the prototroch varies considerably between different lineages. To resolve this contradiction we investigated the development of the prototroch from its formation to its disappearance in the model organism *Platynereis dumerilii* (Audouin & Milne Edwards, 1833). *P. dumerilii* is a lecithotrophic organism with a rapid larval development of only a few days. Our results confirm that the number of cells constituting the prototroch is constant due to cleavage arrest and that the prototroch disappears after the fifth day of development. We compared our results to the planktotrophic larvae of the echiuran *Thalassema thalassema* (Pallas, 1774), which has a prolonged development of several weeks until settlement occurs. Due to its extended planktonic life-style, it is likely that the prototroch cells (trochoblasts) are replaced or at least supplemented by other cells. The result of our investigation sheds light on the developmental dynamics of the prototroch and the alleged stereotypy of the cellular compositions of ciliated bands.



Main Meeting, FG Morphology
Oral presentation

Dentitional metamorphosis in caecilian amphibians: a reanalysis

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Caecilians are fossorial pantropical amphibians renowned for their remarkable diversity of reproductive modes and life histories. Their dentition varies throughout ontogeny e.g., juveniles of some species bear fetal or vernal teeth used to peel off the mother's skin post-partum or post hatching or scrape off oviductal epithelium in utero. The ontogeny of dentition was studied across various caecilian species and currently recognised families mostly from 3D- reconstructions obtained through microCT scanning. Ontogenetic differences in tooth number especially concern dental tooth series but teeth of dentigerous bones of the upper jaw also varied markedly in number and morphology. Interspecific differences in tooth number and ontogeny were also detected. Tooth number was positively correlated to body size in many study species. An updated knowledge on dentitional metamorphosis of caecilians help to draw conclusions about life history evolution and supports comparative morphology.



Main Meeting, FG Behavioural Biology
Oral presentation

Traffic noise influences the acoustic communication signal of the bush cricket *Tettigonia viridissima* (Orthoptera)

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For sexual reproduction many species of mammals, birds and insects use acoustic communication for long distance signaling. However, this acoustic communication channel can be disturbed by biotic and abiotic influences, including anthropogenic noise.

Besides vertebrates, insects might be affected by anthropogenic noise. Many species of Orthoptera depend on acoustic communication for mate finding.

Here we investigate the tettigoniid species *Tettigonia viridissima* (Orthoptera, Ensifera), which relies on acoustic communication for reproduction. *T. viridissima* is an abundant species in many parts of Germany, occurring in urban habitats as well as in natural habitats. Males produce a long range calling song to attract females by wing stridulation. The calling song is produced daily, preferentially in the evening hours and contains long series of syllables.

In order to test whether signal production was influenced by anthropogenic noise, we exposed animals close to a highway and registered their sound production. The overall stridulatory pattern is unchanged, but during by-passing of a car temporal disruptions occurred. These pauses are longer than pauses occurring without car noise. The probability of the occurrence of car-related pauses negatively correlates to the number of passing cars per minute. This is a first report of direct influences of car noise on calling insects resulting in a changed temporal pattern, which might be important for mate recognition.



Main Meeting Keynote Lectures
Oral presentation

The human and evolutionary origins of animal domestication

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It is difficult to overstate the degree to which domestication has shaped human history. The advent and spread of settled agriculture starting ~11,000 years ago triggered wide ranging transformations that continue to this day: demographic increase, the emergence of social elites and wealth disparities, and impacts on the earth's ecology and atmosphere. Given its fundamental importance, a vast literature from a wide variety of academic disciplines has explored and explained the origins of domestication. In both lay and academic literature, domestication has been posited, explicitly or implicitly, to be the result of human intentionality, often as a deliberate action to either solve a problem or respond to a novel incentive.

This emphasis has led to the uncritical acceptance and circulation of origin myths associated with numerous domestic plants and animals. I will discuss those myths and show that the vast majority of domestic plants and animals have emerged as a result of a continuous, dynamic process characterised by shifts in the nature and intensity of their relationship with humans. Viewed through the lens of modern theories of the domestication process, and through an analysis both ancient and modern relationships between people and a variety of plants, animals, and microbes, I explore the possibility that no species was ever intentionally domesticated. I will then use specific recent case studies that analyse the ancient DNA of pigs and dogs to show how elucidating the spatiotemporal pattern of genomic signatures can lead to insights into not only the origins of domestic animals, but into the evolutionary process writ large.



Main Meeting, FG Ecology
Poster: ECO 9

An integrative approach to study insect diversity in Germany, the project DINA (Diversity of Insects in Nature Protected Areas)

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Insect decline was severe over the last two decades and has also affected nature protected areas in Germany (Hallmann et al. (2017) PLOS ONE 12: e0185809). However, large gaps exist in our understanding of the main factors driving this insect Armageddon. With the project DINA we designed a multi-layer approach, combining natural sciences data on habitats, insect species occurrence and pesticide exposure with discourse formats with citizens, stakeholders and public authorities. This complexity will be broadly covered regarding communication processes and expectation management as well as in co-creation and co-production with stakeholders. Using malaise trapping as a powerful tool for insect monitoring in combination with meta-barcoding and selective manual abundance estimates, we will generate the most complete insect species occurrence data for nature protected areas in Germany up to the present. We predict that nature protected areas shape, topography and habitat diversity influence insect biodiversity. If insect biodiversity differs significantly between nature protected areas with similar habitat compositions, we will test for the influence of landscape usage, especially agricultural practices in the vicinity, and the exposure to various ecotoxic substances, especially pesticides. It is generally believed that the penetration depth of emissions will influence insect biodiversity. Based on our results we will develop recommendations for more effective protection of insect.

On behalf of the project partners: EVK, IZNE, ISOE, JLU, IOER, UKL, ZFMK, supported by BMBF



Main Meeting, FG Morphology
Poster: MOR 22

In vivo: three-dimensional patellar motion in French Bulldogs with patellar luxation at walk and trot

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Seven French Bulldog with no orthopedic anamnesis or apparent abnormal gait patterns exhibited larger femoral external rotations and abduction than other breeds. We were curious of how specifically stifle torsion may affect patellar motion and/or induce patellar luxation. We reanalyzed the stifle-joint x-ray-sequences during walk and trot focusing on patellar motion. To reconstruct 3D-patellar motions relative to the femur we used Scientific Rotoscoping (SR). SR is the manual matching of CT-based virtual bones to biplanar X-ray shadows.

We found Medial Patellar Luxation (MPL) occurring during each gait cycle. MPL is one of the most frequent pathologies in small breed dogs. It is a misalignment of the patella related to the femoral groove. Luxation of the patella can lead to pain, lameness, and the development of osteoarthritis. So far, the analysis and the diagnostic methods are performed in a static manner. Moreover, neither three-dimensional kinematics of the patella for French Bulldogs nor any other breed is known, nor whether this is gait related.

Our results indicate that MPL occurs mainly during the last third of stance and the early swing phase. This finding is only partially in accordance with the literature that has suggested that MPL grade 1 and 2 are mostly related with tibial torsion during the early swing phase. Knowledge of patellar kinematics and dynamics may open alternative pathways for the pathogenesis of patellar luxation, open new possibilities for classifying it, and may help to improve surgical techniques leading to a clinical benefit.



Main Meeting, FG Ecology
Oral presentation

Insectivorous bats integrate social information about species identity, conspecific activity and prey abundance to estimate cost-benefit ratio of interactions

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Animals can use Inadvertent Social Information (ISI) to improve fitness-relevant decisions. Since bats emit high-amplitude species-specific echolocation calls when flying, they provide a constant flow of ISI. Of particular interest is the feeding buzz rate – characteristic call sequences preceding any prey capture – which correlates with insect abundance. Our goal was to systematically test which ISI bats integrate when eavesdropping on others and how this integration affects space-use and interactions, respectively. We used a community-wide approach and investigated the effects of a broad range of playback feeding buzz rates and conspecific activity on eavesdropping responses in 24 bat species combinations in the wild. For the first time, we reveal that finely graded and density-dependent eavesdropping responses are not limited to particular foraging styles or call types, but instead are ubiquitous among insectivorous bats. All bats integrated ISI about calling species identity, prey abundance, and conspecific activity to estimate the cost-benefit ratio of prospective interactions, yet in a species-specific manner. The effect of buzz rate was multifaceted, as bats responded differently to different buzz rates and responses were additionally modulated by heterospecific recognition. Conspecific activity had a negative effect on the eavesdropping responses of all bats. These findings can explain the inconsistent results of previous studies and advance our understanding of the complex nature of con- and heterospecific interactions within bat communities. A comprehensive understanding of how bats incorporate social information into their decision-making will help researchers to explain species distribution patterns and eventually to unravel mechanisms of species coexistence.



Main Meeting, FG Neurobiology
Oral presentation

Myoinhibitory peptide is a co-transmitter in CI and DUM neurons and reduces slow muscle contractions

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Understanding how nervous systems generate motor behavior is a fundamental goal of neurobiology. In insects, peripheral inhibition (γ -aminobutyric acid) and modulation (octopamine) are key elements in motor control strategy, essential for the muscle to transfer neural activity into forces efficiently. However, relatively little is known about neuromodulation from non-conventional substances like neuropeptides.

Transcriptomic and neuropeptidomic techniques have been used in prior work to define the neuropeptidome of the stick insect CNS (Liessem et al., 2018). Here, we report on data obtained from MALDI-TOF single cell profiling of modulatory and motor neurons to restrict this analysis to putative neuropeptide candidates involved in locomotion. We describe for the first time the presence of myoinhibitory peptide (MIP) in dorsal unpaired median (DUM) and common inhibitor (CI) motor neurons, its transport to the extensor tibiae muscle, and its functional relevance for muscle contractions. Moreover, we confirm the presence of the MIP-receptor in leg muscles by transcriptomic analysis and are currently defining its localization with in situ hybridization. We show that application of MIP significantly reduces force and contraction amplitude of primarily slow extensor muscle fibers. These effects support the function of CI motoneuron activity in reducing muscle forces generated by dually and triply innervated fibers, which is likely to make the production of fast muscle fiber contractions more effective as for instance during leg swing in stepping movements.



Main Meeting, FG Developmental Biology
Poster: DEV 3

Evolution of developmental processes underlying head formation in *Drosophila*

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The size and shape of adult organs is controlled by developmental gene products, which are organized in gene regulatory networks (GRNs). To reveal the molecular basis of natural variation in complex trait morphology, we study the evolution of compound eye size and head shape in different *Drosophila* species. As previous studies have shown, the size of the head cuticle and the eyes are negatively correlated in various *Drosophila* species. Ongoing work has shown that the GATA family transcription factor Pannier (Pnr) represents a flexible node in the GRNs. However, genetic tests suggest that the causative genomic changes lie upstream of the pnr locus.

We combine various datasets to identify putative evolving regulators of pnr: 1) Based on a genome wide expression dataset in combination with transcription factor motif analyses, we identified several candidates that bind to regulatory elements of pnr (e.g. Mad, Jim, Zen). 2) Previously published quantitative genetics datasets aiming at revealing candidate changes responsible for intra-specific head cuticle variation revealed genes that may be involved in the observed interspecific variation (e.g. jim, Fasciclin 3, Reticulon-like1). 3) We use allele-specific expression data to identify genes that show signatures of cis-regulatory divergence (e.g. zeste, trf, cort). To test which of these candidate genes is indeed responsible for morphological differences between *D. melanogaster* and *D. mauritiana* we combine reciprocal hemizyosity tests based on CRISPR/Cas9 mutagenesis with developmental genetics approaches. Eventually, we aim at unveiling the role of the identified evolving gene(s) in the GRN underlying head formation in *Drosophila*.



Main Meeting, FG Behavioural Biology
Poster: BEH 20

Using an electric field to find a food source in the weakly electric fish, *Gnathonemus petersii*

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During evolution animals developed many ways of navigating their environment. Weakly electric fish emit electric signals to scan their surroundings (active electrolocation) and in addition can perceive local electric fields originating from natural biological/geological sources (passive electrolocation). During foraging, they use a combination of active and passive electrolocation and other senses to find and identify their prey. Here we studied whether *Gnathonemus petersii* is able to navigate using only passive electrolocation of a stationary electric field in a dark arena without any other landmarks.

We tested three single fish in a symmetrical hole-board arena with 64 (8x8) electrodes arranged in a square on the ground. Prior to each trial, a complex electric field was generated by the electrode array, and food was placed in one of the holes on the ground at a fixed location relative to the electric field. A fish was randomly put in one of the corners of the arena, from where it learned to search for the reward. Besides the electric field, no other sensory cues were available. Fish learned to find the prey quickly, independently of the corner they started from. When the electric field was changed (rotated, turned off), the fish needed more time to find the food, indicating that they used the field to remember and find the location of the reward. By varying electric field geometry and amplitude, we investigated the involvement of active and passive electrolocation as well as egocentric and allocentric strategies for navigating the arena.



Main Meeting, FG Developmental Biology
Poster: DEV 6

The influence of nkx genes on amphibian head development

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Anuran tadpoles have several novel, unique structures which only exist in the larvae and disappear during metamorphosis. The most drastic of these novelties are the rostralia and the derived organisation of cranial muscles that goes along with these. In addition to the primary jaw joint an intramandibular joint between Meckel's cartilage and infrastralia is present. This led to the formation of a novel feeding apparatus which might be a key to the evolutionary success of this group. We investigate the molecular basis of the formation of these larval cartilaginous skeletal elements using functional knock-down as well as overexpression of the nkx genes *bapx1* and *zax* in *Xenopus laevis*, *Bombina orientalis* and *Ambystoma mexicanum*. Overexpression of *bapx1* in *Xenopus laevis* led to the development of additional cartilages within the mandibular arch whereas the development of the primary jaw joint fails after knockdown of *bapx1* in three amphibian species. Knock-down of *zax* in *Xenopus laevis* causes a fatal deformation of the anterior part of the head and leads to missing rostralia. Meckel's cartilage and the infrastrals are fused and no intramandibular joint is present. The lack of *bapx1* in agnathans and its appearance in gnathostomes in combination with its joint-forming function in anurans could shed light on how the jaw evolved. Furthermore, the co-option of the related gene *Zax* in anurans could explain how the rostralia as novelties evolved.



Main Meeting, FG Evolutionary Biology
Oral presentation

Ant workers' susceptibility to paraquat induced oxidative stress in relation to age and reproductive status

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In contrast to most solitary species, fecundity and longevity are positively linked in the social insects. While the queens are highly fecund and rather long-lived, non-reproductive workers rear the queen's offspring and bear the costs of colony maintenance, reflected in their shorter lifespans. Evidently, fecundity and longevity are positively associated even within a caste. Ant workers vary greatly in their reproductive potential, ranging from absolute sterility to totipotency across species. Theory predicts that the lifespan of sterile workers, with the lowest reproductive potential, is optimized solely to increase colony fitness and that they will invest little into their own survival. In contrast, worker-lifespan increases when they switch from being sterile helpers to reproductive individuals. We used four ant species from two continents to test whether experimental manipulation of workers' reproductive potential alters their investment into somatic maintenance. To do so, we removed the queen to induce ovarian activation where possible. We then subjected workers of different ages to an oxidative stress treatment using paraquat. This organic compound induces superoxide anions that prematurely age animals. We monitored worker survival for 12 days and subsequently analyzed the ovary development of all workers to investigate the effect of reproductive activity and age on their resilience to oxidative stress. We found that younger workers survived oxidative stress better than older workers, and the queen's absence increased the survival of younger workers but affected older workers adversely. Fecundity, longevity, and fitness are closely intertwined, and our study helps to disentangle these relationships across ants.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral presentation

The adipokinetic hormones of the lower clades of Diptera: a structural comparison

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With about 152 000 described species, the Diptera is one of the species-rich orders of insects. Historically, flies are divided into two major groups, the lower Diptera (= Nematocera) and the Brachycera with the major clade Cyclorrhapha. Recent phylogenetic studies support the monophyly of Diptera, paraphyly of Nematocera and monophyly of Brachycera and also Cyclorrhapha.

Since primary structures of adipokinetic hormones (AKHs) of the nematoceran infraorder Culicomorpha (mosquitoes) were known, we investigated the complement of AKHs in a species from the nematoceran infraorder Tipulomorpha (crane flies) to look at structural trends. First, the corpora cardiaca (the AKH-synthesizing glands) were dissected from the head and extracted in methanol. The extract was then analysed by liquid chromatography coupled to mass spectrometry. Three AKHs were found, all octapeptides. Two are novel, thus have not been detected before in any organism, and differ from each other only in the aromatic amino acid at position 4 (phenylalanine versus tyrosine). The third peptide had been sequenced before in the tsetse fly, a member of the Cyclorrhapha and differs from the second tipulid AKH by an exchange at position 7 (serine versus glycine). All tipulid AKHs are specific for Diptera. They differ from AKHs of the Culicomorpha (*Aedes*, *Anopheles*) by one (serine vs threonine at position 5) or two amino acids (serine/threonine at position 5, and serine/alanine at position 7).

It is not clear in phylogenies where exactly the Tipulidae are placed; the current results support this.

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Main Meeting, FG Physiology
Poster: PHY 1

Metabolomics of the seal brain: Molecular mechanisms of hypoxia tolerance in marine mammals

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The hooded seal (*Cystophora cristata*) can dive to a depth of 1000 m for a duration of 60 min. During these dives the seal brain experiences low oxygen conditions (hypoxia) that would lead to a loss of neuronal function in other mammals. However, neurons of the hooded seal in slices of the visual cortex remain much longer active under severe hypoxia than those of mice, and persist for up to 3 h. Behavioral, anatomical and physiological adaptations have evolved to cope with hypoxia like high blood hemoglobin and muscle myoglobin content, bradycardia, peripheral vasoconstriction and reduced temperature and metabolism. The brain has a high energy demand and hence consumes a large fraction of the inhaled oxygen. During dives the oxygen supply alone is not enough to maintain its metabolism. Molecular mechanisms have to take place, but how they account for hypoxia tolerance hasn't been subject to many studies. Therefore in this project we aim to compare the metabolome of the visual cortex of the hooded seal to terrestrial relatives (mouse, ferret) to elucidate compounds that might be involved in its hypoxia tolerance. Colorimetric assays as well as liquid chromatography-mass spectrometry (LC-MS) for the identification of metabolites will be performed. Substrates of energy metabolism as well as signaling molecules and secondary metabolites play a major role in this matter and are presumably differentially regulated in species under resting as well as diving conditions to survive imminent hypoxia.



Main Meeting, FG Morphology
Oral presentation

Fluid dynamics within structurally diversified spermathecae in leaf beetles by utilizing up-scaled, transparent and flexible models

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In nature females are often polyandrous and can store sperm from different males in a spermatheca before ovulation. Due to the fact, mating success of males does not guaranty reproductive success, and this results in the postcopulatory mate choice. Despite of the universality of this principle, female structures are much less studied comparing to male ones. Hereby we focused on the spermatheca in leaf beetles and aimed at unveiling its functional morphology by simulating sperm dynamics in the spermatheca. Morphology and material composition gradients were studied by means of micro-computed tomography and confocal laser scanning microscopy. We found rather strong structural diversity of the spermathecae among the studied species in not only external structures but also in internal ones. Despite of it, all species possess a similar pumping structure, which is composed of a C-shaped chamber, muscles, and a resilin enriched region. Focusing on a studied species, which shows a relatively simple shape with an internal protuberance in the spermatheca, we challenged to simulate sperm dynamics in the spermatheca by establishing a method of designing models that were later used in fluid dynamics tests. The tests using the spermatheca models with and without the inner protuberance showed quite different fluid movement between them. Our approach demonstrated that structural variations in the spermatheca affect sperm dynamics, which suggests that shape differences in the spermathecae among species can reflect postcopulatory mate choice strategies. We will discuss the role of our experimental approach in understanding the biomechanical background of the postcopulatory mate choice.



