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ABSTRACTS

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H. Römer[1]
[1]University of Graz, Institute of Zoology, Graz, Austria

No abstract availabe.

KN-02 – 125th ANNIVERSARY CEREMONIAL ADDRESS

125 Jahre Deutsche Zoologische Gesellschaft (DZG) – von der Zootomie zur Epigentik und Kognitionsforschung

F.G. Barth[1]
[1]University of Vienna, Department of Neurobiology, Vienna, Austria

No abstract available.

KN-03

Seeing in the dimmest habitats on Earth The eyes and vision of nocturnal and deep-sea animals

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We humans have evolved to see well in bright daylight. Our excellent senses of colour, and our acute spatial and temporal resolution, are among the best found in the vertebrate world. But this is only true during the day. On a moonless night, when light levels may be more than 100 million times dimmer, we are quite helpless. At light levels where we are nearly blind, our cats are out stalking prey, and moths are flying agilely between flowers on our balconies. While we are sleeping, millions of other animals are relying on their visual systems to survive. The same is true of animals inhabiting the eternal darkness of the deep sea. How is such formidable visual performance possible? In my lecture will try to answer this question by exploring the remarkable eyes and visual systems of nocturnal terrestrial animals, deep-sea fishes and the elusive giant squid.

ABBREVIATIONS: KN, key note talk; IT, invited talk; OP, oral presentation; PP, poster presentation

KN-04

Recent shifts in European pollinators and why we should care

K. Biesmejer[1]
[1]Naturalis Biodiversity Center, Leiden, & University of Amsterdam, Amsterdam, NL

Sorry, talk is canceled!

KN-05

Socially induced phenotypic plasticity in locusts

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Locusts are grasshoppers (Acrididae) that can transform between two extreme phenotypes known as phases. This capacity has evolved in adaptation to the unpredictable precipitation patterns in their arid habitats. Locusts normally occur at very low population densities in a cryptic solitarious phase that avoids conspecifics. Sporadic rains provide opportunities for explosive population growth. The recurrence of drought then drives large numbers of locusts onto dwindling islands of verdure. This crowding triggers a rapid behavioural transition towards increased mobility and mutual attraction that is followed by slower changes in morphology and physiology. The end result is the gregarious phase, which is tailored to a life in dense mobile swarms. Our work has focussed on the proximate causes and consequences of phase change in the Desert Locust, *Schistocerca gregaria.* The sole direct drivers of behavioural gregarisation are sensory stimuli from conspecifics. We have evidence that these stimuli activate specific sets of serotonergic neurones in the thoracic central nervous system. Serotonin then initiates a rapid transition to gregarious behaviour through activation of protein kinase A. The consequences of phase change extend to associative learning: the two phases use different rules to associate novel odours with toxic food. Acute crowding leaves existing food-odour associations intact but specifically blocks the acquisition of new aversive ones. In the field, this simple mechanism enables an adaptive updating of an odour's value from aversive to appetitive. Finally, I will consider the relationship between behavioural plasticity and 'animal personality' in the context of the evolution of phase change.

KN-06

The role of gene flow in the diversification of animals

W. Salzburger[1]
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More than one and a half centuries after the publication of Charles R. Darwin's *The Origin of Species*, the identification of the processes governing the emergence of novel species remains a fundamental question to biology. Why is it that some groups have diversified in a seemingly explosive manner, while other lineages have remained unvaried over millions of years? What are the external factors and environmental conditions that promote diversification? And what is the molecular basis of adaptation, evolutionary innovation and diversification? Providing particularly clear evidence of the power of natural selection, adaptive radiations serve as outstanding systems for studying the mechanisms of evolution. The first wave of genomic investigation across major archetypal adaptive radiations is starting to shed light on the molecular basis of adaptive diversification. Notably, these efforts have not yet identified consistent features of genomic architecture promoting diversification. However, access to a pool of ancient adaptive variation via genetic exchange emerges as an important driver of adaptive radiation.

KN-07

Functional genomics of marine and freshwater sticklebacks

F. C. Jones[1]
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Colonisation of new freshwater habitats has resulted in the repeated adaptive divergence of freshwater sticklebacks from their ancestral marine ecotype. We use these powerful biological replicates of the evolutionary process to identify and functionally dissect the molecular mechanisms underlying adaptive divergence and reproductive isolation. I'll describe how we are using whole genome sequencing and population genomics of stickleback species pairs to identify high-resolution sets of loci underlying parallel adaptive divergence. Many loci fall in non-coding parts of the genome, suggesting non-coding regulatory elements may be particularly important in adaptation. We use a range of methods to functionally dissect the phenotypic effect of these loci. These include transgenic methods to test for divergence in the regulatory potential of marine and freshwater adaptive haplotypes, and powerful new genome editing techniques to knock-out and knock-in adaptive loci. Our ultimate aim is to understand the fitness effects of these loci in natural populations. To do this we study the fitness and survival of naturally occurring recombinant individuals in contact zones between marine and freshwater forms. The ability to identify and functionally dissect adaptive loci in sticklebacks provides powerful insights into the molecular mechanisms underlying adaptation in natural populations.

KN-08 – PUBLIC LECTURE IN GERMAN LANGUAGE

Rabenpolitik: Verständnis und Nutzen von sozialen Beziehungen in komplexen Gemeinschaften

Raven politics: Understandig and use of social relationships in a dynamic avian system

T. Bugnyar[1]
[1]University of Vienna, Department of Cognitive Biology, Vienna, Austria

Complex social life has been proposed as one of the driving forces for the evolution of cognition. Aside a large group size and a high degree of fission-fusion dynamics, the formation and use of valuable relationships (social bonds) have been discussed as the main factors constituting social complexity in mammals. Yet it is debated, if this is also true for birds. Reporting on recent data from captive and wild ravens (Corvus corax), I argue that i) the quality of social relationships of these birds is comparable to that of primates and ii) that the relationship quality between individuals explains various patterns of their advanced conflict management (coalition formation, intervention in fights, post-conflict reconciliation and bystander-affiliation). In addition, I argue that iii) social bonds may be advantageous during foraging but iv) that they may come with the costs of increased aggression by third parties. These findings support the idea that the need for, and use of, bonding partners outside reproduction may be one of the factors driving the cognitive evolution in these large-brained birds.