Main Meeting, FG Evolutionary Biology Keynote Lectures
Oral presentation

The evolution of termite immunity

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A broad suite of immune adaptations have evolved in social insects which hold close parallels with the immune systems of multicellular individuals. However, comparatively little is known about the evolutionary origins of immunity in social insects. We tackle this by identifying immune genes from 18 cockroach and termite species, spanning a gradient of social lifestyles. Termites have undergone contractions of major immune gene families during the early origin of the group, particularly in antimicrobial effector and receptor proteins, followed by later re-expansions in some lineages. In a comparative gene expression analysis, we find that reproductive individuals of a termite invest more in innate immune regulation than other castes. When colonies encounter immune-challenged nestmates, gene expression responses are weak in reproductives but this pattern is reversed when colony members are immune-challenged individually, with reproductives eliciting a greater response to treatment than other castes. Finally, responses to immune challenge were more comprehensive in both subsocial and solitary cockroaches compared to termites, indicating a reduced overall ability to respond to infection in termites. Our study indicates that the emergence of termite sociality was associated with the evolution of a tapered yet caste-adapted immune system.



Main Meeting, FG Evolutionary Biology
Oral presentation

Transgenerational phenotypic plasticity in the cyprinid *Pimephales promelas*

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Transgenerational phenotypic plasticity is a mechanism by which organisms attempt to predict future environmental conditions so as to adaptively match their offspring's phenotypes to their environment. Predator-induced defenses, ranging from behavior to morphology, are a well-studied example of phenotypic plasticity where first attempts have been made to understand their transgenerational transmission. However, most of these studies focus on asexually reproducing organisms with short generation times, thus little is known about the transmission of such defenses during sexual reproduction, which adds another important layer of phenotypic variation to transgenerational plasticity. Here, we report the first results of a comprehensive study on transgenerational antipredator phenotypic plasticity in a sexually reproducing common prey cyprinid fish with allopaternal care, the fathead minnow *Pimephales promelas*. Predation risk was simulated by continuously exposing fish in split-clutch rearing designs to either conspecific alarm cues that are released across aquatic taxa upon injury by a predator, or a control water treatment. Afterwards, we set up breeding combinations allowing us to control for parental vs. offspring effects via environmental match/mismatch designs, paternal vs. maternal precopulatory effects, postcopulatory effects of parental care by parents from different environments and grandparental vs. parental effects. Over a 2-year period, we then assessed morphology, shoaling behavior and boldness in up to 4200 fish across 18 treatments during three generations. Our results may allow inferences about how environmental information is transmitted across generations and interacts with an individual's own perception of the environment as well as about the evolutionary consequences of transgenerational phenotypic plasticity.



Main Meeting, FG Developmental Biology
Poster: DEV 7

Imaging cardiac valves: correlating histology and function

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The *Drosophila melanogaster* larvae possess a simple linear heart built up by two adjacent rows of cardiomyocytes with a total number of 104 cells with very little variation in cell number. The fly heart is subdivided into a posterior heart chamber and an anterior aorta section, separated by a single intracardiac valve formed by only two cells. These cells regulate directional hemolymph flow (from posterior to anterior) inside the heart tube (Lammers et al., 2017). The pumped hemolymph distributes nutrients, signaling peptides, ECM constituents and metabolites of various pathways to all parts of the body. Interestingly, a total loss of cardiac activity does not affect viability in principle but has dramatic effects on fitness and longevity of flies (Drechsler et al., 2013). Within the *Drosophila* larval heart tube, flow directionality is supposed to be regulated by the coordinated contraction of the cardiomyocytes and a single intracardiac valve. The histology of this valve has been revealed by different microscopic techniques including transmission electron microscopy and immunohistochemistry. The presence of large membranous vesicles is a unique characteristic of the valve cells of 3rd instar larvae (Lammers et al., 2017). My research focusses on the identification of genes that affect valve cell specification, differentiation and function. By using different microscopic approaches I would like to analyze hemolymph flow in valve mutants and the physiological impairments caused by valve cell malformation.



Symposium: Form and function of motion systems: new approaches, new opportunities, new challenges

Oral presentation

The shape of locomotion: a method for large scale analyses of intra-limb coordination

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Coordinated movements of body segments can be considered the collective output of the movement apparatus and its control, which varies with evolutionary, ontogenetic, and immediate context. However, when comparing the inter-segmental coordination of closely related taxa, it may be hard to pinpoint and quantify the exact manifestation of this variation, especially if large numbers of groups are under investigation. Limitations stem from the complex interrelation of morphology, posture, and adjacent joints. In consequence, the kinematic study of coordination disposes of a more restricted computational toolbox than for example geometric morphometrics, although both fields are equally data driven. I present a novel quantitative method that overcomes these limitations. The method exploits the potential of the Fourier Series to isolate affine components (i.e. mean, amplitude, phase) of signals. By removing affine components to superimpose joint angle profiles, one receives measures of the shape of angular profiles, analogous to procedures in geometric morphometrics. I exemplify this on a data set that covers 75% of all genera of terrestrial ungulates. It has been known that ungulate locomotion is affected by geometric dissimilarity (the classical rhino-giraffe comparison). It can be shown that an even stronger, non-morphological variability component is associated with clearance, i.e. how animals adjust or adapt to substrate structure. This novel method enables the derivation and test of alternative hypotheses about intra-limb coordination in unprecedented phylogenetic detail and scale, thereby improving the understanding of the biomechanical and evolutionary principles that shape locomotion.



Main Meeting, FG Ecology Keynote Lectures
Oral presentation

Valuing intraspecific variation in plant-animal interactions: from individual traits to restoration sites and agro- ecosystems

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Intraspecific variation in phenotypic traits is increasingly regarded as fundamental driver of species interactions and related ecosystem processes. Trait variation in plant species can have profound effects on organisms associated with plants, and consequently it may influence different ecosystem processes related to animal-plant and microbe-plant interactions. Considering interactions between animals and plants, it can be assumed that trait variation in plants affects animals on different organizational levels, from individual performance to composition of animal communities. From an applied perspective, the degree of intraspecific variation in plant populations purposely established, for example for agriculture, forestry or restoration, may be of great relevance for beneficial and detrimental interactions between animals and plants, which are fundamentally affecting the functions provided by plants. By taking into account examples from natural, anthropogenically transformed and experimental systems, the presentation will focus on consequences of intraspecific trait variation in wild and cultivated plants on associated animals from an individual to a community perspective. It aims at stimulating a discussion about the role and the value of intraspecific variation in natural and anthropogenic contexts.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral presentation

Once superabundant now at the brink of extinction – why chronotopes matter

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One of the enigmas of the dramatic loss of biodiversity that is happening on a human timescale is that not only rare small-range species are declining but also formerly superabundant widespread species, such as the passenger pigeon or the house sparrow. Although the scenarios are well published, there is as yet no global conservation strategy. Local conservation measures have proven ineffective.

The loss of these superabundants would have larger consequences for the ecosystems than the loss of the rare species. Due to their large distribution it is unlikely that widespread species are affected by changes in their biotope as these are local and heterogeneous processes. Changes in the chronotope (the temporal structure of a habitat), for example by climate-change or light-pollution, affect larger ranges and are thus potential reasons for such global declines.

The European hamster (*Cricetus cricetus*) is such a formerly superabundant widespread species and now Eurasians most rapidly declining mammalian species. It is not an increase in mortality but a progressive decline of the reproduction rate since 1954 which destabilizes populations over huge parts of the distribution area. Today, a female raises on average only 0.5 females for next year's reproduction. The extrapolation of the data suggests a worldwide extinction between the years 2020-2038.

Why the reproductive output has declined is unclear, however, an inadequate timing of reproduction might have an essential role. Thus, classic chronobiologic concepts might be useful to explain former and present threats and selection pressures against superabundants due to former overhunting, climate-change and light-pollution.



Symposium: Form and function of motion systems: new approaches, new opportunities, new challenges

Oral presentation

The caudal fin in gadiforms: heavily modified, an evolutionary novelty or something in-between?

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Cods and allies, the Gadiformes, are one of the most important fish groups for human food and well-known in terms of fisheries ecology. The skull of the cod is often studied in detail in fish morphology classes. But what's about the other end of the fish? The caudal fin skeleton in gadiforms is usually regarded as much derived with some peculiarities puzzling morphologists: several elements present in 'typical' teleostean fish taxa are missing, e.g. the uroneurals, a notochord flexion or a diastema. On the other hand, some gadiform taxa possess additional skeletal elements, as e.g. the X- and Y-bones, which so far resisted to become homologised with certainty. To clarify the homology of caudal fin elements in cods and allies we used clearing and double staining to follow two approaches. First, in a detailed comparative study we compared bone and cartilage structures covering the gadiform diversity including possible outgroups. And second, in an ontogenetic study we documented the caudal fin development in burbot (*Lota lota*). Preliminary results confirmed the huge differences between caudal fins in gadiforms and other teleosts. Also the caudal fin development in gadiforms clearly differs from the situation known from other teleosts: a typical notochord flexion is absent and sequences of development and ossification make comparisons complicated. Our study provides conflicting data: some details support the idea that the gadiform caudal fin is just a highly derived teleosts caudal fin, other findings rather support the idea that the caudal fin in gadiforms presents a new independent development a so called 'neocaudal' or 'pseudocaudal' fin.



Symposium: Form and function of motion systems: new approaches, new opportunities, new challenges

Oral presentation

The muscle fibre-tendon length ratio mainly determines the contraction dynamics and function of the muscle-tendon-complex

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The muscle-tendon-complex (MTC) shows different functions regarding the relation of the lengths of muscle fibres and tendon or aponeurosis. The literature summarises different functions like stabiliser, motor, accelerator, brake, and spring. Unfortunately, these tasks were determined experimentally on different animals investigating different MTC on different limbs. Thus, a clear discrimination of MTC function remains vague due to varying experimental conditions. To shed more light on the impact of the inner length ratio of muscle fibres and tendons on coherent MTC function, we simulated a MTC by using a Hill-type muscle model. The model consists of a contractile element (muscle fibres), a serial element (tendon), and a parallel elastic element (tissue in parallel to the muscle fibres). Ensuring a constant overall length of the MTC, the tendon rest length was varied over a physiological range from 0.1 to 0.9 times MTC length. Typical MTC functions were investigated by simulation of typical physiological experiments. We found that MTC function is largely determined by the inner length ratio. A MTC with long muscle fibres but short tendon is perfectly adjusted for stabilising joints or accelerating limbs; work and power can be maximised. In contrast, short muscle fibres connected to a long tendon are ideal for handling forces greater than the muscle fibre capacity and maximising work storage capacity of the tendon (legged terrestrial locomotion). Moreover, extreme inner length ratios produce MTC specialists. Thus, when short fibres contract isometrically against a long tendon the MTC cannot fully exploit the fibre's maximum force capacity.



Main Meeting, FG Physiology
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 *Macrobdella 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 Morphology
Oral presentation

**Development of the cranial musculoskeletal
system in fetuses of the West African viviparous toad
Nimbaphrynoides occidentalis (Amphibia: Anura:
Bufonidae)**

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Viviparity is exceedingly rare in anuran amphibians. So far, only about 16 species (out of a total of over 7000) are known to be viviparous. Of these, only the West African toad *Nimbaphrynoides occidentalis* has a matrotrophic form of viviparity (the remaining species are ovoviviparous). Previous research indicated that fetuses of *N. occidentalis* start feeding from a very young age on, which necessitates a functioning musculocranial system, among other things. The extent as to which the foetal morphology differs from that of free-living aquatic tadpole larvae has been unclear though. To address this we examined and described the morphology of the chondrocranium, branchial apparatus, and associated musculature of fetuses of *N. occidentalis* representing various developmental stages and compared these with the morphology of larval *Altiphrynoides osgoodi*, its closest relative retaining a free-living tadpole. The overall structural organisation of the chondrocranium, lower jaw and the branchial apparatus of *N. occidentalis* is surprisingly tadpole-like. Although some muscles are reduced or fused, the musculoskeletal system does not differ substantially from that of *A. osgoodi* and other free-swimming bufonid tadpoles. However, there are marked differences in the orientation and proportions of these structures, most prominent among them a downward flexure of the cranial base, which are seemingly related to intrauterine feeding in *N. occidentalis*.



Main Meeting, FG Morphology
Poster: MOR 10

Chaetae of *Owenia fusiformis* indicate annelid-brachiopod relationship

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Transcriptomic and phylogenomics studies yielded an enormous progress in our understanding of the phylogeny of Annelida that forces to re-evaluate morphological characters. Although the position of the Annelida within the Spiralia is still a matter of debate, re-evaluated characters contribute to solving this issue. Herein we exemplify this for annelid chaetae. Chaetae are almost exclusive to Annelida, only occurring in one additional animal group, the Brachiopoda. According to the most recent phylogenomic studies, Oweniidae are considered to form one of the most basally branching annelid subgroup. We studied chaetogenesis in *Owenia fusiformis* Delle Chiaje, 1844 (Oweniidae) in terms of their formation, structure and diversity using transmission electron microscopy, 3D modelling and confocal laser scanning microscopy. We provide evidence that the notopodial capillary chaeta lack an enamel layer characteristic for all annelid chaetae studied thus far. Such a layer is also missing in brachiopods, substantiating the hypothesis of a sister group relationship either between Brachiopoda and Annelida or between Lophophorata and Annelida. It allows evaluating further characters, like lipid content of follicle cells or monociliarity as plesiomorphic in annelids.



Main Meeting, FG Morphology
Poster: MOR 15

**Ultrastructure of wall-pore sensilla in the web spider
Gradungula sorenseni Forster, 1955 (Araneomorphae,
Araneae) indicates olfactory transduction pathways similar
to other euarthropods**

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In arthropods, sensing of many modalities is achieved with the aid of cuticular sensilla and primary ciliary receptor cells assembled therein. For instance, cuticular sensilla may perform mechanoreception, hygroreception, thermoreception, contact-chemoreception (gustation), or chemoreception over a distance (olfaction). In web spiders, mechanoreception and gustation have been convincingly assigned to certain types of sensilla frequently found on their walking legs and pedipalps (trichoid sensilla, tip-pore sensilla). Whether and, if so, how web spiders are able to sense volatile odors remained unanswered questions. Behavioural studies revealed that web spiders use volatile odors for detecting prey and mating partners. However, previous studies failed to find wall-pore sensilla in spiders, known as the typical receptors of olfactory cues in other arachnids, myriapods, and hexapods. Therefore, it seems likely that olfaction is covered by tip-pore sensilla in spiders, even though this would require spatial restriction of different odor-binding and reception systems to the tip-pore region. However, there is an old, insufficiently documented finding of wall-pore sensilla in web spiders, namely in the species *Gradungula sorenseni*. This electron microscopic study provides thorough insights into the outer morphology and microanatomy of wall-pore sensilla in *G. sorenseni*. Remarkable ultrastructural similarities to wall-pore sensilla of other arthropods are noticeable with respect to the dendritic apparatus and composition of the sensillum shaft. This indicates that spiders may also use common pathways of olfactory stimulus transduction, independent of transport of volatile odors through a tip pore.



Main Meeting, FG Behavioural Biology
Poster: BEH 13

Quantifying the acoustic parameters of overlapping echolocation calls in free-flying horseshoe bat aggregations

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Bats are social animals living and flying in groups. They use echolocation to navigate the environment. While echolocation in single bats is more comprehensively studied, group echolocation is more complex and less understood, especially in horseshoe bats. Horseshoe bats have long echolocation calls, where a long constant frequency (CF) part is sandwiched between two short frequency modulated (FM) sections. The long duration calls suffer from spectrotemporal overlap by other bat calls and Doppler-shifted echoes, challenging acoustic analysis of multi-bat situations. Our study addresses this methodological challenge to fill the gap in understanding how horseshoe bats vary their echolocation call parameters when flying alone and together with conspecific or heterospecific bats. We predict that bats will alter their call parameters in multi-bat contexts by 1) increasing FM bandwidth to increase information in dense situations, and by 2) by emitting higher intensity calls (Lombard effect). We further test whether CF-bats also alter their CF frequency to avoid spectral overlap, as FM bats do. We used multi-channel synchronized audio and video to record bat activity in a natural cave habitat. We first obtained independent estimates of the number of simultaneously flying bats based on the video data, peaks in the call spectra, and visual screening of call spectrograms. We then obtained average call parameters such as peak CF bandwidth, terminal frequency bandwidth, and peak amplitudes which were then compared to the number of counted bats. Our study presents a novel approach for studying echolocation in groups of CF bats.



Main Meeting, FG Developmental Biology
Oral presentation

Spatial cell disparity in the colonial choanoflagellate *Salpingoeca rosetta*

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Choanoflagellates are the closest relatives to the multicellular animals, the Metazoa. Many single-celled choanoflagellates can switch between sessile and motile cell morphologies showing temporal cell differentiation. A few choanoflagellate species additionally have the ability to form colonies consisting of hundreds of cells. In contrast to metazoans, these choanoflagellate colonies have been described to consist of similar cells meaning that they exhibit no spatial cell differentiation. Therefore, spatial cell differentiation is used as one of the basic features to define the Metazoa. Recently, the discovery of single cells in colonies of the choanoflagellate *Salpingoeca rosetta* that exhibit a unique cell form challenges this view. We therefore asked: How similar are the cells within a colony really compared to cell of a metazoan cell type such as sponge choanocytes? To answer this question, we used high-resolution TEM serial sections through four *S. rosetta* colonies (40 cells in total), three solitary cells and five choanocytes of the sponge *Oscarella carmela* to reconstruct the organelle composition (food vacuoles, mitochondria, nuclei, etc) of each cell. Our data indicate that cells within a choanoflagellate colony exhibit a higher spatial cell disparity than sponge choanocytes from the same choanocyte chamber. As an additional data set, we reconstructed the ultra-structural euchromatin/heterochromatin composition in each nucleus to compare the diversity of chromatin ratios and architecture of differentiated sponge choanocytes to colonial *S. rosetta* cells. Our aim is to search for euchromatin/heterochromatin dynamics comparable to those during metazoan cell differentiation.



Main Meeting, FG Behaviour Keynote Lectures
Oral presentation

Goats who stare at scientists – human-directed behaviour in livestock

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Research on the cognitive capacities of non-human animals (i.e. their ability to acquire, process, store and use information) has gained increasing attention over the last decades. Compared to the amount of investigations conducted on primates and dogs, studies on farm animal cognition appear under-represented. This lack of research is surprising because knowledge of the mental capacities of farm animals can directly affect their welfare. For example, a detailed understanding of how farm animals perceive and communicate with handlers is crucial to improving management conditions through positive human-animal interactions. In this overview, I will summarise recent advances in studies on the cognitive capacities of domestic goats, focusing especially on how goats interact with humans. To this end, modified socio-cognitive test paradigms from comparative psychological research in canids and primates have been applied. Like dogs, goats differentiate between human attentive states and show human-directed behaviour when they are confronted with an unsolvable problem. Based on these findings, I will briefly outline how applied research could benefit from these results, considering that subtle human behavioural changes can affect the behaviour of farm animals.



Main Meeting, FG Ecology
Oral presentation

**For they had brought destruction upon themselves:
How host and not parasite variation predicts the outcome of
a symbiotic interaction**

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The fitness and virulence of parasites are often determined by how many resources they can wrangle out of their hosts. Host defenses that help to keep these resources from the parasites will then reduce virulence and parasite fitness. Here we study the protective effects of host brood care and brood size regulation on a parasite. We use the biparental brood-caring burying beetle and its phoretic *Poecilochirus* mites as a model. Since paternal brood care does not seem to benefit the offspring in a clean laboratory setting, the male presence has been suggested to strengthen the defense against parasites. We manipulated male presence and found no effect on the fitness of the parasitic mites or the beetle offspring. We further manipulated parasite dose and beetle brood size and found no effect of parasite dose on beetle fitness, but larger beetle broods to harm parasite success. The specific pattern we observed suggests that beetle larvae are strong competitors and consume the carrion resource before all parasites develop. They thus starve the parasites. These results shed new light on the observation that the parasites appear to reduce host brood size early on – potentially to prevent later competition.



Main Meeting, FG Developmental Biology
Oral presentation

The *glu* gene is required for the sexual dimorphic head development in workers of the honeybee *Apis mellifera*

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Sexual dimorphism is common to many animal species and manifests in various morphological traits. In honeybees, males and the two castes of females can be distinguished by various sexual features such as the size of the eyes, shape of the metathoracic leg with its bristles and number of antennal and abdominal segments. How these striking differences between sex morphs are specified during development is a pending question.

In many insect species doublesex (*dsx*) acts as a master regulator of sexual differentiation. *dsx* specifies sexual morphological traits as well as sexual behaviours. Recent functional studies in the honeybee, however, showed that another regulator beside *dsx* is required during sexual differentiation to realise distinct morphological outcomes. An inactivation of *dsx* in female honeybees showed no effect on sexual dimorphic head, leg and abdomen morphology (Roth (2019) PLoS Biol, 17, e3000171). We used next generation transcriptome sequencing in honeybee embryos to identify other developmental regulators of sexual dimorphism. Comparison of alternative spliced transcripts in male and female embryos led to the discovery of the gene *glubschauge* (*glu*) that is sex-specifically spliced in the honeybee embryo. Mutating *glu* using the CRISPR/Cas9 method indicates that *glu* is required for the development of the female compound eye.



Main Meeting, FG Ecology

Oral presentation

Host plant use in the range-expanding butterfly *Pieris mannii*

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Besides phenotypic plasticity and genetic adaptation, movement is one of the essential ways in which organisms can respond to environmental change. In phytophagous insects, range expansions critically depend on the availability of suitable host plants in the new area. Often, range expansions in such species are therefore associated with host shifts by using secondary or novel hosts if primary hosts are lacking. However, we are currently lacking a solid understanding of the role of host plant shifts for expanding taxa. Here, we examined host plant preferences in a currently range-expanding butterfly species (*Pieris mannii*) by comparing female and offspring host plant preference of individuals originating from core and leading edge populations. To this end, we performed oviposition choice experiments and larval feeding preference tests in the laboratory using primary and potentially novel host plants. We predicted that individuals from newly established populations show an increased diet breadth compared to those from core populations. Such patterns were confirmed for oviposition choice. Interestingly, offspring and female preferences did not match, which might be explained by a higher selective pressure on females for the incorporation of new suitable hosts in order to colonize new areas, while larvae have generally less opportunity for choice than females. Our data indicate a higher flexibility in oviposition behavior for the newly compared with the source populations, outlining the importance of adaptive variability and shifts in biotic interactions during the process of range expansion.



Main Meeting, FG Evolutionary Biology
Poster: EVO 2

Resurrecting genomes: whole genome amplification and sequencing of *Daphnia* resting eggs

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The accumulation of resting eggs from planktonic organisms in sediment allows direct insights into past populations and shifts in inter- and intraspecific variation. Thanks to the rise of new genomic resources, the resting egg bank enables researchers to address evolutionary, ecological and environmental questions. *Daphnia* are a genus of freshwater microcrustaceans and have become a popular genomic model due to their status as keystone species, well-characterized ecological interactions and cyclical parthenogenetic life-cycle. The analysis of eggs from dated sediment cores allows to investigate hybridization dynamics linked to anthropogenic ecological changes in the *Daphnia longispina* complex. Genomic studies that can be conducted directly without hatching and culturing several genetically identical individuals are limited by extremely small amounts of DNA in single *Daphnia* resting eggs. We thus performed whole genome amplification to obtain DNA amounts suitable for genome re-sequencing. Using this approach, we successfully amplified and sequenced genomes from *Daphnia* resting eggs from a North German lake that could be identified as *D. galeata*. Resting eggs derived from three different time periods allowed us to study the lakes' population dynamics in the past several decades. Pre-sequencing quality control steps were conducted to quickly assess possible contamination. Further resequencing of resting eggs from different time periods from several northern German lakes will help to characterize genomic changes through time and to uncover hybridization dynamics in the *Daphnia longispina* complex.



Main Meeting Keynote Lectures
Oral presentation

Reverse-engineering the locomotion of a stem amniote – insights from a multidisciplinary approach

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Reconstructing the locomotion of key vertebrate fossil specimens offers insights into their palaeobiology and helps to conceptualize major transitions in vertebrate evolution. Estimating the locomotor behaviour of a fossil species, however, remains a challenge because of the limited information preserved and the lack of a direct correspondence between form and function. *Orobates pabsti* from the Bromacker quarry in Thuringa, central Germany, is a representative of the diadectids, i.e., the likely fossil sister taxon to modern amniotes. Also, hundreds of tetrapod tracks have been recovered from the same site and some of these were assigned to *Orobates* as the trackmaker. This unique combination of an articulated nearly complete early tetrapod specimen and fossilized evidence of the same species' locomotor behavior was the starting point for an in-depth reconstruction of the locomotion. The reconstruction involved experimental as well as computer-aided modelling approaches ('virtual paleontology'). Starting from a large space of potential solutions, unlikely postures and gaits were step-wise excluded based on quantitative data. Research into the fossil's anatomy, the fossil's potential joint mobility and simulated potential movements within fossil tracks, a comparative analysis of extant tetrapod locomotor biomechanics using x-ray motion analysis, and finally into a bio-inspired walking machine (OroBOT) will be summarized. The locomotor reconstruction demonstrates that *Orobates* exhibited more advanced locomotion than has been assumed for earlier tetrapods, which suggests that advanced terrestrial locomotion preceded the diversification of crown amniotes.



Main Meeting, FG Developmental Biology Keynote Lectures
Oral presentation

From the Biogenetic law to the hour-glass model: is there a conserved stage in vertebrate development?

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Ernst Haeckel formulated his biogenetic law in 1872, famously stating that ontogeny recapitulates phylogeny. Haeckel was in his turn influenced by pre-Darwinian thinkers such as Karl Ernst von Baer, who had noted that earlier developmental stages show similarities not seen in the adults. I give an overview of the tradition emanating from Haeckel and other comparative embryologists and morphologists, which has often been neglected in discussions about the history of EvoDevo and evolutionary biology. I emphasize contributions from Russian and German scientists, to compensate for the Anglo-American bias in the literature. One example is that Haeckel inspired Victor Franz in Jena, whose ideas about "biometabolic modi" are similar to those of a Russian comparative morphologist that visited Jena repeatedly, A. N. Sewertzoff, who made important contributions to what we now call heterochrony research. His student I. I. Schmalhausen became an important contributor to the synthetic theory of evolution and there are important parallels between Schmalhausen's ideas (stabilizing selection, autonomization) and C. H. Waddington's (canalization, genetic assimilation) on developmental constraints. The "hour-glass" model was developed by Dennis Duboule and Rudy Raff in the 1990s as an explanation for the conservation of the phylotypic stage in vertebrates, i.e. why developmental constraints are strongest at this mid-embryonic stage and not earlier or later in development. The model is still controversial and I end with a discussion of the current status of this model.



Main Meeting Keynote Lectures
Oral presentation

The evolutionary origins and impact of the horse on human history

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The horse was one of the last large mammals to be domesticated. It, however, probably represents the animal that most impacted human history. Horses changed the way we made war, but also allowed us to travel well above our own speed, globalizing the world and the circulation of goods, languages and diseases, for the first time. Our own activities have also circled back to the horse, which resulted in the development of hundreds of domestic breeds and pushed all wild populations to extinction. The evolutionary history underlying horse domestication remains controversial, and difficult to fully reconstruct from patterns of present-day DNA variation alone. On the contrary, time traveling provides a unique possibility to bypass current limitations and directly catch the domestication process red-handed. Within the framework of the ERC PEGASUS project, we have endeavoured to sequence complete horse genomes from across their whole temporal and geographical domestication range. Our current genome dataset includes hundreds of ancient horse genomes fully sequenced. This allows us to document the genetic changes accompanying horse domestication at unprecedented scales, revealing unexpected features of the whole population dynamics underlying horse domestication as well as key historical turning points, from the earliest domestication stages to the most recent expansion of major equine civilisations.



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

First insights into the phylogeography of *Palaemon varians* on the European coastline

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The Atlantic ditch shrimp *Palaemon varians* (Leach, 1813) has a patchy distribution throughout brackish habitats, especially river estuaries and salt marshes along the European coastlines (Dolmen (2004) Sarsia, 89, p. 8). This small-scale distribution provides a high isolation potential and thus we may expect significant genetic differentiation within the species range. So far, little is known about the population diversity of *P. varians*, and hence, we set out to investigate the phylogeography of this species. Using newly generated in combination with publicly available sequence data of a fragment of the mitochondrial cytochrome oxidase subunit 1 gene, we characterized the genetic diversity and differentiation of populations along European coasts. The results so far confirm our expectation of significant population differentiation among regions, hint at cryptic invasions but also highlight significant geographic gaps in the sampled populations.



Main Meeting, FG Physiology
Oral presentation

Insights into the venom composition and its biological functions of the endoparasitoid wasp *Pimpla turionellae* (Hymenoptera: Ichneumonidae)

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In the process of oviposition, the female endoparasitoid wasp *Pimpla turionellae* L. (Hymenoptera: Ichneumonidae) injects venom into the host, to ensure the successful parasitization and the development of their progeny. Previous studies showed that the venom harbors active substances with diversified biological functions, such as neurotoxicity or immune suppression. However, venomomics studies that unravel the venom composition and evolution, and address which function they show are still underrepresented. Here, we discuss the venom evolution in *P. turionellae* based on first results of our proteo-transcriptomic analysis. To identify the major venom components, an integrated transcriptomic and proteomic approach was applied. The liquid chromatography-mass spectrometric (LC-MS) data of the crude venom from the venom glands was combined with an in-house analysis pipeline applying a multiple assembly approach of venom gland and body tissue transcriptomes. Among the identified proteins, peptidases constituted the most abundant family followed by protease inhibitors, oxidases, peptides, and novel venom peptides and proteins. Peptidases and protease inhibitors are reported as a common component of several parasitoid wasp venoms. Furthermore, we identified knottin-like peptides with an ICK typical 6C-scaffold, which might have pivotal neurotoxic/paralytic effects on the pupal host. Currently, the activity of novel candidates, which are promising for pharmaceutical and agrochemical applications are being tested.



Main Meeting, FG Neurobiology Keynote Lectures
Oral presentation

Waking at night. Slow-wave oscillations in *Drosophila*

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Slow-wave rhythms characteristic of deep sleep oscillate in the delta band (0.5 – 4 Hz) and can be found across various brain regions in vertebrates. Across systems it is however unclear how oscillations arise and whether they are the functional unit steering behavior. Here, we discover sleep-relevant delta oscillations in *Drosophila*. We find that slow-wave oscillations in the sleep-regulating R5 (R2) network increase with sleep need. Optical multi-unit voltage recordings reveal that single R5 neurons get synchronized by sensory and circadian input pathways. We show that this synchronization depends on NMDA receptor (NMDARs) coincidence detector function and on an interplay of cholinergic and glutamatergic inputs setting the frequency. Genetically targeting the coincidence detector function of NMDARs in R5, and thus the uncovered mechanism underlying synchronization, abolished network-specific slow-wave oscillations. It also disrupted sleep and facilitated light-induced waking, directly establishing a role for slow-wave oscillations in regulating sleep and sensory gating. We therefore propose that the synchronization-based increase in oscillatory power likely represents an evolutionarily conserved, potentially 'optimal', strategy for constructing sleepregulating sensory gates.



Main Meeting, FG Physiology
Poster: PHY 2

Molecular, cellular and physiological consequences of hybridization in *Danio*

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Hybrids, i.e. crosses between species, occur much more frequently in nature than assumed until recently and seem to play an enormous, but so far little studied role in evolution. Thus, hybrids are often invasive species and pose a challenge to many ecosystems. However there is no evidence of hybrid *Danio* species in the wild yet, but studies have proven that some *Danio* species are capable of hybridization. Our first approach to establish a hybridization procedure and the basal gene expression of three *Danio* species in our lab: *D. rerio*, *D. albolineatus* and *D. aesculapii* by comparing their transcriptomes in three different tissues (brain, liver and gonads). What are the molecular consequences of hybridization? Are genes expressed randomly? Are genes from a particular species preferred? Are there differences in tissues? To answer those questions we first looked at the transcriptomes of the parental species. 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.



Main Meeting, FG Evolutionary Biology
Oral presentation

Chemoreceptor diversity and lineage specific gains and losses in the stinging wasps, ants and bees (Hymenoptera: Aculeata)

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Chemoreception is crucial for insects since it allows detection and evaluation of food and mating partners, and enables nestmate recognition in social insects. Stinging wasps (Hymenoptera: Aculeata) evolved different degrees of sociality, feeding behaviours and utilize different food sources. Eusocial wasps presumably have a higher chemical information throughput than their solitary relatives and wasps collecting plant tissue need to have differently tuned chemoreceptors than wasps preying on insects. Thus, lifestyle shifts likely placed selective pressure on the evolution of chemoreceptor repertoires. In order to investigate how lifestyle shifts affected the chemoreceptor repertoire evolution in Hymenoptera, we searched chemoreceptive tissue transcriptomes of apoid wasps for chemoreceptor gene sequences and reconciled the phylogeny of wasps with the phylogeny of these chemoreceptor genes. We show that a high number of olfactory receptors were lost in the lineage leading to bees relative to the evolutionary timeframe in which they happened. Intriguingly herbivorous sawflies and fig wasps also have relatively small chemoreceptor repertoires which could indicate that Hymenoptera searching for plants possibly require fewer chemoreceptors than parasitoids or carnivorous predators. We currently study the chemoreceptor repertoire of additional aculeate wasp lineages, including solitary wasps closely related to ants and vespidae wasps in order to increase the phylogenetic resolution of the ancestral chemoreceptor repertoire reconstruction aiming to identify phylogenetic lineages with significant gains and losses over time. This will allow us to gain insights into the role of different degrees of sociality, feeding behaviours, and food sources on the evolution of chemoreceptor repertoires in the Aculeata.



Main Meeting, FG Developmental Biology
Oral presentation

Organizing the Organizer: A novel role for Ets4 in axis specification and cell migration in the spider *Parasteatoda tepidariorum*

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Axis determination is a fundamental process during animal development. In vertebrates as well as in spiders an organizing centre plays an important role during this process. In spiders the organizer is composed of a cluster of migratory cells (the cumulus) that induce the dorsoventral body axis via the secretion of Decapentaplegic (the ligand for the BMP receptor). This study reveals that the transcription factor Ets4 is required to keep cumulus cells in the cluster and to activate the expression of cumulus specific genes like hunchback and twist. Loss of Ets4 expression is leading to ventralized spider embryos. Interestingly, ectopic expression of Ets4 is sufficient to induce cell delamination and migration by inducing a mesoderm-like cell fate.



Main Meeting, FG Physiology Keynote Lectures
Oral presentation

Plant toxins as a driver of insect-plant coevolution

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Plants produce a tremendous variety of toxic compounds to defend themselves against herbivorous parasites such as insects. Remarkably, many insects can not only cope with plant toxins but also store them in their bodies to ward off predators, a strategy referred to as sequestration. In conceptual terms, this means that insects can use plants in at least two ways, i.e. as a dietary resource and as a source of defensive compounds. We study the physiological mechanisms underlying insect resistance to host plant toxins and found that resistance and sequestration sometimes intertwine. Specifically, sequestration of plant toxins requires resistance traits different from those needed to consume toxins in the insects' diet. In consequence, predators selecting for sequestration can spur the coevolutionary arms race between insects and plants. Moreover, we found recently that acquisition of plant toxins for defense even drives specific associations with particular host plants in insects that are dietary generalists. Based on our findings, we propose that sequestration is an important mechanism mediating ecological interactions across at least three trophic levels. Despite of sequestration being common among insects, the underlying mechanisms and the resulting physiological costs of sequestration are largely unknown. Using a variety of approaches in a comparative, evolutionary framework, we aim on understanding the mechanistic basis of sequestration as well as the resulting physiological implications. Our overall goal is the advancement of coevolutionary theory by integrating insect physiology, analytical chemistry, and ecology.



Main Meeting, FG Morphology Keynote Lectures
Oral presentation

Enter the labyrinth – Functional morphological and phylogenetic signals of the organ of balance in vertebrates

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Since Hyrtl denied in 1873 functional morphological signals in the anatomy of the inner ear of vertebrates, many studies accepted this challenge. However, the results of these studies were as contradictory as the groups of investigation, ranging from aquatic (e.g., sharks, whales) to land-living (e.g., mammals, reptiles) to flying species (e.g., birds). Common to all, the vestibular system is responsible in detecting the equilibrium and spatial orientation of an organism during locomotion. However, it is not clear which anatomical signal represents the mode of locomotion (height and width vs. diameter of the three semicircular canals) and if and how the phylogeny influences this morphology.

Located and enclosed in the petrosal bone at the base of the occipital region, this sensory system and its anatomy can be analysed in extant species, but also fossil taxa, using non-destructive micro-CT scanning and analyses of the virtually reconstructed bony labyrinths. Traditional morphometrics use three-dimensional measurements of these models and, in some cases, standardize the values prior to statistical analyses (e.g., Pfaff et al. (2015) Proc B, Vol. 282, 20150744). In contrast, geometric morphometric approaches are using homologous points (landmarks, semilandmarks) and the respective superimposition of the data (e.g., Grohé et al. (2018) Sci Rep, Vol. 8, 2301). Both methods analyse the data applying multivariate statistic tools (e.g., PCA, Procrustes analyses).

This talk highlights the most important studies of the bony labyrinth in vertebrates and gives an outlook into the future of these functional morphological studies.



Main Meeting, Walther Arndt Prize
Oral presentation

Evolution of visual system development – morphology meets genomics

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The size and shape of an organism and its organs is tightly controlled during embryonic and postembryonic development to ensure proper functionality. However, in the light of the breath-taking diversity of body forms observed in nature, adult features are certainly target for evolutionary changes. This contradiction suggests that developmental gene regulatory networks (GRNs) are constrained to a certain level, but nodes within this network are prone to change to give rise to morphological divergence. We have previously shown that the three closely related *Drosophila* species *D. melanogaster*, *D. simulans* and *D. mauritiana* exhibit natural variation in eye size and overall head morphology. In this survey, *D. melanogaster* has the smallest eyes and *D. mauritiana* has the largest eyes. The aim of our research is to identify flexible nodes within the GRN underlying adult head formation in these three *Drosophila* species. To this end, we combine unbiased genome-wide approaches like quantitative trait loci (QTL) mapping and comparative transcriptomics with developmental genetics and geometric morphometrics to identify genes and developmental processes responsible for the observed differences in head morphology.



Main Meeting, FG Evolutionary Biology
Oral presentation

Imperiled by an expanding pathogen: using management units of the fire salamander to channel species conservation

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In the wake of rapidly declining global biodiversity, conservation management has to focus on the preservation of populations to maintain and maximize the genetic diversity and the evolutionary potential of a species. Globally, biodiversity is threatened by climate change, pollution, and habitat destruction as well as by emerging infectious diseases. Currently, *Batrachochytrium salamandrivorans* (Bsal), an introduced pathogenic chytrid fungus is expanding through Central Europe and has been severely affecting populations of the fire salamander (*Salamandra salamandra*), leading to rapid declines and regional extinctions. In the face of a threat bringing this species potentially to the brink of extinction, ex situ management of fire salamander populations has been suggested as one of the most promising approaches to conserve the genetic diversity as a last resort. We conducted a study aiming to identify management units of the fire salamander in Germany, the species' main area of distribution, where Bsal is rapidly spreading. We sampled ~60 populations of *S. salamandra* across Germany and determined their genetic composition by microsatellite analysis, ddRAD sequencing, and mitochondrial sequence analysis. The identified genetic units represent the most important populations worth being protected and the candidates for an ex situ project in Germany to save the genetic diversity and adaptations present. Here, we present the final results of the study and how they get implemented into the first ex situ programs.



Main Meeting, FG Evolutionary Biology
Poster: EVO 15

Inter- and intraspecific variation and function of the obligate endosymbiont *Blochmannia* in African *Camponotus* species

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Carpenter ants of the genus *Camponotus* are one of the most successful and species-rich ant genera (Bolton (2006), Harvard University Press). All members of this genus possess an obligate intracellular bacterial mutualist, *Blochmannia*, which might be one reason for its evolutionary success (Feldhaar (2007), BMC Biology, 5: 1-11). In particular, the bacterial genome encodes for an urease that allows for the recycling of nitrogen from urea and it retained all but one metabolic pathways to synthesize essential amino acids for its host (Feldhaar (2007), BMC Biology, 5: 1-11; Zientz (2004), Microbiology and Molecular Biology Reviews, 68(4): 745-770).