KN-09

Life on the edge? Local adaptation and emerging reproductive isolation in extremophile fishes

M. Plath[1]
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Extremophile organisms survive under harsh environmental conditions (characterized by the presence of physicochemical stressors) that are inhospitable for most eukaryotes. To cope with these stressors, extremophiles have often evolved complex adaptations. Populations inhabiting naturally occurring extreme environments thus represent ‘evolutionary experiments’ that allow studying the evolutionary potential of species to habituate/adapt to altered ecological conditions, which may also allow generating predictions about the potential of organisms to habituate/adapt to human-induced stressors. A surprising number of teleost fishes can be found in extreme environments, including waters that are nearly devoid of oxygen, hot desert waters, Arctic and Antarctic waters with temperatures below freezing, salinities far above sea concentrations, or even in habitats that temporarily fall dry. My own research has focused on the repeated adaptation to habitats containing toxic hydrogen sulfide (H_2S) and/or permanently dark (cave) habitats in the species complex of the neotropical freshwater fish *Poecilia mexicana*. One of the major questions in this context is whether parallel phenotypes diversify via parallel genetic changes or if alternative genomic routes lead to the same phenotype(s) (i.e., the old ‘parallel versus convergent evolution’ debate). More generally, I will elaborate on the hypothesis that the degree of parallelism increases with increasing level of biological organization (e.g., from genes to anatomical/morphological traits), and I will compare the degree of parallel evolution from genome-wide SNPs, over genes and pathways, to complex character suites (e.g., life history, morphology). Finally, I will present evidence for the emergence of reproductive isolation as a consequence of local adaptation in sulfide-adapted fish (ecological speciation) and discuss mechanisms promoting reproductive isolation.

PRICE GIVING CEREMONY

Werner-Rathmayer-Preis to Thomas Lindner

Nachahmungseffekt bei *Poecilia wingei*

T. Lindner[1]
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Ziel meiner Untersuchung war, die Partnerwahl beim südamerikanischen, lebendgebärenden Zahnkarpfen *Poecilia wingei* zu untersuchen. Besonders interessierte mich der Nachahmungseffekt, der im Englischen mit „Mate choice copying“ bezeichnet wird. Unter diesem verhaltensbiologischen Phänomen versteht man einen Effekt, bei dem ein Individuum keine eigene und von Dritten völlig unabhängige Wahl für einen potentiellen Geschlechtspartner trifft. Die Beobachtung der Präferenz eines anderen gleichgeschlechtlichen Individuums (welches in der Regel derselben Art angehört) für einen Sexualpartner beeinflusst die eigene Wahl. Die beobachtete Präferenz wird teilweise, oder sogar vollständig übernommen. Um diese Frage bei *Poecilia wingei* zu klären, wurden zwei Versuchsreihen durchgeführt: Nachahmungsexperimente mit allen nötigen Komponenten zum Nachweis eines Effektes und Kontrollexperimente, in denen die provozierende Komponente zur Nachahmung jeweils fehlte. Die gewonnenen Ergebnisse deuten auf das Vorhandensein eines weiblichen, intraspezifischen Nachahmungseffektes hin, unterschiedliche Resultate aus den beiden Versuchsreihen konnten nicht anders erklärt werden. Die Erkenntnisse können bei der Zucht auf bestimmte männliche Merkmale genutzt werden und liefern zudem artspezifische Informationen zu *Poecilia wingei*.

Horst-Wiehe-Preis to Alexander Blanke

The Palaeoptera problem and the evolution of head structures of dicondylic insects

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The phylogenetic relationships of dragonflies (Odonata), mayflies (Ephemeroptera), and all other winged insects (Neoptera) is one of the major problems in systematic entomology. Three hypotheses are discussed: the Chiastomyaria hypothesis (Ephemeroptera + Neoptera), the Metapterygota hypothesis (Odonata + Neoptera), and the Palaeoptera hypothesis (Odonata + Ephemeroptera). In my thesis, I analysed the head morphology of Zygentoma, Ephemeroptera and Odonata using state-of-the-art imaging methods in order to study especially the internal head anatomy. A formal phylogenetic analysis of the resulting cephalic characters supported the Palaeoptera hypothesis which was surprising, since former analyses using this character system supported the Metapterygota hypothesis. The talk will also give a brief overview of future research directions in this scientific field.

Walther-Arndt-Forschungspreis to Mirjam Knörnschild

Vocal Communication and social cognition in bats

M. Knörnschild[1]
[1]Free University Berlin, Animal Behavior Lab, Berlin, Germany

Bats are a highly promising taxon for studies on mammalian vocal communication and social cognition for two reasons. Firstly, echolocating bats exhibit remarkable control during signal production and precise auditory perception, which is a preadaptation for sophisticated and flexible vocal communication. Secondly, many bat species are gregarious and long-lived, which gives individuals ample opportunities to interact with and learn from conspecifics, thus shaping both their vocalizations and their behavior, e.g. their foraging behavior. The first part of my talk focusses on vocal communication in the greater sac-winged bat *Saccopteryx bilineata*. This bat learns new vocalizations by imitating tutors, which results in culturally transmitted song dialects, and engages in a conspicuous babbling behavior reminiscent of the babbling of human infants. Babbling is considered to be crucial for mastering the phonological challenges of vocal repertoire acquisition in different species, including humans. Apart from humans, *S. bilineata* is the only mammal known to date that is both a babbler and a vocal imitator, which makes this species highly interesting for comparative studies of language evolution. In the second part of my talk, I discuss the cognitive abilities of flower-visiting bats, *Glossophaga soricina*, in a social context, specifically their social learning capacities. Flower-visiting bats are extremely well suited to study vertical and horizontal information transfer as well as learning from heterospecifics.

TALKS AND POSTERS - TOPICAL SESSIONS

OP-BB-IT-01

Combining comparative cognition and animal welfare: From lab science to zoo-based research

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Comparing the cognitive capacities of different animal species is essential to understand the evolutionary origins of cognition, but getting access to various species can be very challenging. Zoos, housing large ranges of animal taxa, would offer ideal research environments, but zoo-based studies on cognition are still very rare. Even the European Association for Zoos and Aquariums (EAZA) stressed the need of an improved scientific practice in zoos. In addition, zoos also offer great opportunities for urgently needed scientific outreach and communication to the public. Zoos, on the other hand, profit from the welfare aspect of scientific studies, as cognitive challenges can enhance the lives of zoo animals, known as cognitive enrichment. Using my experience from lab-based research on monkeys, I am currently developing and validating portable touchscreen computer systems at Zoo Heidelberg, Germany, to facilitate zoo-based research. Methodological variations in experimental conditions can strongly influence animals' performances in cognitive tests, and the use of touchscreen computers to explore the cognitive abilities of nonhuman animals has shown to be highly applicable. The newly developed setups can be used in various zoo environments and, importantly, with different species (e.g. primates, birds), offering the unique opportunity to conduct comparative studies on different animal species and taxa. To examine the influence of the touchscreen studies on animal wellbeing, behavioural observations are conducted. I discuss my studies on monkey cognition in the lab, and illustrate how increasing zoo-based research can facilitate cognitive studies, enhance animal welfare, and support science communication.