However, it is remarkable that the distribution and diversity of *Blochmannia* throughout the tribe Camponotini is not yet fully analysed. Preceding phylogenetic studies mainly focussed on interspecific endosymbiont distribution and diversity worldwide, except Africa. Therefore, we used 16S barcoding to identify the closest *Blochmannia* associates of six African *Camponotus* species from the Ivory Coast. These African *Blochmannia* appear to be most closely related to *Blochmannia* from *Camponotus* species from South, Central and southern North America.

We have started to generate endosymbiont free colonies and preliminary results indicate that although, adult workers and the queen seem to be not affected, treated colonies stopped to produce brood. An effect previously shown for endosymbiont free colonies of *C. floridanus* (Feldhaar (2007), BMC Biology, 5: 1-11).



Main Meeting, FG Morphology
Poster: MOR 2

The nervous system of cheilostome bryozoans

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Bryozoans are sessile aquatic suspension feeders in mainly marine, but also freshwater habitats. They form colonies composed of numerous individuals called zooids. Most extant species belong to the group of Cheilostomata that, among other characters, have a calcified body wall. The nervous system of this group is little investigated and several authors of the 20th century faced problems in the examination of these small animals. Essential morphological data originated from neuronal tracing techniques using methylene blue vital staining (Lutaud (1969) *Zeitschrift für Zellforschung*, 99, 302) and silver impregnation (Lutaud (1973) *Zeitschrift für Zellforschung*, 140, 217) that were later complemented by immunohistochemical experiments (Schwaha 2015, *BMC Evolutionary Biology*, 15, 223). In our study we focus on the analysis and characterization of the nervous system, based on data from representatives of all main cheilostome taxa. We employed a range of complementary traditional and modern techniques to evaluate each of these methods for neuroanatomical research purposes. First results show the location of the brain at the base of the lophophore, from where nerve cords embrace the mouth opening to form a circumpharyngeal nerve ring. Two neurite bundles project from the brain to innervate the lophophore as well as peripheral areas, such as the body wall and parietal muscles via the tentacle sheath. Three nerve chords display the main nerves of the visceral nervous system. This data will be the basis for a ground pattern reconstruction of the cheilostome nervous system.



Main Meeting, FG Developmental Biology
Oral presentation

FoxB, a new and highly conserved key factor in arthropod dorsal-ventral limb patterning

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Forkhead box (Fox) transcription factors evolved early in animal evolution and represent important components of conserved gene regulatory networks involved in many aspects of animal development. Most research concerning Fox genes, however, is on vertebrates and only a relatively low number of studies investigate Fox gene function in invertebrates. In addition, the focus of attention is often restricted to a few well-characterized Fox genes such as FoxA (forkhead), FoxC (crocodile) and FoxQ2. Although arthropods represent the largest and most diverse animal group, most other Fox genes have not been investigated in detail, not even in the arthropod model species *Drosophila melanogaster*. In our Fox gene screen, we identified a Fox gene with a highly-conserved expression pattern along the ventral ectoderm of arthropod and onychophoran limbs. Functional investigation of FoxB in the spider *Parasteatoda tepidariorum* reveals a hitherto unrecognized important function of FoxB upstream of wingless (wg) and decapentaplegic (dpp) in the gene regulatory network orchestrating dorsal-ventral limb patterning.



Main Meeting, FG Behavioural Biology
Poster: BEH 10

Chicken and quails as roommates: A rearing condition affects welfare and behaviour

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Animal welfare has become a huge question nowadays, especially in farm animals. To improve the welfare of animals one must consider its main aspects: the biological functioning, emotional states and natural behaviour of the animals. Considering the natural behaviour, it is helpful to compare the lifestyle of our domestic animals with their wild ancestors' lifestyle. Social interactions of wild animals are not restricted to conspecifics and predators. It might happen that the ancestor of the domestic chicken (*Gallus gallus domesticus*), which is the jungle fowl (*Gallus gallus*), got in contact with other Galliform bird species, like a wild quail (*Coturnix japonica*). Therefore, we considered to rear domestic broiler chickens and domestic layer quails together in two mixed groups (each group containing ten birds per species) for a social environmental enrichment, to create a more realistic natural scenario in a livestock setting. As controls we had two pure groups per species at similar stocking densities. Behavioural parameters related to welfare were expected to improve in mixed groups. In an open field test, we found that fear of quails as well as of chickens in the mixed groups was reduced compared to their conspecific counterparts in the respective pure groups (Quails, Mann-Whitney, $W=515.5$; $p=0.015$; Chickens, LME, $F_{1,56}=7.008$; $p=0.011$). Furthermore, a social interspecific preference test revealed a reduced discrimination between species for animals reared in mixed groups (LME, $F_{1,45.841}=4.72$, $p=0.035$). To conclude, social environmental enrichment seems to be a promising technique to enhance animal welfare in livestock animals.



Main Meeting, FG Morphology
Oral presentation

High-resolution 3D microscopy and the homology of genital organ components in spiders

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Many arachnids have evolved specialised genital organs in the male. Spiders for example have modified the pedipalp appendages to serve as an intromittent organ. The pedipalp tarsus bears the bulbus organ, which can take up the sperm that is discharged from the male genital opening, store it, and transfer it into the female during copulation. In the majority of spiders, the bulbus organ is a complex structure composed of several heavily sclerotised sclerites connected by less sclerotized cuticle (membranes, haematodochae). This complexity hampers the identification of homologous parts in different species and has led to conflicting homology hypotheses. We have studied bulbus organ morphology in the common house spider *Parasteatoda tepidariorum*, a member of the Theridiidae (cobweb spiders). Using histological sectioning and 3D reconstruction of data from serial bloc face electron microscopy and contrast-enhanced micro-CT, we document the interplay of membranes with the sclerites. Based on these data we argue that the sclerite previously identified as the conductor is actually the theridioid tegular apophysis, and that *P. tepidariorum* has a well-developed median apophysis, that however is intimately fused with the embolus sclerite.



Main Meeting, FG Neurobiology
Oral presentation

Specific features in the Neuropeptidome of the bumble bee, *Bombus terrestris*

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Neuropeptides are intercellular signaling molecules that are primarily produced by neurosecretory cells of the central nervous system and that regulate many physiological functions, including behavior, in animals. Recently, neuropeptide mimetics have been proposed as candidates for species-specific greener pesticides that target key physiological functions of pest insects without harming beneficial insects such as pollinators. In order to demonstrate the specificity of such peptide mimetics, we first search for lineage-specific features in the neuroendocrine systems of pest insects. At the same time, we need to overview the neuropeptides of the beneficial insects to avoid collateral damage when applying these mimetics. While profound knowledge exists for the honey bee *Apis mellifera*, the neuroendocrine system of bumble bees, which are likewise important natural pollinators, is poorly known. The aim of the present study is to close this gap by identifying neuropeptide genes, and the respective mature neuropeptides in the large earth bumblebee, *Bombus terrestris*. For that purpose, we have combined genomic information, immunohistochemistry and mass spectrometry experiments. In total, we identified around 50 neuropeptide genes and confirmed the processing of most predictable mature peptides and protein hormones. Apparently, bumble bee lacks several neuropeptide genes found in many other insects, making these genes good candidates for the development of peptidomimetics against pest insects. Another interesting feature in the bumble bee is the lack of the tryptopyrokinins which are present in the majority of insect capa genes. The results are compared to neuropeptidome data from *Apis mellifera* to find features common to both hymenopteran lineages.



Symposium: Form and function of motion systems: new approaches, new opportunities, new challenges; Keynote
Oral presentation

Skeletal mechanics and the evolution of function across major transitions in vertebrate evolution

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Methods such as tomographic imaging and computational biomechanics have enhanced the study of function in living and extinct animals. One such computational approach is finite element analysis (FEA), a method that reconstructs stress, strain and deformation in a structure experiencing simulated functional loads. Application of FEA follows the principle that the vertebrate skeleton is responsible for withstanding functional loading in the organism, and remodels in response to load. A signature of function should therefore be evident in the form of the skeleton. Using FEA and associated methods to reconstruct and estimate functional loads, I here present work from my lab quantifying the evolutionary mechanics of the vertebrate skull across major evolutionary transitions. I focus firstly on the evolution of mammals, and how the skull accommodates the shift in loading associated with the evolution of the mammalian jaw joint and the shift loss of postdentary bones into the middle ear. Then I focus on the evolution of the skull across the water to land transition. I explore how far can we use an understanding of extant cranial function to understand the functional consequences of cranial morphological evolution as vertebrates acquire limbs and digits and begin to diverge from aquatic habitats.



Main Meeting, FG Morphology
Oral presentation

The evolution of head morphology in ants: analysis of an understudied character complex

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With currently 13.555 valid species, ants are the largest clade of eusocial insects. They occur in almost all terrestrial habitats and play a crucial role in various ecosystems. With their enormous diversity in behavior, dietary specializations and morphology, they are a highly attractive subject in evolutionary biology and related disciplines. However, despite of numerous studies dedicated to the group, morphological research has been neglected to an astonishing degree. As organisms interact with their environment through their morphological structures, a detailed knowledge of the phenotype and its variations is crucial for understanding the phylogeny and evolution, but also important in a wider biological context, including functional morphology or behavior. In recent years, molecular studies yielded many insights into the phylogeny of Formicidae. However, since anatomical data are presently lacking for most clades, evolutionary interpretations are often very limited. In this project we will improve this situation by systematically producing detailed morphological documentations for carefully selected representatives of ants, starting with the head as the most complex body region. Combined with a robust phylogeny, this will allow a reliable reconstruction of the evolution on the phenotypic level. Preliminary results suggest important and previously undocumented differences of the endoskeleton, the foregut and its musculature, and glands across ant lineages. It is apparent that the observed features have functional implications in most cases. However, more work needs to be done to reconstruct evolutionary pathways in a broader phylogenetic context in Formicidae, including also stemgroup members of the family.



Main Meeting, FG Behavioural Biology
Oral presentation

Regulation of worker reproduction in *Camponotus maculatus*

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In eusocial hymenopterans, mutual control of worker reproduction (i.e. policing) is essential for the resolution of the queen-worker conflict over reproduction. Colonies of the formicine ant *Camponotus maculatus* are headed by a single reproducing queen and workers usually refrain from reproduction in presence of the queen. However, in the absence of a fertile queen workers start laying eggs and eventually produce males parthenogenetically. We studied factors that could potentially influence worker reproduction. For example, which caste – minors or majors – primarily lays eggs and how egg policing is influenced by the presence or absence of queen or worker laid eggs. Surprisingly we found in video assays that minors in the presence of majors lay eggs, although majors usually have a higher reproductive potential. Besides, queen-laid eggs had a higher survival probability than worker-laid eggs in isolated worker groups. Intensive worker-egg policing was observed shortly (24 hours) after worker separation from the queenright colony but was significantly reduced with each consecutive day of isolation. We also compared the cuticular hydrocarbon profile of *C. maculatus* queens and workers and queen and worker laid eggs, respectively. Thereby we found differences in queen and worker CHC profiles. Finally, we investigate whether worker ovary development is suppressed not only by the presence of a fertile queen, but also by contact with queen eggs. This study will help to understand the role of queen signals for conflict resolution in social insects by providing important insights into the regulation of worker reproduction in *C. maculatus*.



Main Meeting, FG Behavioural Biology
Poster: BEH 7

Fluffy feathers: the significance of neoptile feathers for camouflage

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Camouflage is a widespread strategy to evade predation and hence increase survival. The importance of camouflage for survival may change over different life stages. In birds, previous studies focused on egg and adult camouflage. In contrast, little attention has been paid to the importance of camouflage during the juvenile stage despite chicks experiencing high mortality and being vulnerable to predators. Many precocial chicks have a natal plumage that increases background matching and features elements of disruptive colouration. In this project, we will examine whether and how integumentary structures and appendages such as neoptile feathers contribute to body concealment in snowy plover chicks (*Charadrius nivosus*) by digitally manipulating and analysing photographs of one to three-day old chicks. Neoptile feathers are shed with fledging and are typically associated with thermoregulation. However, they also contribute to the outline of the chicks. We hypothesize that these contour feathers create a transition zone between chick and background with intermediate values for colour, luminance and pattern energy, making it harder to detect the outline of the chick against the background. Associating neoptile feathers with camouflage is a novel and untested concept in camouflage research. We will identify structural feather characteristics that maximize camouflage by varying number, thickness and transparency of digitally added artificial contour feathers fitted to random objects. This work will identify likely mechanisms how integumentary structures increase the camouflage of organisms and further our understanding about effective camouflage strategies in nature.



Main Meeting, FG Physiology
Oral presentation

Identification of ABC transporters involved in the elimination of diflubenzuron using *Tribolium castaneum* as a pest model

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The control of pest insect populations is largely reliant on insecticides. However, development of resistance to insecticidal agents challenges sustainability of pest control. Several studies have shown that ABC transporters contribute to insecticide resistance because they function as efflux pumps to facilitate elimination of insecticidal compounds.

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 more than 70 ABC genes, which group into eight subfamilies ABCA-H. Subfamilies ABCA-C and ABCG contain genes that encode multidrug resistance proteins suggested to be involved in insecticide resistance.

To gain a broader insight into the involvement of ABC transporters in insecticide resistance, we systematically analyzed the contribution of individual transporters of subfamilies A-C to the acquired tolerance towards diflubenzuron in *T. castaneum*, which is highly susceptible to this insecticide without adaption. We analyzed TcABC gene expression in different tissues of DFB sensitive and tolerant beetles. Additionally, we established competitive fluorescence-based elimination assays, silenced TcABC gene expression by RNAi and analyzed mortality. In this way, we identified several TcABCs that contribute to DFB resistance to more or less extent. We also demonstrated that ABC inhibitors can act as sensitizers to increase the efficiency of diflubenzuron in *T. castaneum*. In summary, we provide evidence that a set of different ABC transporters is involved in the elimination of diflubenzuron with TcABCC-5V contributing a major part to the transport capacity.



Main Meeting, FG Behavioural Biology
Poster: BEH 8

Adaptive shaping of the behavioral and neuroendocrine phenotype to the adolescent social niche in female guinea pigs

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For social animals, the environment is highly influenced by interactions among conspecifics. Stable group-living allows for communication via consistent behavioral cues among group members, often resulting in the generation and maintenance of individualized social niches. Early phases in life have been identified as sensitive phases for individuals to modify their phenotype to match their environment. However, it is not known to what extent individuals, especially females, can adjust their behavior to their social environment in adolescence and adulthood. Adolescence has recently been proposed as a sensitive phase for behavioral development. In adolescence, individuals can directly assess the social environment via interactions with conspecifics and modify their behavior, and there is a high fitness incentive for behavioral adjustment with the onset of the reproductive phase. Therefore, the social environment likely contributes to individualization of the behavioral phenotype during adolescence. Using guinea pigs as a model system, we investigated how dominance rank attained in adolescence shapes the development of the behavioral phenotype and the underlying neuroendocrine mechanisms in females. Furthermore, we manipulated the dominance rank in adulthood to determine whether reshaping is possible. Preliminary results indicate that the social environment plays a role in shaping the neuroendocrine profile; females that were subdominant in adolescence tended to have a stronger cortisol response to a challenge than dominant females. Further behavioral and neuroendocrine results are currently under analysis, and this project will contribute substantially to the question of whether individuals conform adaptively to their social environment during adolescence and adulthood.



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

Falling to pieces? – fragmentation, regeneration and sexual reproduction in the heteronemertean species *Lineus sanguineus* (Rathke, 1799)

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Many animal species are capable of regeneration of lost body parts. Regeneration of posterior body parts is fairly common, but the ability to regenerate a head is found in only few species. Within Nemertea (ribbon worms) several species independently gained the ability to regenerate a head. The cosmopolitan heteronemertean species *Lineus sanguineus* (Rathke, 1799) found in temperate waters has already been studied for more than 150 years for its spontaneous fragmentation and the remarkable regeneration capacity of entire individuals from the resulting very small body fragments. Formerly, *L. sanguineus* was divided into four separate species based on geographic distribution, but molecular analyses revealed that these belong to only one species. Its outstanding regenerative abilities are thought to provide the basis for asexual reproduction, which appears to be the dominant mode of reproduction in this species. So far, only anecdotal accounts of sexual reproduction exist and oogenesis is commonly regarded as abortive. However, current molecular data suggest sexual reproduction as catalyst for genetic exchange. From the results of regeneration studies, it can be assumed that sexual reproduction only takes place in winter months and asexual fragmentation occurs predominantly in summer. To gain further insight into asexual and sexual reproduction of *L. sanguineus* and their effect on genetic population structure, we investigated populations from different localities. In two of these (Norway, France) the reproductive behavior under different temperature and illumination regimes was studied. Our results underpin the occurrence of genetic exchange and of gametogenesis in at least some specimens at lower temperatures.



Symposium: Form and function of motion systems: new approaches, new opportunities, new challenges

Oral presentation

Three-dimensional deformation of the Achilles tendon insertion in mice: the enthesal fibrocartilage as a water cushion

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The insertion of the Achilles tendon to the Calcaneus transmits forces between soft and hard tissue. From an adaptationist perspective, the insertional tissues are expected to distribute stress homogeneously, in spite of the abrupt change in tissue elastic behavior. But it remains yet unclear, whether and how they achieve those properties.

The collagen fibers follow approximately straight courses along the tendon. Before they insert, the fibers curve over the posterior Calcaneus surface while passing through an unmineralized fibrocartilage. According to their curvature, they can exert pressure on the extrafibrillar matrix which is rich in water. Therefore the fibrocartilage is expected to lose volume under pressure. We compared the deformation of the proximal tendon and the distal fibrocartilage within three-dimensional images of relaxed and loaded Achilles tendon insertions from mice [*Mus musculus*, strain C57BL/6J, n = 3], acquired using synchrotron radiation-based micro-computed tomography with propagation-based phase-contrast. Forces were measured during the entire period of the experiment.

The tomographic images are the first to render the three-dimensional deformation of intact tendon insertions. The permanent stretch of the experiment leads to a relative volume loss of 20 % in the non-mineralized fibrocartilage, which is twice as high as in the tendon proper. The scans of the loaded insertions reveal that pressed out liquid accumulates in the retrocalcaneal bursa.

These findings contribute to the interpretation of the fibrocartilage as a poroelastic composite that inhibits water loss by its low permeability. Therefore, under dynamic loads the fibers could exert pressure on a “water cushion”.



Main Meeting, FG Morphology
Oral presentation

Tracking tendon fibers to their insertion

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At tendon insertions into bone, forces are transferred between tissues with extremely different mechanical behavior. Such transitions are prone to inhomogeneous distributions of stress which makes them potential weak spots. Therefore the presence of structural features leading to a homogenization of stress is hypothesized. We analysed data from phase-contrast micro-computed tomography with a template-based algorithm to track the fibers of the Achilles tendon in mice [*Mus musculus*, C57BL6J, n=3] on their way to the insertion. The fiber courses were analysed with regard to properties, that could contribute to a homogenization of stress: fiber branching and twist. Template-based fiber tracking results in plausible fiber courses. A moderately twisted course of the fibers within the tendon is found. Fiber branching occurs over the complete examined length of the tendon. Digitalization of the fiber courses is an important step toward three-dimensional mechanical models on the basis of structural information.



Main Meeting, FG Ecology Keynote Lectures
Oral presentation

Flickering lights below the ground: what molecules tell us about an invisible world

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Soil-living decomposers form an important link between the above- and belowground world because they feed on dead organic material, and at the same time make nutrients available for plants that were fixed in plant organic matter. They are therefore fundamental for ecosystem functioning and ecosystem services, but processes that structure decomposer communities or affect their functioning are not well understood. Understanding how historical climate changes, mass extinction events and evolutionary innovations above the ground affected the evolution of decomposers below the ground can shed light on these processes.

Oribatid mites (Oribatida, Acari) and springtails (Collembola, Hexapoda) are important and species rich decomposers in virtually any soil of extant ecosystems and their fossil record indicates that they formed part of the terrestrial soil system ever since the Early Devonian. However, due to their small size and diversity they are difficult to observe, culture and determine, but recent biochemical and genetic studies are uncovering the complexity of their trophic interactions and evolutionary history in the soil system.

I will explain why oribatid mites and springtails can shed light on the evolution of soils and the functioning of decomposer systems over geological time and show how molecular methods help us to identify processes that impact decomposer systems. I will discuss why we need to gain more detailed understanding of the actual diversity of decomposer communities and also highlight some of the problems and pitfalls faced when studying belowground diversity.