OP-BB-IT-02

Consistent individual differences in behaviour as part of a broader pace-of-life syndrome

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Based on a heuristic framework links between physiological and life-history traits coevolved in response to long-term selection pressures forming the pace-of-life syndrome (POLS). Although the POLS is supported at the between-species level, it remains open whether these links exist also among individuals within populations and whether between-individual differences in behaviour, i.e. personality traits, are part of a broader POLS. Here, I will present results of two empirical studies and review the current literature on the behaviour-integrating POLS. First, using a laboratory experiment, I found individual consistency in exploration and resting metabolic rate (RMR) under different environmental conditions in grey mouse lemurs (*Microcebus murinus*; Primates). Individuals with high RMR were more explorative and expressed less energy-saving torpor. Second, I tested for among- and between-individual (co)variation between energy metabolism, behavioural phenotype and life-history in free-ranging eastern chipmunks (*Tamias striatus*; Rodentia). I found large among-individual differences in torpor use that were related to RMR and had consequences for survival and reproductive success, indicating that among-individual differences in heterothermy-based energy-saving and metabolism are part of the POLS. However, there was no clear support for covariation with behavioural traits in this species. These mixed findings are in line with other empirical studies and call for a refinement of the POLS hypothesis into a more broadly formalized model, which is tailored to specific ecological conditions.

OP-BB-01

Scent marking: honest, uncheatable indicator of social status or just smelly?

K. Luzynski[1]
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Scent marking is important for signaling an individual's condition, social status, territory location, and sexual receptivity for a plethora of taxa. In house mice (Mus musculus musculus), scent marking is a testosterone-mediated behavior with marked dimorphism between the sexes, and may indicate an individual's social status, e.g., there is increased marking in aggressive males compared to socially defeated mice. Furthermore, there is evidence that scent marking predicts the outcome of agonistic interactions such that high markers are more likely to defeat low markers. Scent marking is thought to be a cheat-proof signal of social status; however, previous results were based on short-term, aggressive interactions, and studies are needed to examine differences in marking in more natural contexts. We examined the relationship of social status and scent marking from wild-derived house mice (F1 offspring from wild-caught) in semi-natural enclosures. Over a period of 20 weeks we measured social interactions, reproductive success, territoriality, urine composition, and scent marks of 32 males and 32 females in 8 semi-natural enclosures. This study design allows wild house mice to compete at multiple levels and more likely to predict natural phenomena compared to results gathered from head-to-head fighting bouts in controlled arenas. Our results challenge the honesty of scent marking as a signal of social status and suggest that there is a complex relationship between scent marks, status, and sex.

OP-BB-02

Change her phenotype, change her choice: chemosensory self-referencing in a cricket promotes polyandry but not inbreeding avoidance

S. Steiger[1], A. Capodeanu-Nägler[1], J. Rapkin[1], S. Sakaluk[1], J. Hunt[1]
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An individual's ability to assess the similarity between its own phenotype and that of the individuals it encounters can provide a reliable measure of relatedness, thereby facilitating inbreeding avoidance, optimal outbreeding or altruistic behavior towards kin. Although self-referencing is believed to be widespread, definitive evidence is scarce and its role in recognition controversial. Here we provide direct evidence for a chemosensory self-referencing mechanism in the decorated cricket *Gryllodes sigillatus* using inbred lines. Females of this species are known to imbue males with their own cuticular hydrocarbons (CHCs) at mating and use these cues to avoid previous mating partners. We modified the CHC profile of females after mating and found that they altered their subsequent mate choice decisions, which were now based on their new olfactory phenotype. These results indicate that females use self-referencing, but this self-referencing is not based on an innate or early learned template of self, rather they compare a conspecific phenotype with their own in real time. A further study, in which we performed over 450 mating trials, suggest that they do not engage in self-referencing to avoid mating with genetically similar males, but chemosensory self-referencing is only used to avoid previous mating partners, thereby facilitating polyandry.

OP-BB-03

The effect of temperature on the vibrational and chemical signals of males of the red mason bee, *Osmia bicornis* (L.)

T. Conrad[1], C. Stöcker[1], M. Ayasse[1]
[1]Ulm University, Ulm, Germany

Abiotic factors such as fluctuations in air temperature are known to have a major influence on most animals, especially poikilotherm insects, because they depend on the temperature to be high enough to function. Previous studies have already shown that acoustic, vibrational, chemical and visual communication signals can all be affected by changes in temperature. In the red mason bee, *Osmia bicornis*, which emerges early in spring and is therefore subject to extensive temperature changes, females choose suitable males based on, among other criteria, their vibrations and chemical signals. However, research into the effect of temperature changes in these bees has so far focused on overwintering females. We therefore investigated if the environmental temperature has an influence on the male's mating signals by measuring vibrations using a laservibrometer and collecting male and female odor at low and high temperatures. Our results showed that rejected males differed in their vibrations between the two temperature settings but accepted ones did not. Furthermore we found that the differences in odor profiles were greater between temperature settings than between males and females. We conclude that temperature strongly influences the male mating signals and therefore may have a major impact on sexual selection in this species. This is an important aspect to consider, not only in future studies on mating behavior, but also in view of climate change.

OP-BB-04

The hot male hypothesis:
Do male katydids signal their energetic costs by body temperature?

B. Erregger[1], M. Hartbauer[1], H. Kovac[1], A. Stabentheiner[1], H. Römer[1]
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Males of a trilling species of the *Mecopoda* complex use multimodal signals for communication. In addition to continuous, intense calling songs (103 dB SPL at 15cm) they generate three different types of substrate-borne vibrations in close temporal relationship with the air-borne sound signal. Song production is energetically costly for the sender, indicated by a 12-fold increase of CO_2 production rate compared to resting. During singing the thorax temperature increases by more than 8 °C. The strong linear correlation between metabolic rate and temperature increase in males let us suggest that females might use this sensory modality as a further cue for mate choice, in addition to air-borne sound and substrate vibration signals. The combined information in these different modalities facilitates the evaluation of the quality of a sender, each being effective over different distances to the sender. Males of a tropical cricket (subfamily *Anurogryllus)* also increase their thorax temperature during singing. However, in *Anurogryllus* both males and females increase their thorax temperature without singing, by vibrating their wings. Thus, in this species the thermal cues may have switched from a cue into a signal, because "silent signallers" decouple thermal signals from acoustic signal production.