Main Meeting, FG Morphology
Poster: MOR 20

Three-dimensional forelimb kinematic analysis of *Tamandua tetradactyla* (Mammalia: Xenarthra) during walking, climbing, and balancing

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Tamanduas utilize a diverse set of locomotor behaviours. Being excellent climbers using an abducted forelimb posture, they also exhibit morphological adaptations to hook-and-pull-digging. As members of the Xenarthra, they belong to a sister-clade to all other eutherian mammals, which makes them intriguing study animals for research on adaptation and evolution in locomotion in mammals.

We used the marker-less X-ray of moving morphology (XROMM) method to visualize and quantify the three-dimensional movements of the scapula, humerus, ulna, and radius of two adult individuals. First, bi-planar high-speed X-ray videos were recorded during different locomotor behaviours: Walking on a level treadmill, climbing a vertical wooden pole, and balancing on a horizontal wooden pole. Surface models for each bone were created using museum collection material. After scaling these models to match the size of recorded tamanduas' bones, they were combined to form a digital hierarchical marionette following the marker-less XROMM workflow. The marionette was then oriented in such a way that the bone models matched the imaged bones in each X-ray video frame. The resulting key-frame animation allows to measure 6 degrees of freedom movements of the scapular fulcrum, the glenohumeral joint, the humeroulnar joint and the humeroradial joint. Based on this data for the first time the complex kinematics of tamanduas will be described and a joint movement's contributions to the overall movement will be quantified. The new data will be compared to other members of the Xenarthra in order to further characterize postcranial form and function of this branch of eutherian evolution.



Main Meeting, FG Neurobiology
Poster: NEU 1

Comparative study of auditory signal processing in insect neuronal networks

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In acoustically communicating bushcrickets (Tettigoniidae) different mate finding strategies are associated with morphological adaptations in their sound receiving hearing organs. To unravel specific adaptations to different calling systems we used anatomical and neuronal measurements (multichannel and extra-/intracellular recordings) and compared the auditory processing of intraspecific acoustic signals in a broadband singer (*Mecopoda elongata*, Tettigoniidae: Mecopodinae) and a narrowband singer (*Ancylecha fenestrata*, Tettigoniidae: Phaneropterinae). *M. elongata* use chorusing broadband signals to attract females, which perform phonotaxis. In *A. fenestrata* however, males fulfill the tasks of song production and phonotactic mate finding, while females (narrowband) answer occasional to the male's song. This combination of both tasks exposes *A. fenestrata* males to an increased risk to be spotted by predators and requires locating the female precisely just using sketchy acoustical cues.

We discovered a sex specific auditory fovea in the male's ear, an overrepresentation of the carrier frequency of the female call response at about 10 kHz, by an unusually high number of sensory units that encode the female call frequency. In contradiction to the steady-rising frequency distribution in *M. elongata*, this auditory fovea in *A. fenestrata* results in an increased neuronal input to the auditory path that influences the signal processing along the auditory pathway. Here, we compared neuronal signals at successively ascending levels in the auditory pathway in both sexes of *A. fenestrata* and *M. elongata*. With these datasets, we hope to answer the question whether more input to a central network leads to enhanced perception of specific acoustic cues.



Main Meeting, FG Ecology
Oral presentation

A rethink of ecological niches

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The concept of ecological niches has been extremely successful in the field of ecology and with the growing interest in inter-individual variation within populations, it is desirable to adopt the concept for the study of individualization. Niches have been treated in many conceptual papers with a number of different formal definitions, the most popular one being Hutchinson's ecological niche as the n -dimensional environmental hypervolume that allows a non-negative population growth rate. I here argue that none of the formal variants is very suitable for studying individualized niches. However, the concept of the niche has already been tweaked already to make it suitable for a number of different contexts and although most variants make reference to the n -dimensional environmental hypervolume, they are not always applying it according to the original definition. I think it is time to acknowledge these discrepancies and propose a modified concept of the niche that unites the fields of ecology and evolution and allows a study of individualization from a niche perspective.



Main Meeting, FG Physiology
Poster: PHY 3

Effect of Neuroglobin knockout to hypoxia tolerance in zebrafish (*Danio rerio*)

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The vertebrate globin family includes beside Hemoglobin (Hb) and Myoglobin (Mb), Neuroglobin (Ngb), Cytoglobin (Cygb), Androglobin (Adgb), Globin X (GbX), Globin Y (GbY) and Globin E (GbE). Globins are small respiratory iron-heme proteins that bind their ligands reversibly and occur in multicellular animals, fungi, plants and bacteria. There is still little known about the physiology role of some of the globins. This also stands for Ngb.

Ngb structure resembles that of a characteristic Mb. Ngb consists of 150 amino acids with a molecular mass of 16 kDA and constitutes a typical globin fold. Expression analysis in vertebrates reveals a conserved pattern mainly restricted to neuronal tissues. To date Ngb function is still debated. ROS and nitrosative stress protection is possible. Recent findings suggest a role in oxygen supply to neuronal cells. Moreover, in fish and diving mammals a neuroprotective role for Ngb is conceivable under low oxygen conditions.

Our Workgroup generated a Ngb knockout line in zebrafish with CRISPR/Cas9 technology. Since Ngb knockout may result in reduced oxygen supply and altered hypoxia tolerance, we will monitor developmental effects under normoxic and hypoxic conditions, e.g. delayed development and morphological defects, such as malformation of larvae. To assay physiological malfunction in Ngb knockout fish we will examine the hypoxia response on a molecular basis.



Main Meeting, FG Behaviour Keynote Lectures
Oral presentation

‘Sharkspeare’ & ‘Sharkira’ – Sharks may not write poems or songs, but they can still hit the right notes in many cognitive tasks

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While most people associate sharks with a whole bunch of sensational attributes, being clever is not usually one of them. Over the last ten years we have been assessing learning and memory functions in two elasmobranch representatives, i.e. the grey bamboo shark (*Chiloscyllium griseum*) and the ocellate river stingray (*Potamotrygon motoro*) on a behavioural and neuronal level. In two-alternative forced choice experiments we showed that sharks are cognitively on par with other vertebrates, mastering a wide range of tasks, including object recognition, categorization and perception of illusory contours. More recently, we conducted several studies assessing numerical abilities and serial reversal learning. Results of these studies indicate that small numbers below ten can be distinguished from one another if there is a minimum difference of two, i.e. 5:3 can be distinguished but not 5:4. Stingrays seem to perform better than sharks which may relate to different ecological needs. Conversely, sharks performed much better than stingrays, and even better than Malawi cichlids, in two serial reversal tasks, reducing the number of sessions needed to reach criterion with an increasing number of reversals down to the minimum of 3 and 1, respectively. While most of our experiments have used visual cues as stimuli, experiments over the last year have shown that bamboo sharks can also discriminate sounds. Hearing occurs most likely in the low frequency range; therefore, sounds between 30 Hz and 280 Hz were tested. In the process, a ‘Go/no Go’ method was for the first time successfully applied in an elasmobranch species.



Main Meeting, FG Behavioural Biology
Poster: BEH 17

Discrimination and generalisation of natural temporal patterns various behaviour context in the weakly electric fish *Mormyrus rume probosciostris*

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By discharging an electric organ, the weakly electric fish *Mormyrus rume probosciostris* emits brief electric organ discharges (EOD) of constant amplitude and waveform. Each EOD builds up an electric field around the fish, which the fish can sense with cutaneous electroreceptor organs. During 'active electrolocation', *M. rume* can thus detect and analyse nearby objects. During electro-communication, the EODs are perceived by conspecifics. By analysing EOD waveforms, the receiver can get 'identity information' of the sender, i.e., information about the species, the sex and the individual. EODs are emitted at a variable rate, i.e., the inter-discharge intervals (IDI) strongly fluctuate depending on the behavioural context. Previous experiments have shown that *M. rume* can be trained to discriminate between different temporal IDI-patterns recorded during different behaviours of the sender fish. Here we tested whether *M. rume* spontaneously classifies the behavioural contexts of a conspecific by perceiving the corresponding IDI-pattern. Alternatively, the fish might perceive similarities between IDI patterns based on statistical resemblance and not on behavioural type.

We trained four individuals of *M. rume* to select an IDI-pattern recorded from a conspecific during 'exploring' (S+) and to reject a 'resting' pattern (S-). When the fish have learned this discrimination, transfer tests are conducted during which 2 novel patterns are presented. Both the S+ and the S- patterns are varied systematically to deviate from the training conditions. First results indicate that fish prefer patterns that are similar to their S+ as long as the alternative pattern differs strongly enough.



Main Meeting, FG Ecology
Poster: ECO 10

A sensitive and quick assay of environmental effects on the vertebrate nervous system

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With the ever-growing multitude of substances that we release in our environment the need for thoroughly assessing their potential effects on humans and other animals calls for refined and quick assay systems.

Here we describe a system that quickly and automatically detects even minute environmental effects on a behavioral response of a well-established vertebrate model species. Our system is comparably cheap and simple to operate and accurately detects even small changes in the rapid escape starts of semi-fixed larvae of zebrafish (*Danio rerio*). The system delivers brief vibrational stimuli to elicit the escapes and uses an arrangement of photodiodes to automatically monitor latency and directionality of the subsequent rapid escape tail-bending. The system allows the practical use of an extremely sensitive assay that, otherwise would require expensive high-speed video and be too time-consuming to be of any practical use. Using a multiplexed version of the setup to simultaneously monitor several larvae we could quickly demonstrate the effects of several drugs and, perhaps most notably of 'insect-specific' insecticides on a vertebrate brain.



Main Meeting, FG Behavioural Biology
Poster: BEH 5

Is sensation affected by molting? Insights into an outstanding behavior using the model organism *Drosophila melanogaster*

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The life cycle of holometabolous insects is characterized by two remarkable features: metamorphosis and ecdysis. Whereas metamorphosis represents the total reorganization from larvae to winged adults, ecdysis is responsible for larvae growth by periodical shedding of the cuticle. The main molting hormone, 20-hydroxyecdysone, emerges from the pre-cursor molecule cholesterol, which has to be absorbed from the diet. For perceiving sensory stimuli from the environment *Drosophila* larva possess three main external gustatory and olfactory organs: the dorsal, terminal and ventral organ. These cuticular sensory organs are innervated by sensory receptor neurons that transmit information from the periphery and associated ganglia to the brain of the larvae. During ecdysis, the chitinous external organs and related anatomical structures e.g. the mouthparts, the pharynx and the foregut have to be shed and reorganized. To classify ecdysis related timepoints automatically during post-embryonal development of *Drosophila* larva, we have established a camera monitoring system. In addition, we want to investigate ecdysis sequence dependent differences in the innervation of cuticular sensory organs using high-resolution microscopy. Together with classical behavioural experiments on different diets, we aim to gain more insight and understanding for this remarkable behavior, which has contributed greatly to the enormous evolutionary success of insects.



Main Meeting, FG Physiology
Oral presentation

Optimal hematocrit theory under consideration of natural blood dopers and diving animals

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In humans and higher animals, a trade-off between sufficiently high erythrocyte concentrations to bind oxygen and sufficiently low blood viscosity to allow rapid blood flow has been achieved during evolution. Optimal hematocrit theory has been successful in predicting hematocrit values of about 0.4, in very good agreement with the normal values observed for humans and many animal species. However, according to those calculations, the optimal value should be independent of the mechanical load of the body. This is in contradiction to the exertional increase in hematocrit observed in some animals called natural blood dopers and to the illegal practice of blood boosting in high-performance sports. In this study, we calculate the optimal hematocrit under two different constraints – under a constant driving pressure and under constant cardiac power – and show that the optimal hematocrit in the latter case is higher than the normal value, ranging from 0.5 to 0.7. We use this result to explain the tendency to better exertional performance at an increased hematocrit. Finally, the increased hematocrit in endurance divers such as seals is explained on theoretical grounds.

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Symposium: Form and function of motion systems: new approaches, new opportunities, new challenges

Oral presentation

Chewing mechanisms change across metamorphosis in salamanders

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Food processing includes all types of mechanical reduction or preparation of food before swallowing. While at least two different mechanisms of intraoral food processing are known for metamorphosed salamanders, we lack data on processing behaviors in salamanders with larval morphology. As most salamanders metamorphose from a gill-bearing larva to a post-metamorphic stage, they undergo drastic changes in their craniovisceral region. In fact, a recent study revealed that prey capture kinematics show minor differences between larval and metamorphosed salamanders. It was hypothesized that larval salamanders cannot employ the same processing mechanism as metamorphosed animals based on morphological constraints. Salamandrid newts are ideal to test this hypothesis because they exhibit facultative paedomorphosis, where both paedomorphic (animals that skip metamorphosis) and metamorphic (animals that undergo metamorphosis) adults coexist in the same population. Accordingly, facultative paedomorphic salamanders allow direct comparison of form-function relationships in animals from the same population with very different morphology but within the same developmental stage (adults) and similar size. Here, we used high-speed videography and morphological approaches to analyse food processing in paedomorphic and metamorphic Alpine newts (*Ichthyosaura alpestris*). The results show that intraoral prey processing of the Alpine newts differs significantly between individuals with metamorphic and paedomorphic morphology. This suggests that changes in the morphology of the feeding apparatus during the ontogeny of salamanders affect one phase of the feeding event (i.e. processing), while other phases can remain largely unaffected (e.g. capture).



Main Meeting, Horst Wiehe Prize
Oral presentation

Reciprocity in Norway rats (*Rattus norvegicus*)

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If only those behaviours evolve that increase the actor's own survival and reproductive success, then it might come as a surprise that cooperative behaviours, i.e. providing benefits to others, are a widespread phenomenon. Many animals cooperate even with unrelated individuals in various contexts. One possibility to explain the evolution of such cooperative behaviour is reciprocity. Here, individuals help cooperative partners and exchange favours repeatedly. Reciprocity is a ubiquitous and important human trait, which we use daily. Still, the evolution of this behaviour is largely unclear, mainly because it is believed to be too cognitively demanding for other animals and to be limited to specific situations. In contrast to this, I propose that reciprocity is not necessarily cognitively demanding and likely to be widespread. In my talk, I will shed light on the mechanisms of reciprocity in Norway rats. In a series of studies, my colleagues and I have demonstrated that rats reciprocate help between and within different commodities and independent of kinship. They most likely form attitudes towards social partners that are based on the last encounter, which they remember over long time spans. Making decisions based on attitudes appears cognitively less complex than calculating values of received and given favours. Thus, reciprocity might be in fact more widespread in other non-human animals than commonly believed.



Main Meeting, FG Morphology
Oral presentation

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 biological and materials characterization techniques such as SEM, TEM, 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 (comprised of individual units arranged 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 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 Ecology
Poster: ECO 5

How to adapt to feeding on the main secondary metabolites of *Physalis* plants? Ask a specialist and a generalist species of Lepidoptera!

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Naturally occurring withanolides are secondary metabolites with promising biological activities *in vivo* and *in vitro*. The role of withanolide synthesis in plants is still conjectural though numerous studies strongly indicate a potent feeding deterrent effect against insect larvae and other herbivores. In contrast to the potential medical applications of withanolides, the ecological effects on herbivores have not been studied intensively. Our research focuses on the specialised adaptation of the noctuid moth *Heliothis subflexa* and the closely related generalist species *Heliothis virescens*. We recently demonstrated that *H. subflexa* larvae not only exploit their host plant *Physalis peruviana* as a food source, but also benefit from the striking immune modulating activity of the plant-based withanolides. These findings raise questions on the mechanisms by which *H. subflexa* overcame the inhibitory effects of these compounds. Withanolides form a group of C28 steroids built on an ergostane skeleton. The high reactivity of the unsaturated carbonyl system suggests an activation after ingestion in the insect gut by e.g. P450 enzymes, which are known to be involved in metabolite detoxification in other lepidopteran species. Preventing this activation in *H. subflexa* larvae might explain their apparent tolerance to withanolides. We here present the results of feeding assays in which both heliothine moth species were fed with defined amounts of purified withanolides that we performed to elucidate their potential metabolism or metabolic circumvention. Subsequent analysis of the faeces, gut and the rest body via LC-MS allows us to detect differences in withanolide metabolism between both species.



Main Meeting, FG Evolutionary Biology
Poster: EVO 3

Comparative analysis of genomic repeat content in grasshoppers reveals phylogenetic similarities as well as unexpected differences

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Eukaryotic organisms vary widely in genome size and a large part of this variation is explained by differences in the abundance of repetitive elements. However, the phylogenetic distribution and evolutionary turnover rates of repetitive elements are largely unknown. We therefore used de novo repeat identification based on low coverage whole-genome sequencing to characterize the repeatomes of six species of Gomphocerine grasshoppers, an insect clade characterised by unusually large as well as variable genome sizes. The genome sizes of these species ranged from 8.4 to 14.0 pg DNA per haploid genome and thus our study embraces the second largest insect genome documented so far. Estimated repeat content ranged from 79 to 96% and was strongly correlated with genome size. Most individuals showed a right-skewed distribution of repeat cluster abundances, indicative of many different elements being present at generally low frequencies, while the two grasshopper species with the largest genomes were dominated by a single cluster of satellite DNA. Overall, we found a strong phylogenetic signal in the grasshopper repeatomes, indicating that multiple repetitive element families may have expanded or contracted subsequent to lineage divergence. Overall, retrotransposons were unexpectedly scarce, whereas helitrons and satellite DNA were often highly abundant. We suggest that the expansion of satellite DNA might be secondary and possibly favoured by selection as a means to stabilise greatly expanded genomes.



Symposium: Form and function of motion systems: new approaches, new opportunities, new challenges

Oral presentation

Agility: limb stiffness in jumping dogs with different level of skill

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A considerable body of work has examined the dynamics of different dog gaits, but there are no studies that focused on limb dynamics in jumping. Jumping is an essential part of dog agility, a dog sport in which handlers direct their dogs through an obstacle course in a limited time. In agility dogs are categorized into grades depending on their success in competition, which was used to define beginner (low grade) and advanced dogs (highest grade). We hypothesized that limb parameters like limb length and stiffness indicate the skill level of dogs. We analyzed global limb parameters in jumping for 10 advanced and 10 beginner dogs. In experiments, we collected 3D kinematics and ground reaction forces during dog jumping at high forward speeds.

Results for limb stiffness indicate a pole-like mechanism with switching forelimb roles, in take-off to achieve jumping height and in landing to transfer vertical velocity into horizontal velocity. In skilled dogs, the forelimbs are stiffer than in beginner dogs. Beginner dogs exhibited more bent limb configuration, and larger limb compression during the stance phases. Due to the reduction of the mechanical advantage, more compliant (flexed) limbs are associated with a larger amount of eccentric muscle contraction which might be relevant to explain frequently occurring soft tissue injuries in the shoulder region in beginner dogs. Our results indicate that limb stiffness is a promising parameter for measuring training level in agility.



Main Meeting, FG Morphology
Poster: MOR 19

Functional ultrastructure of the posterior legs of *Lithobius forficatus* (Chilopoda: Lithobiomorpha) with emphasis on telopodal glands

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Centipedes display a broad diversity of solitary, aggregated, and compound epidermal glands enabling the animals to deter competitors, ectoparasites and potential predators, to kill harmful soil bacteria and fungi, to initiate and support mating, to provide components for egg production, or to assist cleaning activities. Aggregated defense glands may be present on the sternites of Geophilomorpha, called sternal glands, as well as on the inner face of the distal podomeres of the posteriormost legs (including the ultimate legs) in some Lithobiomorpha, called telopodal glands. Flanking our proteomic and transcriptomic analyses to reveal their biochemical properties, we explored the ultrastructural organization of the telopodal glands of the lithobiid *Lithobius forficatus* with the aim to explore potential structural disparities that may indicate differential secretion qualities. Using SEM and TEM techniques we detected that the telopodal glands consist of 4 cells, namely (1) a canal cell, (2) an intermediary cell forming a collar around the apices of (3) a small and granulated secretory cell (type-1 cell) and (4) an elongated, non-granulated secretory cell (type-2 cell) encasing a voluminous, tubular reservoir. There is no gland-associated musculature but many neurites, in part myelinated, that can be observed at the base of glandular epithelium thereby getting in close contact to the bottom of the type-2 secretory cells. The ultrastructure of closely aggregated telopodal glands closely resembles that described for sternal glands and venom glands.