OP-BB-05 - Fish sing differently in noisy waters: Males of two goby species similarly adapt their use of courtship calls to the acoustic environment

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[2]Instituto Superior de Psicologia Aplicada – Instituto Universitario, Unidade de Investigacao em Eco-Etologia, Lissabon, Portugal
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Question - Increasing levels of background noise in our oceans are a major cause of concern, and are likely to hamper acoustic communication under water. When signals used during courtship and reproduction are affected, this could lead to a decrease in reproductive success within affected populations. However, because behaviour is often flexible, animals may be able to change their signals to overcome the loss of signal efficacy. The ability to adapt communication to the acoustic environment has been found in mammals, birds and frogs, but evidence in fish is still very scarce.
Methods - We chose two closely related species that have more than one call type in their repertoire: the two-spotted goby (*Gobiusculus flavescens*) and the painted goby (*Pomatoschistus pictus*). Males of both these species use two different call types during courtship. The two-spotted goby is semi-pelagic and lives in kelp forests, while the painted goby is benthic and lives on sandy bottoms. In two separate aquarium experiments in different years and countries, we compared male courtship behaviour in a noisy versus a quiet environment for these two species.
Results - Males of both species reacted similarly to increased noise levels: they reduced the use of one of their courtship call types, but not of the other. In both species, males reduced the use of the call type that was most masked by the experimental noise.
Conclusions - We present clear evidence that some fishes are able to adapt their acoustic behaviour to the acoustic environment. Our results indicate that the two goby species studied are able to assess the efficacy of their signals and that they can flexibly use call types that fit to the acoustic environment. Fish may thus be more flexible in their acoustic behaviour than generally assumed. The call type that was reduced under noisy conditions has been previously shown to contain information about male condition in the painted goby, and may thus be an important signal of male quality. We discuss how the reduction of a specific courtship signal may lead to different choices by females and therefore affect the direction and/or the strength of sexual selection.

OP-BB-06 - Species specificity of male antennal courtship in *Leptopilina* wasps

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In many species of parasitic wasps, antennal stroking by the male during courtship is necessary to elicit receptiveness in the female. Most probably, male antennal pheromones are transferred during antennal stroking, which might allow the female to recognize the courting male as conspecific. This hypothesis is supported by the fact, that males possess glandular structures in their antennae. However, it is neither known whether the antennal stroking is species specific, nor has any proposed pheromone been chemically identified. Here we show that the antennal courtship of *Leptopilina*, a parasitoid of *Drosophila,* is indeed species specific. To test this we needed males to court heterospecific females, which normally does not happen. However, by transferring the female sex pheromones of *L. heterotoma*, *L. boulardi*, and *L. victoriae* between females of different species we were able to elicit intraspecific courtship. Males of all three species readily courted both conspecific and heterospecific females treated with the pheromone extract. However, males elicited readiness to mate only in conspecific females, but never in heterospecific females. Chemical analysis revealed the presence of long chained double unsaturated hydrocarbons on the antennae of males, which are not found in the CHC profile of females. The composition of these unsaturated hydrocarbons differs both qualitatively and quantitatively between species. Females could recognize conspecific females using these compounds, which thus most probably form the male antennal pheromone of *Leptopilina*.

OP-BB-07

Reproductive behaviour of bank vole (*Myodes glareolus*) females as a function of infanticide risk and mating interest

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Infanticide, the killing of conspecific young, is a widespread behaviour in the animal kingdom. Minimizing the infanticide risk comes at the expense of searching for mating opportunities. Therefore, iteroparous species are faced with a reproductive trade-off between current and future reproduction. The present study investigated this trade-off by observing the behaviour of bank vole females as a function of infanticide risk and mating interest under laboratory conditions. Two levels of infanticide risk were simulated via exposure to olfactory cues (i) the scent of the sire - low risk and (ii) the scent of a non-sire male - high risk. Since bank voles are able to conceive another litter while still weaning the present one a male should represent both a potential threat and a mating opportunity. Integrating both, we predicted that under a high infanticide risk females are faced with a reproductive trade-off between protecting their young and searching for a potential mating partner which is in favour of the first. To observe the behaviour females and their corresponding litter were transferred into indoor arenas and confronted with the different scent types on successive days. We found that females adjust their behaviour according to the potential infanticide risk presented. Under a high risk they increased their protection effort while decreasing their mate search effort compared to the presence of a low risk. Individuals therefore recognize different levels of infanticide risk and adjust their behaviour accordingly. The mating interest reflects in aspects of the reproductive behaviour as well. Bank vole females are therefore faced with a reproductive trade-off between current and future reproduction that shapes their behaviour.

OP-BB-08

Distribution of paternity within a large, semi-captive group of Japanese macaques (*Macaca fuscata*)

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Japanese macaques (*Macaca fuscata)* live in female-bonded groups containing several female matrilines and, generally, unrelated males, which are the dispersing sex. We investigated the distribution of paternity in a large semi-captive group of Japanese macaques (*N = 140 individuals*). The group originates from a founder population of 40 individuals, which were imported to Landskron (Austria) in 1996, and no transfer of individuals occurred since then. Therefore, we assume a high risk of inbreeding, which leads to the question of whether any countermeasures are taken to lower the possible disadvantageous effects of this risk. Furthermore, we were interested in the dominance status of fathers. Paternity could have been identified in 43 individuals out of a total of 85 descendants and data showed that reproduction among closely related individuals was as frequent as expected by chance (permutation tests, n.s.). However, analysis of behavioural data collected during the breeding season showed that females significantly avoid sexually motivated contact with closely related males ($\rho = -0.692$, $p = 0.004$, $n = 15$) but not vice versa ($\rho = -0.202$, *n.s.*, $n = 18$). This may represent a behavioural mechanism to avoid inbreeding among closely related mating partners on the part of the females which - in the light of at least one observed kin mating - does not appear to be perfectly efficient. Furthermore, the results showed that high ranking males were not able to monopolize paternity, probably due to the high ratio of adult males to females in this population.