Symposium: Form and function of motion systems: new approaches, new opportunities, new challenges

Oral presentation

A three-dimensional model of the dog's locomotor system

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The domestic dog is the only species with more than 300 breeds. This fact is reflected in a large variability of body sizes (e.g. chihuahua – great dane) and body types (e.g. sighthound – bulldog). Thus, the dog is a fascinating model system to investigate the connections between body structure and joint load during locomotion, as well as between joint load and degenerative diseases of the musculoskeletal system (e.g. dysplasia). Above all, we want to understand how body size, physique and agility as well as diseases affect the gait-related mechanics and control of the joints in dogs. To understand joint load, a simulation model was used for the evaluation of the internal and thus invisible power transmission. The model was checked for plausibility with the aid of external data. In addition, it is scalable to other dog breeds and can be adapted to partial questions.



Main Meeting, FG Evolutionary Biology
Poster: EVO 14

The role of transposable elements (TEs) in the evolution of odorant receptor (OR) genes in ants

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Transposable elements (TEs) are DNA sequences present in almost every eukaryotic species and have the ability to change their position within the genome. TEs can cause mutations, for example by transposition or by aberrant recombination (Kent et al. 2017), which in turn can cause gene duplications or the reshuffling of regulatory sequences (Klein and O'Neill, 2017). These TE mediated mutations can have phenotypic effects which have been shown to confer fitness advantages in some cases. Here, we study the role of TEs in the evolution of ant genomes, focusing on the dramatic diversification of the Odorant Receptor (OR) repertoires in this family of insects (McKenzie and Kronauer, 2018). For this we generated annotations of TEs and on average 439 OR genes per available ant genome for a comprehensive comparative analyses. Our findings suggest that TEs are important contributors to ant genome evolution. In particular, they contributed to the diversification of the OR gene family in the ants.

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Main Meeting, FG Neurobiology
Poster: NEU 4

Lifestyle matters: Brain morphology in cursorial and stationary hunting spiders

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The specific lifestyle of an animal is reflected in the structure of brain areas that process sensory information. Spiders (Araneae) include stationary species that build webs for prey capture and cursorial species that do not build webs. These distinct lifestyles are associated with major differences in sensory equipment. We investigated if brain morphology differs depending on lifestyle. To this aim, we analyzed the brains of four spider species: two cursorial hunters, *Marpissa muscosa* (Salticidae) and *Pardosa amentata* (Lycosidae), which strongly rely on visual cues, and two stationary web building hunters, *Argiope bruennichi* (Araneidae) and *Parasteatoda tepidariorum* (Theridiidae), which detect prey using vibrational cues. We predicted that the differences in primary sensory input between the different species are mirrored by differences in those brain areas that process the incoming information. By means of microCT analysis, paraffin histology and immunohistochemistry we show that the brains of the investigated species differ in number, arrangement, structure and volume of neuropils. These differences are especially pronounced in the visual system of the brain and pertain to first order, second order and higher order brain centers. While the investigated cursorial hunters have large visual neuropils and mushroom bodies, these are smaller or even absent in the investigated stationary hunters. Our results thus demonstrate that depending on the sensory specializations, profound differences in spider brain morphology exist.



Main Meeting, FG Developmental Biology
Oral presentation

Developmental and cellular insights into oogenesis in the sea anemone *Nematostella vectensis*

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The development and growth of oocytes (oogenesis) is a very resource-intensive developmental process, which is therefore tightly controlled by nutrient availability in most animals, including cnidarians. In contrast to hydrozoans (e.g. *Hydra*), where oocytes develop from pluripotent 'interstitial' stem cells (i-cells) and are nurtured by nurse cells, the developmental and cellular origin of oocytes and their yolk components are unknown in any non-hydrozoan cnidarian. We have therefore studied oogenesis and vitellogenesis in the sea anemone *Nematostella vectensis*, and have used a combination of candidate gene expression (e.g. *vasa*, *piwi*, vitellogenin), single-cell transcriptomics, nutrient and bead uptake assay, and transgenesis approaches. We have identified a potential *vasa*+/*piwi*+ oocyte stem or progenitor cell population outside the gonad of *Nematostella*. Transgenic lines have revealed their location, progeny and developmental potency in maturing juveniles and adults. Nutrient and bead uptake experiments have shown that specific gastrodermal regions of *Nematostella*, including vitellogenin-expressing somatic gonad cells, show high phagocytosis activity, high levels of vitellogenin transcripts, and high fatty acid and glucose uptake potentials, and could therefore contribute to yolk production. Altogether, we provide the first molecular and cellular insights into oogenesis, vitellogenesis, and the location of the underlying cell types, from any non-hydrozoan cnidarian. Our data also forms the basis for further characterizing the molecular control of oocyte determination, differentiation and/or growth under starving conditions in *Nematostella vectensis*.



Main Meeting, FG Morphology
Oral presentation

Functional morphology of the middle ear of *Homo* and *Pan*

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Comparing hearing capacities of humans and chimpanzees reveals distinct differences with humans possessing a number of derived auditory characteristics. The functional basis for these differences is not yet understood but morphological differences in the ear region of humans and chimpanzees exist. Our aim was thus to experimentally study the functional morphology of the outer and middle ear of non-human apes for the first time by measuring the middle ear transfer function (METF) on cadavers of common chimpanzees, bonobos and humans. We recorded stapes footplate vibrations using Laser-Doppler-Vibrometry after gaining access to the tympanic cavity. Middle ears were excited acoustically through the external ear canal (EAC) and the investigated frequency bandwidth ranged between 0.1 and 10 kHz. In the low frequencies, the magnitude of the METF of *Pan* is greater compared to that of humans. This likely relates to a lower stiffness of the larger eardrum of *Pan*. Humans and *Pan* show a decrease in magnitude of the METF after 1 kHz. While the METF in humans continuously decreases until the end of the measuring range, it slopes upwards around 4-5 kHz in *Pan* progressing above the human curve. However, after adding the simulated pressure gain of the EAC, the magnitude of the human METF increases around 4 kHz which is also seen as a characteristic of the human mid-frequency hearing range. Our experiments indicate that auditory capacities of *Homo* and *Pan* are related to morphology, opening up new avenues for studying the evolution of hearing in fossil hominins.



Main Meeting, FG Ecology
Poster: ECO 6

Using microscopic tooth wear to infer biotic and abiotic factors in western chimpanzees (*Pan troglodytes verus*) feeding ecology

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Microscopic tooth wear studies have been used to reveal dietary proclivities related to variations in biotic and abiotic factors in primates. While the focus has been primarily on comparisons between species, little is known to what extent biotic (e.g. sex- or age-related dietary proclivities) and abiotic (e.g. periodical dust accumulation) factors are reflected in microscopic tooth wear patterns within one population, as this can provide insights into social structure, life history changes or habitat use.

Here we investigate the 3D surface texture (3DST) on upper and lower molars of 41 western chimpanzees from the Taï National Park (Ivory Coast) and relate them to dietary and environmental data previously collected for this population. We then employ 3DST analysis to a sample of 47 western chimpanzee molars from neighboring NE Liberia where no ecological data are available.

We find in the Taï sample both sex- and seasonal-specific 3DST signatures, while age-related dietary shifts are less obvious. While 3DST does not distinguished well between sex and age in the Liberia sample, the signatures are overall similar to those of Taï individuals that died during the dry (dusty) period.

Our results indicate that intra-population biotic factors are reflected in 3DST but caution against using the same 3DSTs to infer diet from different populations. However, our findings suggest that seasonality (dry vs. wet periods) is well reflected in 3DSTs, regardless of dietary differences. Our approach therefore bears the great potential for using microscopic tooth wear analysis in reconstructing the (paleo)-ecology of living and fossil primates.



Main Meeting, FG Behavioural Biology
Poster: BEH 1

How novel is new? Revisiting the novel object paradigm

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Consistent individual differences in behavioural phenotypes have been the subject of intense research for the last few decades. Such individual differences are variously called animal personalities or temperament, since the goal is to study general responses to environmental challenges, such as individual-differences in risk-taking, exploration and novelty-seeking. Temperament traits are typically measured through standardized testing paradigms and one frequently used paradigm is the novel object test. In novel object tests, animals are exposed to new objects and their reaction is quantified in terms of approach latency, distance, arousal or activity. However, demonstrating individual consistency requires multiple testing sessions. Researchers therefore face the dilemma of using the same or different 'novel' objects in repeated trials. Repeated exposure of an individual to the same stimulus can result in habituation, while exposure to different objects can result in different responses – both processes may result in an underestimation of individual consistency. In the absence of detailed knowledge about animal memory and cognition, it is also difficult to judge when a time interval between trials is long enough, so that individuals respond to the same object as if it was entirely novel. We performed a quantitative assessment of published data on novel-object trials to evaluate the properties of this testing paradigm. We will present a formal meta-analysis that assess the importance of genuine novelty and time gap in novel-object trials.



Main Meeting, FG Morphology
Oral presentation

Experimental taphonomy of cyclostome muscle tissue and the implications for the agnathan fossil record

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Cyclostomes have a spotty fossil record due to their lack of ossified structures and low preservation potential. The loss of morphological information during the decay of the carcass, before fossilisation, can have a significant impact upon interpretations of fossils. Understanding this process is critical, currently attempted through experimental decay studies. Here, we present unpublished fossils whose muscle tissue was preserved in phosphate, thus retaining its original shape and position. To better inform on the succession of structural decay taphonomy experiments were carried out on extant river lampreys (*Lampetra fluviatilis*) obtained in the field. Samples of these lampreys were decayed in two experiment set-ups (open with O₂ contact, and anoxic) in accelerated conditions at 24°C for 14 days. Subsequently the samples were critically point dried and analysed with X-ray tomography at the SLS Synchrotron near Zurich. The structure of the myomeres and respective patterns of decay were the focus of the analysis. The results show that samples of both set-ups follow approximately the same patterns of decay. The rate of disarticulation depends on the type of muscle fibre and position in the body. Myoseptal tendons attached to the notochord demonstrated the highest resistance to disarticulation and represent the only muscle element still articulated in later decay samples. They are also the most distinguishable soft tissue element preserved in the fossils. While results from decay experiments cannot directly inform on patterns of information loss in fossils, we can still observe correlations between some structures demonstrating decay resistance and their potential for preservation.



Main Meeting, FG Developmental Biology
Oral presentation

Temperature and insulin signaling regulate body size in *Hydra* by the Wnt/TGF- β pathway

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How multicellular organisms assess and control their size is a fundamental question in biology, yet the molecular and genetic mechanisms that control organ or organism size remain largely unsolved. The freshwater polyp *Hydra* demonstrates a high capacity to adapt its body size to different surrounding temperatures. Here we identify the molecular mechanisms controlling this phenotypic plasticity and show that temperature-induced cell number changes are controlled by Wnt- and TGF- β signaling. Further we show that insulin-like peptide receptor (INSR) and forkhead box protein O (FoxO) are important genetic drivers of size determination controlling the same developmental regulators. Thus, environmental and genetic factors directly affect developmental mechanisms in which cell number is the strongest determinant of body size. These findings identify the basic mechanisms on how size is regulated on an organismic level and how phenotypic plasticity is integrated into conserved developmental pathways, all in an evolutionary informative model organism.



Main Meeting, FG Developmental Biology
Poster: DEV 8

Neuropeptide processing in arthropods: non-redundant functions of PC1/3 and PC2 in the beetle *Tribolium castaneum*

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Insect neuropeptide signalling helps maintaining the physiological balance and is required for many aspects of behaviour, reproduction and development. Internal cleavage of neuropeptide precursors is catalysed by prohormone convertases (PCs). In vertebrate models PC1/3 and PC2 are active in the neurosecretory pathway, both of which are conserved in most insects. Notably, the fruit fly as the main insect model has only retained PC2, therefore we are investigating the function of separate orthologues in the beetle *Tribolium* as an alternative model for insect molecular biology.

We find that PC2 is abundantly expressed in cells of the larval nervous system whereas PC1/3 is restricted to few identifiable cells of the posterior brain and the suboesophageal ganglion. Pupal RNAi-knockdown of both genes leads to reduced viability and infertility of the injected females, caused by a failure of proper oocyte maturation and of the egg-laying process. Larval RNAi is lethal in case of PC2 whereas knockdown of PC1/3 slows down growth and leads to supernumerary moults. Our findings show that both factors act in parallel but have non-redundant functions. To understand the principles of combinatorial processing we are exploring ways to identify neuropeptide targets of PC1/3 and PC2 by peptidomics analysis. We are aiming to pin down the observed phenotypes to specific secreted peptides and by this means to understand how both enzymes exert their biological functions. We suggest that maintaining both orthologues confers greater evolutionary adaptability to an insect lineage than relying on a single gene for the internal cleavage of peptide precursors.



Main Meeting, FG Morphology
Poster: MOR 11

The osteology of *Liza aurata* (Teleostei: Mugiliformes) – A basis for a phylogenetic evaluation of grey mullets

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The Mugiliformes are a worldwide distributed taxon of extremely uniform fish. Some of the 79 species that are currently distinguished are important for fisheries and aquaculture all over the world. But, due to their similar external morphologies the identification of the species is quite troublesome. Furthermore, phylogenetic analysis of the relationships within the grey mullets based on these characters are even more difficult to conduct. However, in the past many studies focused on the external features of the grey mullets and only a handful took a closer look at their internal skeletal morphology. That is why phylogenetic comparisons to other taxa were limited to certain character complexes, e.g. the branchial arches or the pelvic girdle. And even though an osteology of another species of the grey mullets is available, no phylogenetic analyses with the therein presented data were conducted. These phylogenetic analyses based on the internal as well as the external morphology of the Mugiliformes, however, seem to be necessary: although the phylogenetic position of the grey mullets was limited to the taxon Ovalentaria within the tree of fishes using a broad genetic approach, the exact relationships to the other taxa in this group are still unknown. A morphological analysis can provide additional data to help resolve these phylogenetic relationships. The osteology of *Liza aurata* will be a basis for such a study. It will help reconstruct the grundplan of the Mugiliformes which then can be the starting point for a broader morphological analysis.



Main Meeting, FG Behavioural Biology
Oral presentation

Sex, snacks, sibs – and their impact on mound building in a cichlid fish: The evolution of an extended phenotype

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Animals often construct and shape their environment. In many fishes, parents provide a safe environment by intensively caring for the young and / or spawning in protected areas as nests or caves, which they oftentimes greatly modify or construct themselves. Such “extra-bodily” traits can be conceptualized as extended phenotypes. *Pelvicachromis taeniatus* is a West African cichlid fish that breeds in caves and shows intense biparental care. This species shows kin mating preference, which seems to be adaptive because, among other reasons, related parents provide better brood care. Commonly, male cave owners build small mounds out of substrate, e.g. sand, in front of the cave hindering competitors or egg predators from entering. Here, first we examined the impact of food availability and presence of females on mound building activity of males. Second, we investigated whether male-female genetic relatedness of a breeding pair affects mound height or building activity. Our results indicate that genetic relatedness positively affected building activity resulting in higher mounds in related pairs. This confirms previous findings that relatives perform better and are more cooperative during reproduction probably due to kin selection. Furthermore, our studies reveal that male mound construction is costly as it was condition dependent and sensitive to environmental variation (food availability or presence of females). In conclusion, mounds may function as extended phenotype honestly signaling male quality.



Main Meeting, FG Physiology
Poster: PHY 4

Analysis of ABC subfamily G transporters from the red flour beetle, *Tribolium castaneum*

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ATP-binding cassette (ABC) transporters are integral membrane proteins that mediate ATP-dependent translocation of a wide range of substrates across cellular membranes. In insects, they have been implicated in pesticide tolerance. The genome of the well-described model beetle and pest *Tribolium castaneum* contains more than 70 TcABC genes, which group into the eight known insect subfamilies ABCA-H. Next to subfamilies ABCA-C, also subfamily ABCG contains genes that encode multidrug resistance proteins that have been suggested to be involved in insecticide resistance in few cases. The aim of this study is to identify TcABCG transporters that might contribute to diflubenzuron resistance in *T. castaneum*. For this purpose, we determined the expression profiles of all 14 TcABCG genes in different tissues and at different developmental stages. We found that some TcABCG genes exhibited high transcript levels in the fat body. Then we analyzed transcript levels in response to diflubenzuron treatment and could identify two genes, TcABCG-4F and TcABCG-4G, which were particularly upregulated in response to diflubenzuron treatment. The next step is to identify the TcABCG transporters that are potentially involved in diflubenzuron elimination by RNA interference injecting dsRNAs to silence gene expression. In summary, we provide first evidence that TcABCG transporters contribute to the elimination of diflubenzuron.



Main Meeting, FG Evolutionary Biology
Oral presentation

Finding a Ruff wingman: modelling male-male cooperation under strong sexual selection

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A core element of sexual selection theory is male-male competition. In some systems, strong competition for females compels certain males into fragile alliances to outcompete others. Sexual selection can also lead to alternative reproductive tactics among males, resulting in divergent behavioural and morphological phenotypes. Lekking Ruffs (*Philomachus pugnax*), combine male-male cooperation with alternative reproductive tactics in two displaying male morphs: Independents and Satellites. Independents are aggressive lekking males that defend territories against other Independents. The dominance hierarchy among Independents determines their reproductive success. Satellites are non-aggressive co-displaying males that are able to sneak copulations, as females seemingly prefer mating on the territories of Independents that have a Satellite associate. These co-displaying alliances are often labile: Satellites may swap allies among or across leks, while Independents may reject Satellite competitors. Variation in mating success among lekking Independents may determine their willingness to co-display with Satellites although the presence of cooperation partner benefits and their magnitude is unclear. We developed a mathematical model to find mutually beneficial Independent-Satellite pairings. Based on published data from natural leks, we parameterized the model. Currently, it is unknown how Satellites change the copulation distribution on leks; therefore, we investigated four hypothetical scenarios of how Satellites change the lek copulation distribution. Two scenarios yielded realistic Satellite copulation estimates and mutually beneficial co-displays. Our model provides clear and testable predictions when and how male-male cooperation arises as an alternative reproductive tactic.



Main Meeting, FG Ecology
Oral presentation

Natural vs anthropogenic barriers to butterfly dispersal – insights from landscape genetics

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The population genetic structure of a species reflects the way individuals within populations are affected by physical attributes of the environment. Barriers to dispersal may well affect genetic structure by reducing or preventing gene flow. Gene flow may be hampered by natural (e.g. rivers, forests, mountains) or anthropogenic (e.g. settlements, roads) barriers. Fine-scale landscape genetics can provide a way of examining the importance of these factors. Here, we investigate the genetic structure of the Sooty Copper (*Lycaena tityrus*) in an alpine environment. We sampled 171 individuals in the Ötz valley system, Austria, and additionally 15 individuals in five outgroups. Genetic structure was assessed by double digest restriction-site associated DNA sequencing (ddRADseq), yielding 12,806 single nucleotide polymorphisms (SNPs). We show surprisingly weak genetic structuring in this putatively sedentary species. However, ravines caused genetic differences among sub-populations, and more surprisingly, roads had more effect on genetic differences than rivers. We conclude that the Sooty Copper is not only threatened by agricultural intensification, but also by habitat fragmentation caused by roads.



Main Meeting, FG Evolutionary Biology
Oral presentation

Rapid but narrow - Adaptation of *Drosophila* to toxic mould

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The ubiquitous encounters between animals and microbes has led to adaptations through (co-)evolutionary processes. The highly diverse taxa of insects have adapted to such encounters, including the presence of xenobiotic noxious substances produced by harmful environmental microorganisms. Microorganisms employ these noxious chemicals in a chemical warfare against predators and competitors. In particular on ephemeral resources, such as decaying fruits, severe forms of this interference competition can be observed, driving co-evolutionary adaptations.

We conducted experimental evolution with the highly adaptable saprophagous insect *Drosophila melanogaster* in order to analyse whether one single, maybe dominant, feature of an environmental microbe is the driving force of evolutionary adaptation in the insect. For this we selected *D. melanogaster* populations through repeated larval development on a toxin-producing mould that infests the breeding substrate. To disentangle the different aspects of mould infestation we used four selection regimes, which enable us to separate the toxic component from other mould characteristics. We further combined our selection experiment with transcriptome analysis to identify shifts in gene expression due to the selection regimes and mould confrontation.

Populations that repeatedly developed in presence of the toxin-producing mould or the pure mycotoxin rapidly adapted to breeding conditions and showed higher viability in subsequent confrontations. Yet, populations that were selected for tolerance to the isolated mycotoxin had no advantage in toxic mould confrontation. Moreover, distinctive changes in gene expression patterns were only related to the selection-regime including the toxin-producing fungus. Thus, it is the complexity of the selection agent that leads to complex adaptations.



Main Meeting, FG Developmental Biology
Poster: DEV 5

Gene regulatory networks of sense organ development: Level of conservation and basis for diversification?

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Perception of environmental stimuli through sensory systems is crucial for the survival of any organism. The diversity of sensory organs is in no way inferior to the great morphological diversity present in the animal kingdom. Over the last decades, the morphology, cellular architecture and developmental origin of various arthropod sense organs was intensively studied. The genetic basis of sensory organ development, especially detailed gene regulatory networks (GRNs) and their evolution, are less well understood. Within the arthropods many sensory modalities are perceived through diverse cuticular external sensilla innervated by neurons.

In *D. melanogaster* it is known that such sensilla develop from epithelial cells, where proneural cell clusters are determined by the expression of proneural genes. Lateral Inhibition via the Notch signaling pathway refines the differentiation into sensory organ precursors (SOP). The fate of the SOP is further influenced by, so-called SOP identity genes.

I will study the level of GRN conservation and where alterations in the GRNs occur during development leading to the diversification of external arthropod sensory organs following Macro and Micro-Evo-Devo approaches. Using comparative candidate gene expression and functional studies in the spider *Parasteatoda tepidariorum* I will identify the level of conservation across arthropods. To reveal detailed changes in the GRNs I will investigate the development of diversified bristle patterns on the ovipositor of closely related *Drosophila* species.



Main Meeting, FG Evolutionary Biology
Oral presentation

Wolbachia*-Induced Cytoplasmic Incompatibility in *Cardiocondyla obscurior

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Microbial symbionts have shaped the evolution and diversity of multicellular species. Their symbiotic nature can range from being beneficial (mutualistic), detrimental (parasites/pathogen) or near-neutral (commensal). Many ant taxa are infected with *Wolbachia*, a common manipulator of reproductive systems in other insects (via feminization, parthenogenesis, cytoplasmic incompatibility or male killing), but their role in ant evolution is unclear. We are interested in analyzing *Wolbachia*-ant interactions in more detail. As a model, we use *Cardiocondyla obscurior* populations from Brazil and Japan/Taiwan which are infected with two different *Wolbachia* strains. We are especially interested in understanding unidirectional hybrid breakdown resulting from allopatric crosses, where only crosses of queens from Brazil with males from Japan failed to produce viable brood while the reciprocal crosses show no fitness loss. Using antibiotic (Rifampicin) treatment to selectively reduce the *Wolbachia* level in experimental colonies we show that this is a result of cytoplasmic incompatibility, which can occur when an infected male is crossed to a non-infected female, or to a female with another *Wolbachia* strain as in our example. Our results indicate the presence of a parasitic *Wolbachia* strain in the Asian lineages of *C. obscurior* and a more neutral *Wolbachia* strain in the Brazilian population.



Main Meeting, FG Evolutionary Biology
Oral presentation

Evolution in action: Adaptation of the sexual communication system in an invasive moth species

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The noctuid moth *Spodoptera frugiperda* (Sf), which is native to North and South America, has invaded the African continent in 2016. The species consists of two genetically different strains, the corn-strain and rice-strain, which differ amongst other factors in their sexual communication. As Africa is a novel environment for Sf, where eight other *Spodoptera* species occur that partially overlap in their pheromone composition with Sf, communication interference could influence the sexual behavior of the invasive species. To test whether strain-specific and/or geographic variation exists, we investigated the sexual communication system of populations from West Africa (Benin and Nigeria) by using a combination of genetic, chemical, electrophysiological, and behavioral observation methods. We found that African populations (consisting of corn-strain and rice-corn-hybrid descendants) exhibited no strain-specific variation in their sexual communication, i.e. both genotypes have the same pheromone profile, EAG responses, and onset time of mating. However, we found geographic variation in the pheromone composition and the electroantennogram response between African and American populations. The sex pheromone of African corn-strain females was similar to American rice-strain females and exhibited higher percentages of the male attracting minor component (Z)-7-dodecenyl acetate (Z7-12:Ac). In addition, African Sf males exhibited the highest antennal sensitivity towards Z7-12:Ac, while American males showed highest sensitivity towards the major pheromone component. These results suggest that the invasive African Sf population adapted its sexual communication system by increasing the production of and sensitivity to the minor pheromone component Z7-12:Ac in order to avoid communication interference with local species.



Main Meeting, FG Evolutionary Biology
Poster: EVO 1

Fiber-type distribution in the shoulder muscles of hominoids: implications for a link between muscle architectural parameters and locomotor modes

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The superfamily Hominoidea comprises large-bodied orthograde primates, including humans and non-human apes. Non-human apes rely heavily on various forms of forelimb-dominated arboreal locomotion. In contrast, the human forelimb lost its function in body support and propulsion as bipedalism evolved. The high diversity of locomotor behaviour reflects species-specific adaptations that evolved to navigate specific environments. Such adaptations have altered the musculoskeletal system in each hominoid species.

Skeletal muscles contain two overarching muscle fiber types – type I and type II fibers. They display different contractile properties, including maximum velocity and time to fatigue and thus determine the muscle function. Muscles containing high amounts of type I fibers are thought to mainly adopt postural roles while muscles with high amounts of type II fibers serve for fast, propulsive movement (Sickles and Pinkstaff (1981) *American Journal of Anatomy*, 160.2, 187).

In this study, we investigate differences in fiber type distribution in the shoulder muscles of hominoids. We relate these differences to locomotion and evolutionary ecology. Specifically, we test the expectation that the non-postural function of the human forelimb will be reflected by a reduction in the proportion of type I fibers, compared to non-human apes.

Muscle tissue samples were collected from a gorilla, chimpanzee, bonobo and orangutan. Immunohistochemistry was used together with DAB and fluorescent staining to detect the overall amount and distribution of fast-twitch type II fibers. We compared our results to previously published data on human shoulder muscles.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral presentation

Ultraconserved elements help to resolve evolutionary relationships across several time scales in the honey ant genus *Myrmecocystus*

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Ultraconserved elements (UCEs) have been successfully used as molecular markers in multiple phylogenomic studies across a diverse range of taxa. UCEs were shown to give higher node support and more resolution in phylogenetic analyses compared to traditional multi-locus Sanger Sequencing (Blaimer et al. 2015). The identification of more than 2500 UCEs in the Hymenoptera and the design of corresponding RNA baits (Faircloth et al. 2015, Branstetter et al. 2017) now enables comprehensive phylogenomic analyses in the Hymenoptera including the Formicidae with high confidence.

We present results from several phylogenetic studies that leveraged UCE sequences to examine relationships within the New World honey ant genus *Myrmecocystus*. We reconstructed a well-supported genus-level tree that is largely congruent with a previous mtDNA analysis, which supports the subgeneric organization proposed by Snelling (1976) while calls into question the validity of some species groups. On the other hand, a comprehensive analysis of *M. mendax* populations combining UCE and mtDNA data revealed unexpected genetic diversity, and together with morphological data suggests incipient divergence. Overall, our findings illustrate the strength of UCEs in resolving evolutionary relationships across taxonomic levels, and highlight undescribed diversity in a honey ant species inhabiting a highly biodiverse region of the American Southwest.



Main Meeting, FG Ecology
Oral presentation

Can parasitoids shift the outcome in an antagonistic nursery pollination system? An ecological detective story

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Nursery pollination systems are species interactions where pollinators are parasitic on their plant-partner. While the plants depend on associated insects for pollination, the insects do so on the plants' fruits and structures for larval development. These interactions vary in their outcome from highly specialised and truly mutualistic to antagonistic. Where exactly these interactions may be placed along the gradient between mutualism and antagonism may depend on the complex ecological context, where third parties – such as co-pollinators, exploiters, predators or parasites – can play an important role. We used *Hadena bicruris* (Noctuidae), and its host plant *Silene latifolia* (Caryophyllaceae) as model system. We analysed if and how parasitism of a pollinator/seed predator by a natural enemy may increase individual plant fitness and shift the outcome of the interaction. In a series of experiments, we analysed the change in seed predation with and without parasitoids and how this can be translated into plant fitness taking seed germination and plant competition into account.



Main Meeting, FG Ecology
Oral presentation

Acoustic ecology and host specificity of frog-biting midges (Diptera: Corethrellidae)

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Phonotactically foraging female frog-biting midges (*Corethrella* spp.) use male anuran advertisement calls to locate their blood hosts. It is likely that acoustic preferences in *Corethrella* have evolved in close correspondence to local host communities, however, we still know very little about the exact parameters favoring selection for certain host species and/or call variants. At our primary study site in lowland Pacific Costa Rica, we investigated mechanisms of host choice and levels of specificity among the frog-biting midge community, integrating catch data from acoustic traps and feeding midges collected directly from frog hosts. We found that the midges use rather generalist acoustic templates to detect suitable blood hosts. Being based on elementary spectral and temporal call parameters, these templates only allow for low levels of acoustic niche differentiation, whereas observed higher levels of host specificity are likely to be based on a multimodal perception of additional (non-acoustic) cues, in the close range. We discuss the influence of frog host communities and potential key host species on (acoustic) host partitioning in *Corethrella*, and its role in the evolution of anuran communication networks.



Main Meeting, FG Behavioural Biology
Poster: BEH 6

Does inbreeding affect shoaling in juveniles of the West African cichlid *Pelvicachromis taeniatus*?

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Shoaling is wide spread in fishes. Environmental factors (e.g. temperature, light or predation), but also physical traits of the shoal members (e.g. body size) and their familiarity or genetic relatedness have been shown to influence shoaling performance or individual shoaling preference. Inbreeding increases the genetic relatedness within sibling shoals, potentially facilitating cooperation among shoal members due to kin selection, but it could also increase the risk of inbreeding depression (worse performance of inbred shoals). Whether inbreeding affects shoaling behavior is unknown. The biparental West African cichlid *Pelvicachromis taeniatus* prefers kin over non-kin as mating partners which seems to be adaptive because of inclusive fitness benefits and better brood care of related parents. Deleterious effects of inbreeding regarding juvenile growth or mortality have not been observed in this species. After juvenile *P. taeniatus* have left their parents, they form loose shoals. Here, we address the question whether inbreeding affects the shoaling behavior of juvenile *P. taeniatus*. Using a computer-based tracking software, allowing automatic identification of unmarked individuals, we tracked shoals consisting of in- or outbred full-siblings and analyzed their shoaling behavior (time swimming, distance travelled, synchronicity and average speed, shoal density). Furthermore, we compared the reaction to a tactical disturbance cue between in- and outbred shoals. We aim to elucidate potential kin selected benefits and cost of inbreeding, i.e. inbreeding depression, on grouping behavior. Our results will contribute to a better understanding of the consequences of inbreeding on social evolution.



Main Meeting, FG Neurobiology
Poster: NEU 5

Reproductive status-dependent gene expression of the neuropeptides dynorphin and neurokinin B in the brain of 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 neuropeptides, neurokinin B (NKB) and the endogenous opioid peptide dynorphin A (Dyn) are strongly implicated in the control of GnRH release with opposing effects. They colocalize together with the neuropeptide kisspeptin in the arcuate nucleus (ARC) of the hypothalamus. This neuron population is thought to constitute the GnRH pulse generator whereby NKB appears to have activating and Dyn to have inhibiting function on GnRH release. To assess whether these neuropeptides are involved in the mechanism of reproductive suppression we investigated the gene expression of Dyn and NKB by means of in situ hybridisation in wild-caught females with different reproductive status. We found distinct expression patterns of Dyn and NKB in several areas of the telencephalon and diencephalon with both genes being expressed in the middle and caudal part of the ARC. Quantitative analysis of gene expression within this nucleus revealed significant differences in relation to reproductive phenotype. Breeding females had increased gene expression of NKB and decreased gene expression of Dyn compared to nonbreeders. These data agree with the proposed model of GnRH pulse generation and suggest that, similar to other mammals, this ARC neuron population is responsible for generating the pulsatile release of GnRH in Damaraland mole-rats.



Main Meeting, FG Morphology
Poster: MOR 14

Ultrastructure of the pigmented eye in the larva of *Carinina ochracea* (Palaeonemertea, Nemertea) reveals a novel, potentially mixed type of photoreceptor cell

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Since the times of Darwin, the evolution of eyes has fascinated evolutionary biologists. After the strict definition, pigmented eyes consist of minimally two cell types: the shading-pigment cell (SPC) and photoreceptor cell (PRC). Two types of PRCs are distinguished among metazoans based on the nature of elaboration of the cell-membrane housing the photoreceptive pigments (opsins). The membrane is either elaborated by microvilli-projections (rhabdomeric, r-PRC) or by projections of the ciliary membrane (ciliary, c-PRC). As a rule, c-PRCs are found in pigmented eyes of Deuterostomia, while Protostomia (Ecdysozoa and Spiralia) possess pigmented eyes with r-PRCs. This is also the case in Nemertea (ribbon worms), a spiralian clade comprising approximately 1,300 worm-shaped species. However, in pelagic larval stages of Spiralia, this rule is occasionally violated: In some clades, such as Brachiopoda, Entoprocta, Gastropoda, and Nemertea, pigmented larval eyes (larval ocelli) with c-PRCs have been reported. To complement the data on PRC-types in Nemertea, we investigated the larval ocellus of *Carinina ochracea* (Palaeonemertea, Nemertea) ultrastructurally. The pigmented eye of larval *C. ochracea* comprise SPCs and several c-PRCs with branched cilia. The c-PRCs, however, also possess potentially rhabdomeric microvilli. The results strengthen the hypothesis of c-PRCs being the ancestral photoreceptive cell type in pigmented eyes of spiralian larvae. The occurrence of mixed PRCs with both photoreceptive cilia and microvilli in a larval ocellus is an unusual case warranting further investigation.



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

What shapes the assembly of land snail communities on Vietnam's limestone karsts?

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The rich biodiversity of Vietnam's limestone karsts has fascinated scientists for a long time. The island-like nature of these habitats can separate individual communities of limestone-associated organisms from each other, which allows for the existence of multiple unique taxon assemblages. Underlying mechanisms of community assembly, however, remained long unknown. Two major processes that could be involved in the assembly of karst communities are interspecific competition and filtering of taxa due to geographical factors, which generally result in contrary patterns of community structure: overdispersion and clustering of ecologically relevant characters. In the present study, communities of operculate land snails of the genus *Cyclophorus* (Caenogastropoda: Cyclophoridae) from different limestone karst areas in Vietnam were investigated. Molecular phylogenetic and geometric morphometric data were used to detect patterns of overdispersion and clustering in individual *Cyclophorus* communities. Most of the studied communities were phylogenetically and morphologically overdispersed, which indicates that interspecific competition is likely the major process shaping their assembly.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral presentation

Cryptic diversity revealed: operculate land snails (*Cyclophorus* spp.) on limestone karsts in Vietnam

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The limestone karsts of Vietnam harbor a highly diverse fauna. Many limestone-associated taxa, however, are only poorly known and countless species are still expected to be discovered. As Vietnam's karst habitats are threatened due to the quarrying of limestone, a thorough examination of their biodiversity is needed. Operculate land snails of the genus *Cyclophorus* (Caenogastropoda) are generally common in karst regions and individual species, which often differ considerably from each other in shell morphology, have typically relatively small distribution ranges. Representatives with a very similar shell morphology, however, have been reported from large parts of Vietnam. Molecular phylogenetic, geometric morphometric and species delimitation analyses revealed that these snails belong to several different species, a number of them previously unknown to science. The geographic distribution of these species is typically allopatric. Convergent evolution and interspecific competition probably played a role in their evolutionary history. It seems likely that so far undiscovered morphologically cryptic taxa have also evolved in other groups of limestone-associated organisms.



Main Meeting, FG Systematics, Diversity and Biogeography Keynote Lectures
Oral presentation

Evolutionary venomics of pancrustaceans

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Venoms are important key adaptations that evolved at least 80 times convergently in the animal kingdom. Toxins are actively employed as venom components by complex morphological structures for defence, predation or competition in every major animal lineage. Despite this obviously important role venom systems play for the survival and the ecology of many taxa they remain unexplored for most species. So far species from few groups are more extensively studied, such as snakes, scorpions, spiders, cone snails and centipedes. This imbalance of explored venomous lineages (and lacking genome data) is also one reason why the processes of toxin gene evolution and the mechanisms how venoms evolve are not yet fully understood.

Modern evolutionary venomics applies a plethora of –omics methods, such as transcriptomics, proteomics and genomics to understand how venom diversity and toxin compositions evolve. The recent technological advances allow now to study much smaller, and so far neglected organisms.

Results of venom studies of remipede crustaceans (*Xibalbanus tulumensis*), the likely sister group of hexapods, and of robber flies (Asilidae) are being discussed. Both groups feature complex venom cocktails that harbour similar several new, lineage specific venom components. In particular, they secrete cysteine inhibitor knot peptides (ICKs) that are potent bio-resources for agrochemical or pharmaceutical research. Comparative genomics indicates that the processes by which toxins evolve might be more heterogeneous in pancrustacean lineages than previously assumed. High quality genome data of venom species is crucial to unravel this diverse, possibly multi-modal processes that shape venom composition and toxin gene evolution.



Main Meeting, FG Behavioural Biology
Oral presentation

Evolution of problem-solving as an adaptation to a manmade environment

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Urbanization is an uprising, global trend that often comes at the cost of destruction of animals' natural habitats. It is no surprise that due to the loss of natural territory, diverse wildlife (e.g. birds, rodents, raccoons, coyotes, and mountain lions) establish commensal lifestyle with humans. To cope with novel foraging challenges in urban areas, animals have been reported to express enhanced problem-solving performance not found in rural populations of the same species. Enhanced problem-solving skills in urban wildlife could arise from different life-experience (i.e. plasticity) of rural and urban populations, but could also be a product of the evolution of cognitive abilities.

To test whether cognition can be an evolutionary adaptation to a manmade environment, we experimentally tested problem-solving performance of three subspecies of wild mice (*Mus musculus*) which established a commensal lifestyle with humans at different time points in history. To control for any potential differences in animals' history not attributable to the degree of commensalism, experiments were conducted on two populations of each subspecies raised under standardized laboratory conditions. In four problem-solving setups, we compared the populations' solving ability, the latency to approach, and the interaction time with the setup. Our preliminary results suggest that populations living commensally with humans for longer periods evolved enhanced problem-solving performance. As populations do not differ in latency to approach and interaction time, the difference in problem-solving abilities cannot be explained by non-cognitive factors. This data infers that urbanization can lead to evolution of certain aspects of cognition in animals.



Main Meeting, FG Ecology
Poster: ECO 8

Nutritional stress in fluctuating environments: a case study on *Daphnia*

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Recent studies showed that animals tend to respond differently to fluctuating versus constant resource supply even when the average supply is the same. We combine experiments with modelling to study the growth responses of an aquatic key herbivore on nutritional variability and fluctuating temperature. We use controlled laboratory experiments and Dynamic Energy Budget models to gain information on how organisms with the ability to store resources and to adjust their nutrient acquisition may respond to changes in the temporal structure of environmental fluctuations.



Main Meeting, FG Morphology
Poster: MOR 7

Muscle damage and regeneration a balancing act

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The muscle is a complex structure and function unit and has numerous mechanisms for regeneration and repair after training or damage. For that reason, the muscle is on focus in various research topics. Because of its unique intra- and extracellular interactions which enable contracting for different motions as well as ensure stability it is a very important tissue. If the muscle would be strained, by training or damaged by an injury, the sensitive network will be disturbed. Fortunately, there is a very good repair and regeneration system to prevent the muscle from large damage.