OP-BB-09

Traumatic experiences in early infancy have lifelong effects on social integration of chimpanzees (*Pan troglodytes*)

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Early traumatic experiences such as loss of the mother are known to affect later psychosocial functioning in humans, whereas less is known regarding these effects on our closest living relatives, the chimpanzees. Previously, we investigated the effects of early maternal loss and long-term isolation on three groups of ex-laboratory chimpanzees who experienced an either early (ELDs, n=10) or later onset of long-term deprivation (LLDs, n=8) in terms of being single caged for decades. Here we expand this line of research by comparing these re-socialised ex-laboratory chimpanzees to two groups of zoo chimpanzees consisting of non-deprived (NDs, n=16) and wild-caught early maternally deprived subjects (EMDs, n=7) that have been living in stable groups for many years. We focused on individual social network measures based on the toleration of passive close proximity and social grooming and compared these measures between the different deprivation classes. Our study revealed that ex-laboratory chimpanzees were more selective with respect to their toleration of conspecifics close-by subsequent to re-socialisation than were zoo chimpanzees. However, ex-laboratory chimpanzees partially recovered during their second year of group life, indicating that social stability is important for tolerating conspecifics near-by. Social grooming, in contrast, differed significantly between non-deprived chimpanzees and chimpanzees who were traumatized by capture and maternal loss in early infancy, i.e., EMDs as well as ELDs. LLDs did not differ from either NDs or EMDs. Thus, we conclude that early traumatic experiences affect the social integration of chimpanzees throughout their lifetime which becomes evident in their social grooming networks.

OP-BB-10

Stay or leave, help or breed? Decisions in the life of a cooperatively breeding bird

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Helping in facultative cooperatively breeding species is not mandatory, which leads to high variability in life-history traits. A critical decision for an individual's future reproductive success is to stay and help or to disperse. Learning from experienced breeders or getting access to potential mating partners are possible direct fitness benefits prompting individuals to help others on the expense of postponed own reproduction. For group members who are closely related to the brood, indirect fitness benefits can also be a reason to help. We investigated causes and implications of different tactics in the highly variable breeding system of the El Oro Parakeet (*Pyrrhura orcesi*). Decisions were influenced by genetic and environmental factors: Individuals helping at their parents' nest (related helpers) had a lower body mass than individuals which left, but the first year status as related or unrelated helper did not predict future reproductive success. For dispersing individuals, the probability to reproduce increased with the dispersal distance. Males acted more often as helpers and inexperienced male breeders benefited from their partner's experience as a breeder, mainly due to the strong influence of mother's experience on egg survival. Females preferred males with high mean locus heterozygosity irrespective of their experience, indicating that females are able to assess male genetic quality and choose their partner accordingly. We conclude that the advantages of various decisions differ individually and that the best tactic depends on body condition of fledglings, sex and genetic quality.

OP-BB-11

The significance of multi-level sociality in cooperative breeders

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Cooperative breeders serve as models to study the evolution of cooperation and altruism, because in these systems individuals forego own reproduction and expend effort to benefit others, which cuts across fundamental predictions of the theory of natural selection. Until now, most research on cooperative breeding has focused on the group level, despite the fact that many cooperatively breeding species exhibit multi-level sociality. Here we show that different levels of sociality may simultaneously and interactively influence Darwinian fitness of helpers and breeders. The social structure of the cooperatively breeding cichlid fish *Neolamprologus pulcher* comprises two distinct levels: individuals form groups and groups cluster in colonies. Our long-term field data show that larger groups enjoy higher survival and productivity. Groups located at higher densities also benefit from better survival chances, but productivity is interactively influenced by density: larger groups benefit from low densities, while small groups are more productive at higher densities. This outcome is likely caused by effects of competition and cooperation between groups. At high densities, groups frequently engage in territorial conflicts, but our additional experiments show that they can also benefit from the anti-predator behaviour of neighbouring groups. For small groups, the benefits of between-group cooperation appear to outweigh the costs of between-group conflict, whereas this does not apply to large groups. Our results highlight that the exclusive focus on within-group cooperation in the study of highly social animals may limit the understanding of the evolutionary mechanisms underlying cooperation and altruism, because the costs and benefits of sociality may greatly vary between different levels of social organization.

OP-BB-12

Costs and benefits of cognition measured in male laboratory mice

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Short living species such as mice are able to cope with a wide diversity of environmental challenges. The environment an individual is born into may be uncomplex and predictable or cognitively challenging with a wide range of unpredictability. How such differences in life history affect behavioral and physiological parameters is not fully understood. All in all, there are few indications for a vital role of cognitive skills for fitness and mate choice, but measuring costs and benefits of cognition still is a challenging task. The aim of this study was to analyze costs and benefits of cognition and its physiological and behavioral impact on male C57BL/6J mice. For this purpose individuals of the experimental group were exposed to a variety of different cognitive challenges throughout their life. Mice of the control group were exposed to the same environment without being cognitively challenged. We took a number of fitness related measures including female choice, weight development, and measurement of resting metabolic rate in order to evaluate the long term effects of differences in the cognitive demands. First results reveal a lower metabolic rate in the experimental group. In the female choice test, however, females spent least time with the cognitively challenged males. Surprisingly and in contrast to the literature record our study thus shows costs of cognition with regard to lower attractiveness to mates. On the other hand their lowered resting metabolic rate can be interpreted as beneficial with regard to a prospectively enlarged lifespan. We continue our experiments with the same mice in order to investigate if these results can be explained by different life history strategies.

OP-BB-13

Discrimination of vortex ring size by harbour seals (*Phoca vitulina*)

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Harbour seals possess highly sensitive vibrissae that enable them to detect water disturbances and track hydrodynamic trails left behind by prey fish. Most of these trails contain vortex rings as a main hydrodynamic component. They may reveal information about their generator as the trails differ depending on the fish species, the fish's body shape, size, and swimming style. Even single vortex rings, created in C-start escape responses or other natural situations, might convey useful information to a seal. In this study, the ability of a blindfolded stationary harbour seal to perceive and discriminate the size of two single vortex rings has been investigated. As vortex ring size correlates with the size of a potential prey fish it can be considered important information for a seal. In a pool two vortex ring generators were fixed under water on either side of a point directly ahead of the stationary seal. Single vortex rings with predefined sizes, velocities, and accelerations similar to those produced by fish were generated consecutively. One of the two vortex rings travelling to the seal's vibrissae was bigger than the other one. The animal had to identify the bigger vortex ring and responded by pushing its muzzle against one of two response targets in a left/right forced choice procedure. First, the seal was taught a set of three stimulus combinations until it reached a highly significant performance. After introducing completely unknown stimulus combinations the performance stayed at a highly significant level. These results lead to the conclusion that the seal did not merely learn the previously taught stimulus combinations but made its decision based on relative size. The ability to successfully analyse vortex rings regarding their size by using hydrodynamic reception should be advantageous for harbour seals when hunting fish.

OP-BB-14

Harbour seals *(Phoca vitulina)* are able to time precisely

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Time is one of the two fundamental dimensions of life. Living in the marine environment might require a precise sense of time as e.g. tides control access to food as well as haul-out places. Just recently a well- developed sense of time was documented for a harbour seal by discriminating time intervals in the second range. The aim of the present study was to investigate the sensitivity of a harbour seal intervals for millisecond to second time intervals, a time scale crucial for vocalizations or motor control. The experiments were conducted under constant condition inside an experimental chamber. In a two-alternative-forced-choice procedure, the harbour seal was required to discriminate between standard and longer comparison time intervals marked by a white circle on a black background that was displayed on a monitor. Time difference thresholds were determined for five standard time intervals in the millisecond to second range (100 ms, 200 ms, 400 ms, 800 ms, 1.600 ms) by a staircase method. In comparison to the seal's performance with second time intervals, the seal showed a higher precision when tested in the millisecond range. However, in contrast to its performance with supra-second intervals, the millisecond timing abilities cannot be described by Weber's law, which might indicate that different timing mechanisms account for these time scales. To conclude, harbour seals can accurately time in the millisecond range. Millisecond-timing is a fundamental clue seals can rely on for fine movements, motion processing and provide a reliable basis for conspecifics communication, which might even extend to other sensory modalities.

OP-BB-15

Grace of oblivion: Adaptive forgetting in the parasitoid wasp *Nasonia vitripennis*

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Generally, the missing reaction to a previously learned stimulus is considered negative. However, the hypothesis of adaptive forgetting states that the absence of expression of previously acquired long-term memory can be adaptive in variable environments, to deal with conflicting information, or when the reliability of information changes with time. This idea was tested using the jewel wasp *N. vitripennis*, a parasitoid of fly pupae, by studying the reaction to less reliable information acquired during development and more reliable information learned by the adult wasp during host encounters. Wasps received experience with cinnamon odour during different stages of ontogeny and were tested for their reaction to this odour in an olfactometer. *N. vitripennis* showed an attraction to cinnamon after exposure to the odour as larva, during moult from the pupal case, and during emergence from the host. Learning at emergence is most likely due to imprinting as it is restricted to a sensitive phase within the first hour of emergence and results in a long-lasting memory, most likely equivalent to long-term memory. Wasps, which were imprinted to a first odour during emergence and were associatively trained as adult to a second odour during host encounters only reacted to the second odour. Control experiments revealed that wasps, which had been associatively trained in host encounters to two different odours, or to an odour bouquet consisting of both odours, were significantly attracted to both odours. This demonstrates that memory constraints can not be used to explain the missing reaction to the odour learned at emergence. To the very best of or knowledge, this is the first support for the adaptive forgetting hypothesis in parasitoid wasps.

OP-BB-16

High-tech meets ethology: sensor technology helps to describe the foraging and social behavior in a tropical bat species

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Recent technological advances allow for automatized recording of animal behavior in free ranging species. However, this technological revolution still did not reach small vertebrates due to the considerable weight of tags combined with the small body size of the majority of mammalian or avian species. Behavior in bats is particularly difficult to study since sophisticated tracking technology in the required weight class is unavailable. In addition, their lives appear cryptic because of their nocturnal activity and high mobility, which makes direct observation very difficult once they have left their roosting sites. To overcome this issue a sensor network based monitoring system is being developed by the BATS-research unit. The system allows for localization of small animals at high spatial and temporal resolution and the simultaneous documentation of encounters among tagged animals. We use light-weight sensor tags to gain new perspectives on bat sociobiology and to link data on bat interactions in flight to mobility patterns during the nightly activity phase. We present the BATS system architecture and first results from a pilot study on the fringe-lipped bat (*Trachops cirrhosus*). We used the sensor network to study the foraging behavior and identified the fringe-lipped bat as a perch hunter. Furthermore, we documented encounters between adult and juvenile individuals of a social group while foraging. To the best of our knowledge this is the first study that directly documents interactions among mother and pup in free-living bats while foraging.

OP-BB-17

I need you mom and dad: variation in offspring dependency on parental care among burying beetles

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Studies on the evolution of parental care mainly focused on the costs and benefits of parental care and the life-history aspects favouring it. However, once care has evolved, offspring in some taxa seem to become increasingly dependent on their parents. Although offspring dependency can come at high extremes for example in altricial birds and some mammals, remarkably little is known about this phenomenon. Beetles of the genus *Nicrophorus* are well-known to provide elaborate biparental care including food provisioning to their offspring. They present an excellent model system to investigate dependency on parental care as offspring of related species show a clear difference in the magnitude of fitness loss in the absence of parents. By manipulating the presence of pre-hatching and/or post-hatching care, we show that offspring of the three burying beetle species *N. orbicollis*, *N. pustulatus* and *N. vespilloides* show high variation in their degree of dependence on parental care. Our results clearly demonstrate that this variation is particularly caused by a differential need in post-hatching, but not pre-hatching care. While in *N. orbicollis* hardly any larvae survive without post-hatching care, larvae of *N. pustulatus* survive pretty well in the absence of parents. Offspring performance of *N. vespilloides* is better than that of *N. orbicollis*, but worse than that of *N. pustulatus*; hence, the dependency of *N. vespilloides* larvae seems to be intermediate. Our study also highlights the adaptive value of brood size regulation through infanticide in the presence of parental care. While larval survival is higher in the absence of parental care in *N. pustulatus*, larval weight appears to benefit from brood size regulation when parents are present.

OP-BB-18

Fight or Flight? A multi-species study of aphid defence

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With more than 4000 different species worldwide aphids are considered a major pest, especially the generalist among them. A great deal of recent scientific work is focused on defence behaviours of those generalist species, but most of the literature either looks at only few species or only one type of behaviour. Knowledge about the aphid defensive repertoire could help when choosing natural agents for biological control of aphid pests. This study investigates the defence behaviours and species relatedness within the family of Aphididae. For this purpose we collected more than 60 species (140 colonies) in Austria and Scotland and classified their defensive repertoire into 6 different behavioural categories. Physical defence in the form of collective twitching and kicking was found in at least 17 species. 50% and 70% of Austrian and Scottish species respectively show more than one defence behaviour. Individual kicking and chemical secretions were the most employed strategies; 14 colonies utilize chemical secretions alone for defence, whereas individual kicking was almost always observed in combination with other behaviours. Previous studies found that between 33-66% of European aphid species are (facultatively) myrmecophile; out of the 35 Austrian aphid species about 50% (18 species, 31 colonies) were (facultativley) ant tended, in Scotland on the other hand only 20 % (9 species,10 colonies)of 45 collected species were tended. Ant tending seems to be mutually exclusive with some of the other behaviours, whereas chemical secretions go along with all the other behaviours, the same holds true for individual kicking.