In the recent past, different methods were used to classify the potential damage of the muscle fibre. Especially fibre typing is a common method to give a presumption on muscle damage. As already mentioned above, the muscle is a complex system, it doesn't seem to be the best way to analyse the muscle only by fibre typing. Other different markers are discussed in the literature but it is noticeable that they all analyse certain issues. Driven by this background we decided to analyse different intra- and extracellular structures histological after muscle stimulation. Electrical stimulation is appropriated to emulate training. Therefore, we decided to have a look at muscle changes after electrical stimulation. Additionally, we observe muscle changes after surgery.

We found that fibre typing is not the one and only method to analyse muscle damage. Furthermore, we figured out several structures which could be helpful for analysing muscle changes.



Main Meeting, FG Evolutionary Biology
Poster: EVO 7

Spatio-temporal genetic population structure of European freshwater jellyfish *Craspedacusta* originating from China: evidence for multiple invasions and cryptic species

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Craspedacusta (Cnidaria, Hydrozoa, Limnomedusae, Olindiidae) is the most widespread freshwater jellyfish in the world. We investigated the spatio-temporal genetic structure in eighteen populations of *Craspedacusta* medusae from Germany, Austria, Czech-Republic and China. Mitochondrial DNA variation at the 16S rRNA- and COI-locus was used to determine genetic diversity within and among populations. We found altogether four mtDNA-haplotypes in field samples and haplotype pairs were grouped in two major clades with genetic divergence at the species level (17.6 % for COI; 4.6 % for 16S), identifying *Craspedacusta* type 1 (subtype 1.1 and 1.2) and *Craspedacusta* type 2 (subtype 2.1 and 2.2). Notably, gender was associated with haplotype in both major clades (males: 1.2 and 2.1; females: 1.1 and 2.2). Medusae from almost all lakes were fixed for a single haplotype (1.1 or 2.1 or 2.2) over space and time. In the majority of lakes only the female type 1.1 was found. However, in Lake Baarer Weiher up to three haplotypes (1.2, 2.1, 2.2) co-occurred. The higher haplotype diversity in this lake corresponded to its special ecology emerging from Principal Component Analysis on physico-chemical lake characteristics. We are the first showing that altogether four haplotypes (dominant and rare ones) of *Craspedacusta* invaded European lakes and that up to three haplotypes are able to coexist within populations. Detection of high gene flow in pelagic jellyfish populations within and among regions or continents can be explained by the strong invasiveness of their inconspicuous benthic dispersal stages such as polyps, frustules or podocysts.



Main Meeting, FG Physiology
Poster: PHY 5

Capsaicin-loaded chitosan nanocapsules coated with wtCFTR-mRNA as a potential treatment of abnormal ion transports in cystic fibrosis

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The underlying problem of cystic fibrosis (CF) is an imbalanced homeostasis of ion and water transports in secretory epithelia causing problems especially in the lung. This imbalance is caused by impaired chloride secretion through the defect cystic fibrosis transmembrane conductance regulator (CFTR) and associated sodium-hyperabsorption via the epithelial sodium channel (ENaC). In this study we aim at establishing a double tracked strategy targeting both proteins to correct abnormal ion transports. We developed chitosan nanocapsules loaded with capsaicin to enhance mucus solubility and to downregulate sodium hyperabsorption, as it has been shown that the vanilloid reduces α ENaC expression. Furthermore, we coated the capsules with wtCFTR-mRNA, based on previous studies of our group, to restore CFTR function. Physicochemical characterization of the capsules showed that addition of capsaicin increased the hydrodynamic diameter by ~60 nm indicating successful encapsulation. Adsorption of mRNA to the surface did not have an effect on the capsules. Dynamic light scattering (DLS) revealed that capsules had an average hydrodynamic diameter of 204.3 ± 8.4 d.nm, Zeta potential of $+63.1 \pm 1.3$ mV and polydispersity index of 0.11 ± 0.01 . The results of DLS measurements were confirmed by asymmetric flow field flow fractionation (AF4). AF4 also showed that the capsules had a slightly elongated shape. Finally, the nanocapsules were stable for 24 h in cell culture transfection medium making them very promising for transfection purposes. These optimized chitosan nanocapsules effectively incorporate capsaicin and adsorb mRNA to the surface thereby being able to restore abnormal ion transports in CF.



Main Meeting, FG Behavioural Biology
Oral presentation

Natural Zeitgeber cannot compensate for the loss of a functional circadian clock in behavioural gating

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The circadian clock regulates a plethora of biological processes, including behaviour. Yet, little data is available on the actual requirement of circadian clocks under natural conditions. Recent experiments in *Drosophila*, a prime organism in circadian research, suggested that locomotor activity under semi-natural conditions is only little affected by an impaired molecular clock. Besides locomotor activity, the classical *Drosophila* model for circadian behaviour is eclosion, which is gated to the morning hours by a central and peripheral clock. Again, it is unknown to which extent the circadian clock is required to ensure proper eclosion timing in the presence of natural Zeitgeber.

Using a newly developed eclosion monitor (WEclMon), we monitored eclosion timing in wildtype and clock mutant flies under quasi-natural conditions. Our main finding is that a functioning molecular clock is required for proper eclosion gating even in presence of all abiotic Zeitgebers, while the temporal eclosion pattern of wildtype flies is similar to that observed in the laboratory. Moreover, clock mutant flies apparently have problems to keep daily rhythmicity when temperature conditions are more strongly changing from one day to the other. The situation is thus different compared to locomotor rhythms under semi-natural or nature-like conditions, and suggests a fitness advantage for flies having an intact clock. Nevertheless, abiotic Zeitgeber seem to be able to temporally organise individual oscillators in mutants lacking PDF signalling involved in timing clock neuron activity.

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Symposium: Form and function of motion systems: new approaches, new opportunities, new challenges

Oral presentation

The smooth transition from many-legged to bipedal locomotion – An application of the ground force interference model

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By using a simple numerical approach studying the interaction of single leg ground forces in polypedal locomotor apparatuses, I could show that the number of propulsive walking legs significantly affects the impact of ipsilateral phase shifts on overall ground force oscillations and therefore body-dynamics. The model relies on three parameters: the ipsilateral phase relations of the legs, the duty factor and the single leg vertical ground reaction forces, which are assumed as symmetrical, averaging body weight over a full stride. However, in contrast to this model's assumptions many polypedal animals reduce ground reaction forces underneath some - mostly the anterior - of their walking legs, in particular at higher running speeds. Thus, some spider, insect and lizard species decrease stance duration and maximum forces of their fore legs when moving close to top speed.

By factoring-in these reductions stepwise into the existing model approach, I will show that the phase dependent behaviour of overall body dynamics and total force amplitudes determined previously for integer numbers of walking legs gradually blend into each other. Accordingly, octopedal animals that reduce stance duration and force maximum of one pair of legs can be considered as functional hexapedes. Likewise, insects reducing foreleg activity are functional quadrupeds and quadrupeds like lizards can employ many advantages of bipedal locomotion, like high stability against sagittal plane disturbances, when apparently still moving with four legs as long as the fore legs' ground forces are significantly smaller than those of the hind legs.



Main Meeting, FG Ecology
Poster: ECO 3

Identification of *Chaoborus* kairomone chemicals that induce defences in *Daphnia*

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Infochemicals play important roles in aquatic ecosystems. They even modify food web interactions, such as by inducing defenses in prey. In one classic but still not fully understood example, the planktonic freshwater crustacean *Daphnia pulex* forms specific morphological defenses (neckteeth) induced by chemical cues (kairomones) released from its predator, the phantom midge larva *Chaoborus*. On the basis of liquid chromatography, mass spectrometry, and chemical synthesis, we report here the chemical identity of the *Chaoborus* kairomone. The biologically active cues consist of fatty acids conjugated to the amino group of glutamine via the N terminus. These cues are involved in *Chaoborus* digestive processes, which explains why they are consistently released despite the disadvantage for its emitter. The identification of the kairomone may allow in-depth studies on multiple aspects of this inducible defense system.



Main Meeting, FG Physiology
Oral presentation

Functional characterization of an ABCG transporter from *Tribolium castaneum*

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The ATP binding cassette (ABC) transporter superfamily mainly contains membrane bound proteins that are involved in the translocation of a large variety of substrates. Our previous studies on ABC transporters from the red flour beetle, *Tribolium castaneum* (Tc) revealed that the genome of this beetle harbors more than 70 TcABC genes, which group into subfamilies ABCA to ABCH encoding full and half transporters. One of these genes is TcABCG-8A, which is expressed in larval fat body and pupal elytra. Crosslinking and bimolecular fluorescence complementation experiments demonstrated that TcABC-G8A forms a homodimer in insect and yeast cells, respectively. Injection of dsRNA to knockdown TcABCG-8A function by RNAi in *T. castaneum* resulted in developmental arrest, molting defects, premature development of an adult eye, and a 50% mortality. These effects resembled phenotypes that were observed following RNAi for the two ecdysone receptors, TcECR-A and TcECR-B. Hence, TcABCG-8A may be involved in the transport of ecdysteroids in target tissues. As RNAi for no other TcABC gene led to similar phenotypes as described above, we conclude that ecdysteroid transport depends on a dimeric form of TcABC-G8A. To dissect TcABC-G8A function in more detail, we quantified TcABC-G8A mRNA levels during larval-to-pupal development and analyzed the effects of TcABC-G8A silencing on the expression of TcE75, which is an early ecdysone-induced gene, in either the absence or presence of tebufenozide, an ecdysone receptor agonist. Our results are in line with the assumption that TcABC-G8A acts as an ecdysteroid transporter in target tissues of this steroid hormone.



Main Meeting, FG Developmental Biology
Poster: DEV 4

Evolution of developmental processes underlying head formation in *Drosophila* on single-cell resolution

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Morphological diversification facilitates adaptation to changing environments. The genetic basis of natural variation of morphology however is still elusive. We aim at applying single-cell RNA-seq (scRNA-seq) to gain in-depth insights into gene expression and regulation dynamics throughout head development in *Drosophila* species on single-cell resolution. Comparative scRNA-seq will be used to identify candidate genes responsible for morphological variation in closely related *Drosophila* species.

To understand key events in development, we will sequence tissue from different time points, evenly covering larval development. For some stages of head development, bulk-RNA-seq data is already available (Torres-Oliva et al., 2018). However, scRNA-seq allows assessing co-expression and, to a degree, spatial localization of gene expression that is not possible by using bulk sequencing methods alone. By using drop-seq methods, it is possible to sequence a large quantity of the cells of the head.

Sister species of *D. melanogaster*, *D. mauritiana* and *D. simulans*, are shown to differ in eye size and shape, as well as face width (Arif et al., 2013; Norry et al., 2000; Posnien et al., 2012). We use these species to gain insight into the genetic basis of these differences and their evolutionary history. By studying evolution in closely related species, potential differentially expressed genes and diverging cell clusters are more likely to be meaningful for understanding morphological differences than when studying distantly related species.



Main Meeting, FG Evolutionary Biology
Poster: EVO 12

The repeatome – abundance, diversity, localization, and activity of repetitive and transposable elements

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The role of transposable elements (TEs) as drivers of genomic change is currently being intensely studied; both disruptive and formative effects have been described to play a role in (eukaryotic) genome evolution and maintenance. Yet, the classification of these and other repetitive elements remains elusive, as they pose inherent challenges to sequencing protocols as well as assembly and annotation algorithms. As a consequence, research often focuses on specific families on TEs rather than a genome-wide assessment.

We approach the genomic repeat content via a genome-wide screening and scoring of 'repetitiveness'. We implemented a score that considers motif length and copy count. This allows to visually inspect the repeat content of whole genomes independent of classification procedures; thus, annotation and classification can be simultaneously validated and complemented. Additionally, this approach allows to visualize and compare species-specific differences of the repeatome. With a focus on vertebrate model-organisms, we also sought to elucidate general patterns of region-specific (relative to protein-coding genes) enrichment/depletion of TEs as well as of age-dependent TE activity. With this we aim to generate a new and better understanding of genomic repetitiveness including the conservation of the repeatome during phylogeny as well as its variation during ontogeny.



Symposium: Form and function of motion systems: new approaches, new opportunities, new challenges

Oral presentation

Investigation of perturbed locomotion compensation using a 3D-kinematic, 3D-dynamic, and neurobiological approach

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One of the main questions in developing walking robots is how the locomotion can be stabilized in uneven terrain. To analyze the compensation of disturbances during running in rats we combine 3D-kinematics, 3D-dynamics and neurobiology.

During the experiments the animals running on a normal treadmill, a treadmill with irregular holes in it and on a walkway with two integrated force plates. The first force plate was lowered 2.5 cm, covered by a piece of paper to hide the hole or uncovered to see the difference. The second plate is on the base level.

To recognize the compensation, we synchronized the measurement of 3D bone movements (biplanar highspeed cineradiography), 3D GRP (force plates) and the muscle activity (EMG) of the triceps and biceps brachii as well as the trapezius and pectoralis muscle.

Each segment of a rat forelimb was marked with implanted tantalum beads to minimize the deviation between measured and real bone movement. The muscle activity was recorded with implanted silicon coated stranded platinum-iridium wires.

Preliminary results show an increasing and elongated triceps activity as well as a stronger biceps activity when the rat steps into the hole. The leg is not so much more stretched than expected. It seems the configuration of the foreleg 'freeze' in the normal touch down position and the leg rotates into the hole. The stronger activation of the muscles can stabilize the joints in an uncomfortable position.



Main Meeting, FG Evolutionary Biology
Poster: EVO 8

Who provides the biological relevant information to sailfin molly females for mate-choice copying? Computer animation provides new insights into a fascinating mate-choice strategy

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Animals use public information during mate choice by observing conspecifics during their sexual interaction and often copy the mate choice of others they just witnessed. This has been experimentally shown for a variety of different species. Beside numerous studies on mate-choice copying, one fundamental question remains: who provides the biologically relevant information observers extract from watching others during their mate choice? To investigate this question, we used computer-animated male and female sailfin mollies *Poecilia latipinna* which varied in the extent and direction of courtship behavior and presented either (1) a mutual driven, (2) a female driven or (3) a male driven courtship scene to focal females during an observation period within a mate-choice copying experiment. In two additional treatments, we tested whether (4) the presence or (5) the absence of male courtship affected female mate choice when no public information was provided. As expected, females copied the mate choice in all three treatments (1) - (3). The copying effect, however, was strongest in the male driven courtship scenario, and weaker in the mutual and female driven courtship scenarios. We hypothesize that model females who actively engage in courtship might be recognized as strong competitors for focal females, which leads to a weaker copying effect. Without public information and lack of male courtship behavior, focal female's preference decreased for a previously preferred male. Females, however, chose consistently when stimulus males showed courtship towards them. Our results provide new insights into the mechanism of mate-choice copying using an innovative method.



Main Meeting, FG Behavioural Biology
Oral presentation

How to run fast – strategies in desert ants

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Fast running locomotion has evolved in several arthropods, particularly in hot and hostile climates. Desert ants of the genus *Cataglyphis* are well-studied examples here. These ants are long-legged scavengers of desert and steppe habitats, and different species have adopted different strategies to achieve high running speeds.

One strategy relies on long legs that allow large stride lengths and resulting high running speeds – stride length maximisers (e.g. Zollikofer, 1994, J. Exp. Biol. 192, 107). *Cataglyphis bicolor* is a typical species following this strategy. These ants are large, ~3.63 mm in alitrunk length, front, middle and hindlegs measuring ~6.72, ~7.97 and ~10.49 mm. Another strategy favours high stride frequencies, a feat that cannot be achieved with long legs due to their large inertial momentum. A typical representative of such short-legged (by long-legged *Cataglyphis* standards) high frequency runners is *C. albicans*. Legs of *C. albicans*, while short in absolute terms (~3.74, ~4.01 and ~5.47 mm), are in isometric proportion to the smaller body size of *C. albicans* (alitrunk ~1.94 mm) compared to *C. bicolor*.

Comparison of these two ant species appears particularly profitable considering their virtually isometric body dimensions, identical habitats, with prey spectra constituting the main species difference. Any differences in walking behaviour can thus be attributed rather confidently to differences in body size.

Stride lengths and frequencies in the two species agree with the concept of spring-loaded inverted pendulum (SLIP) of walking, smaller species exhibiting higher characteristic frequencies of the leg-body oscillator. However, swing and stance durations show idiosyncratic characteristics.



Main Meeting, FG Morphology Keynote Lectures
Oral presentation

Insights into lophotrochozoan evolution – on the morphology and molecular signature of single cells in a mollusk with pronounced ancestral traits

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How did the vast diversity of cell types arise during evolution and how are cell types related to each other? Addressing this question, I study representatives of the phenotypically diverse superphylum Lophotrochozoa with clades as different as mollusks or annelids. The polyplacophoran mollusk *Acanthochitona crinita* exhibits ancestral molluscan and bilaterian traits. Its trochophore larva is a mosaic of embryonic and adult traits such as seven shell plates, an apical organ, a ciliary band, a creeping foot and a differentiated nervous system. I performed whole-body single-cell transcriptomics on the polyplacophoran trochophore using 10x genomics and Next-Seq technology. More than 30 well-supported cell types have been revealed and validated by *in situ* hybridization experiments, among them muscle, intestinal, sensory, ciliary, and neuronal cell types. Interestingly, several cell types give rise to the shell valves and spicules and express genes encoding transcription factors known to be expressed in the nervous system of other bilaterians. For an in-depth characterization of these cell types state-of-the-art techniques such as light sheet fluorescence microscopy are applied. Findings are discussed in the light of the evolution of other lophotrochozoan hard parts such as brachiopod shells and chaetae as well as annelid chaetae. This study contributes to lay the foundation for tracing the evolution of cell types and cell type families across Lophotrochozoa and Bilateria.



Main Meeting, FG Morphology
Oral presentation

Anatomy of some of the smallest free-living crustaceans (Cladocera, Branchiopoda)

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Eucrustacea is a uniquely diverse group, representatives of which have developed a plethora of various forms and life habits. Their body size varies majorly, from 0.1 mm (Tantulocarida) up to 3,7 m (Decapoda). Although morphology and anatomy of different eucrustaceans has been studied rather thoroughly, there is almost no information on the miniaturized forms, except for several studies, which either treat rather large crustaceans or describe only certain aspects of morphology. Extremely small body size of some invertebrates causes transformations such as renunciation of certain physiological functions and organ reductions that seemingly contradict fundamental biological principles.

Smallest (0.2 mm) non-parasitic crustaceans belong to Cladocera (Branchiopoda), and are close relatives of a well-known model organism *Daphnia* sp. Until now there was almost nothing known about their internal anatomy and development, apart from taxonomic studies with schematic drawings. *Alonella nana* (Chydoridae) is the smallest representative of Cladocera (0.2 mm) and has been one of the main subjects of the following study. Its anatomy has been thoroughly studied with different advanced morphological techniques, such as confocal laser microscopy, scanning electron microscopy, transmission electron microscopy and 3D-reconstructions based on histological sections. The results have been compared with the anatomy of crustaceans of different size classes and taxonomic groups in order to identify features that are likely affected by miniaturization.

This study is the first detailed investigation of the anatomy of minute crustaceans and helps to understand effects of such an important evolutionary trend in animals as body size diminution.



Main Meeting, FG Systematics, Biogeography and Diversity
Oral presentation

Spatio-temporal colonization of the genus *Psectrascelis* (Coleoptera, Tenebrionidae) to the Chilean Altiplano

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Geological and climatological events had a particularly great impact on the evolution of life in extremely water limited environments, such as the Atacama Desert in northern Chile where the evolutionary history has been poorly studied. Within the CRC 1211 (Earth – Evolution at the dry limit), we focus on the evolution of darkling beetles of the genus *Psectrascelis*. These beetles belong to the most conspicuous biotic components in Altiplano and represent a hyperdiverse genus with small areas of distribution. To elucidate the evolutionary pattern, we drive phylogenetics analyses and additionally, we estimate the divergences times and the biogeographical history. The results suggest a deep separation between western and eastern lineages during the Pliocene. Then a secondary split by the colonization of the Puna and Prepuna region occurred in the Mid-Pliocene and separated the Coquimbean lineage from the Puna-Prepuna lineages. Finally, the Puna lineage colonized the Altiplano in the mid-Pleistocene from the Prepuna region in the south. The other two species from the eastern lineage colonized the Altiplano in a completely independent history just in Late-Pleistocene. The evolution of *Psectrascelis* in the Altiplano shows a complex history related to the uplift of the Andes and the climatological changes in the Plio-Pleistocene periods.