OP-BB-19

Wormlions like it dark and do not mind having nosy neighbors

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Wormlions (Diptera: Vermileonidae) are small insect larvae that dig pit-traps in sand and ambush small arthropod prey. We studied their competitive interactions and habitat preference and discovered they prefer fully shaded habitats. However, this preference could be moderated, when the quality of the preferred shaded habitat is lowered by surface obstacles or shallow sand, both limiting the constructed pit's size. Repeatability in pit construction and shade preference lasts for at least three successive days. Wormlions are very tolerant to conspecifics, and we show that abiotic factors are the main factors taken into consideration when choosing a habitat. When forcing two wormlions to compete for space, the larger one reduced its pit size more than the smaller one, not in agreement with other studies on trap-building predators, such as spiders and antlions. We suggest that due to their restriction to specific habitats, they occur in high densities, much higher than antlions or spiders, and have to tolerate conspecifics at very short distances. Finally, in contrast to antlions and spiders, we documented no cannibalism in the laboratory, even when literally feeding a large wormlion with a smaller individual directly into its pit. The absence of cannibalism in this species may help reaching the observed high densities in the field.

PP-BB-01

The effect of different UV-light intensities on the orientation behaviour of the honeybee during waggle dance

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Under natural conditions, honeybees perform their waggle dances on a vertical honeycomb, signalling the angle between a food source and solar azimuth as the angle between dancing direction and upward direction in the darkness of the beehive. If the comb is turned horizontally to exclude gravity as a directional cue, they only show oriented dances in the presence of a light source. It is known that orientation under these conditions depends on the wavelength of the light (Edrich et al. 1979; Rossel, Wehner 1984). When bees are stimulated with a green light spot, dances are oriented as if the light source was the sun, i.e. the angle between dancing direction and stimulus is the same as between solar azimuth and food source. But in the presence of a UV-light spot, the dance directions suggest that the artificial light source is interpreted as coming from a part of the sky opposite to the sun. This is thought to help the bees distinguish between the solar and the antisolar hemisphere when other cues are not available. Here we tested the effect of different UV-light intensities on the dance orientation of honeybees on a horizontal comb. First results indicate that dance behaviour differs between stimulation with high and low UV-light intensities not only in its accuracy, but also in the mean direction of the dance. Dance directions obtained in the presence of high UV-light intensities were similar to those under green light conditions and shifted about 90° compared to dances under low UV-light intensities. The similarity between the responses to high UV intensity and green light might be based on the beta-peak, a second absorption maximum of the green-receptor in the UV range and could ensure robust identification of the sun, the brightest source of UV-light in the sky.

PP-BB-02

Ability of the desert locust to compensate for visual deprivation during the final pre-adult and adult stages

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In the desert locust (*Schistocerca gregaria*), vision is a seemingly indispensable prerequisite for many behavior patterns. The question arises as to whether and to what extent other senses can compensate for the loss of vision, and whether this can take place in the adult stage. To answer this question, both compound eyes (but not the ocelli) of nymphs in the final pre-adult stage were blinded, resulting in permanent visual deprivation during adult life. The results were somewhat surprising: Under laboratory conditions, in comparison with sighted controls, the blind locusts did not exhibit any noticeable change in overall agility relative to daily activity, nor any disadvantage in terms of the final molt, reproductive rate or longevity. In their search for a specific food source in an experimental arena with a narrow passage between the compartment where the animals were released and the compartment containing food, in the first trial, visually deprived females needed significantly more time than the sighted controls. However with an increasing number of trials, each performed after one day of food deprivation, the food finding latency of blind locusts approached or even surpassed that of seeing locusts. The blind locusts used the antennae, mouthparts and tarsi more extensively, pointing to a more frequent use of tactile and chemical cues, which they gradually learned to use more efficiently. The results thus indicate that pre-adult and adult locusts can respond to abrupt, permanent changes in their sensory inputs, and have a significant capacity for adaptation.

PP-BB-03

Female zebra finches recognise their eggs based on olfactory cues

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Parental care or investment to unrelated offspring is maladaptive from an evolutionary perspective, since it comes along with costs, in terms of energy and resources that cannot be invested in related offspring at the same time. Therefore selection should favour a mechanism to discriminate between own and foreign eggs. So far, studies on egg recognition have focused on visual cues, such as egg sparkling patterns. The potential of olfactory egg recognition has been completely ignored. However, recent studies show that eggs emit odourants. Here, we investigated whether egg odorants may enable female zebra finches (*Taeniopygia guttata*) to discriminate between their own and a conspecific egg. Zebra finches are colony breeding songbirds. Eggs are monomorphic, i.e. without any sparkling pattern and intraspecific egg dropping frequently occurs. In an olfactory choice chamber, female zebra finches were given the choice between the scent of their own and a conspecific egg. After the onset of incubation, females choose randomly and showed no sign of discrimination. However, at the end of the incubation period, i.e. shortly before hatching, females preferred significantly the odour of their own egg. Currently we are trying to identify the underlying mechanism by cross fostering eggs between conspecific nests. The aim is to find out whether volatiles on the eggshell or from the inside of the egg could serve as recognition cues.

PP-BB-04

Behavioural flexibility in the chemical defense of the parasitoid wasp *Leptopilina heterotoma*

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Chemical defense is one of the most common and effective defense strategies seen among insects. However, the production of defensive secretions is costly for the producing organism and thus, they should only be used in case of real danger. Females of *Leptopilina heterotoma* produce a mix of iridoid compounds in their mandibular glands with (-)-iridomyrmecin as major component. The wasps use this secretion as a deterrent allomone against predators like ants. However, it remains unknown whether their defense behaviour varies towards different predators and which factors cause a possible variation. Using headspace-analysis, we could confirm that *L. heterotoma* females discriminate between predators varying in size and level of aggression, and adjust the the release of their chemical defensive compounds accordingly. *L. heterotoma* females alone or confronted with non-aggressive *Nasonia vitripennis* females, did not release any iridoids. When attacked by *Myrmica* ant workers, the wasps always sprayed their defensive secretion. However, when attacked by smaller *Cardiocondyla* workers, most females did not release any iridoids, regardless of the duration of the attack. Our data suggest that direct contact with a predator of a certain size is necessary to trigger the chemical defence mechanism of *L. heterotoma.*

PP-BB-05

Signalling patterns and interactions during electrocommunication between real and artificial weakly electric fish

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African weakly electric fish (Mormyridae) use an electric organ in their tail to generate electric fields that are emitted as short, often biphasic pulses. These signals are used for both active electrolocation and electrocommunication, which is supported by the existence of independent types of electroreceptors and central processing pathways for both functions. Variations in inter-discharge intervals have been linked to optimization of sensory acquisition during active electrolocation, as well as to the transmission of behavioural states and intentions during electrocommunication. Mormyrids are known to communicate using distinct temporal signalling patterns as well as by synchronizing their discharge activity with other individuals. In addition, their propensity to follow a mobile fish dummy is strongly increased by playbacks of species-specific pulse sequences. Here, we tested how single individuals of *Mormyrus rume* responded to playback sequences of electric signals that were taken from various behavioural contexts, and which were emitted by a moving electric fish dummy. On average, animals did not adopt the overall interval distribution of the playback, but synchronizations to the different pulse sequences occurred frequently and largely independent of the playback's interval distribution. Fish emitted characteristic double pulse patterns exclusively as a reaction to electrical playbacks, and they occurred more frequently if the playback also featured double pulse patterns. Differences in response were found as a reaction to different playback patterns, as well as between individual fish, suggesting individual dispositions in signalling style, some of which correlated with social rank.

PP-BB-06

Mate guarding as alternative to nuptial gift investment in the tropical bushcricket *Letana inflata* (Orthoptera: Tettigoniidae)

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In many Ensifera species spermatophores are transferred as nuptial gifts to female bushcrickets during mating. These nuptial gifts consist of a nutritious spermatophylax and paired ampulla, containing the sperm. Hereby the spermatophylax acts as a sperm protection device: while the female consumes it, sperm wander into the female’s spermatheca. Additionally ingredients in the spermatophylax provide nutrients to fuel the female’s metabolism. Males of the tropical species *Letana inflata* (Brunner von Wattenwyl, 1878) does not seem to transfer a nuptial gift but mate in mean three hours, which is an exceptional extended period of copulation duration in bushcrickets. We hypothesized that the males save the spermatophylax and present only an ampulla with sperm. To examine whether a spermatophylax or only an ampulla is transferred and when, we separated coupling pairs at different times during mating. We also counted the number of sperm in the female’s spermatheca. Males transfer the ampulla within the first minutes of copulation, without a spermatophylax, while the extended coupling duration corresponds with the time the sperm needs to wander into the female’s spermatheca.Therefore, the elongated mating duration replaces the sperm protecting function of the missing spermatophylax and act as mate guardingin this tropical bushcricket species.

PP-BB-07

Does spatial proximity between Greylag geese families indicate alliance formation?

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Close individual proximity may provide benefits in daily situations like agonistic encounters, access to resources, foraging and protection from predation. Furthermore it is a pre-requisite for cooperation. In the present study we consider proximity to conspecifics during resting-periods as an indicator for social tolerance. We investigated spatial proximity between the Greylag geese families (*Anser anser*) of the semi-tame and individually marked flock of the Konrad Lorenz research Station (Austria). Greylag geese live in a complex social system, with goslings staying with the parents for an entire year and benefiting from social support. Previous studies investigating spatial proximity in geese provided evidence for long-term bonding among related females. A total number of 382 distance protocols were collected from 12 goose families in summer 2014, with the number of goslings per family ranging between 1 and 8 (mean = 3.25). Collected data included the distances between the parents and their offspring, the distances to the other families as well as the distance to the closest individual which did not belong to any of the 12 families. The resting locations were monitored too. The number of observations per family ranged from 21 to 41 (mean ± SE = 31.8 ± 1.75).Our results indicate that some families have clear preferences for specific families over others, whereas other families seem to be indifferent. We discuss our findings with respect to social bonding and alliance formation, preferences for a particular common resting place (i.e. philopatry) as well as to kinship between the parents.

PP-BB-08

Evoking ‘Echo Response’ in weakly electric fish by an interactive fish dummy

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African weakly electric fish (Mormyridae) communicate by varying the temporal pattern of their electric organ discharges (EOD). The inter-discharge intervals (IDI) deliver information about the sender’s behaviour like resting, swimming or feeding. In certain social contexts, special electric patterns occur, for example acceleration patterns, which have been associated with aggressive displays. An often observed behaviour is the so-called echo response: a fish produces an EOD with a fixed latency after an EOD of another fish. Here, we wanted to answer the questions whether echo responses carry communicative information and how a fish responds to echoes of a conspecific. To analyse electric and motor reactions to echo responses in *Gnathonemus petersii*, we created a fish dummy, which was able to reply to a real fish’s EOD with an echo at the species-specific delay of 12 ms. For comparison, the fish were also confronted with non-interactive aggressive and resting playbacks emitted by the dummy. The fish reacted to all three playback types with high discharge frequencies and acceleration patterns. IDI-modes averaged at about 24 ms, which corresponds to a frequency of 41.7 Hz. All playback types initiated echo responses in the fish tested. However, by far the most echoes were elicited during the interactive echo-playbacks. The aggressive playbacks evoked a few more echoes than the resting playbacks. Cross-correlation-analysis showed that the fish correlated their signals with the echoing dummy, whereas there were only few correlations with the resting and aggressive playbacks. Our results suggest that the echo response carries communicative information and evokes specific responses in receiving fish.

PP-BB-09

Female cuticular hydrocarbon signals initiate courtship behavior in grasshopper males

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Males and females may select potential mates based on a single cue or may use a whole array of signals to make a decision. Signals can consist of several components within the same sensory modality, or of components involving different sensory channels (multicomponent and multimodal signals, respectively). Gomphocerine grasshoppers, which have been extensively used as model systems for acoustic communication, use species-specific calling songs for sex recognition and mate attraction and provide a potentially interesting system to study multicomponent signaling. The acoustic signal has on close range only a minor impact on the fertilization rate of *Chorthippus* females, indicating that additional communication channels exist and are decisive for mating success. Here we developed a bioassay for grasshoppers to determine if an additional communication channel via cuticular hydrocarbons (CHCs) exists and if grasshopper males use this information for mating decisions (i.e whether or not to court a female). We used two closely related species, *C. biguttulus* and *C. mollis*, in which acoustic communication is so far the only described communication channel. The results of this approach provides evidence that males of *C. biguttulus* and *C. mollis* are able to extract species- and sex-specific information from CHC signals and respond with a courtship song to the odor of conspecific females but not to odors of heterospecific females. Therefore, we conclude that males of *C. biguttulus* and *C. mollis* use multimodal channels for mating decisions, based on acoustic and olfactory cues.

PP-BB-10

Task efficiency and fanning behavior in bumblebees

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The ecological success of social insects is often attributed to division of labor, specifically to an increase in colony efficiency when individuals specialize and perform only a subset of all tasks. One possible explanation for such an increase in colony efficiency is that individual workers show behavioral plasticity and perform a task with higher efficiency with increasing experience. Experiments testing this hypothesis, especially in tasks that are not foraging-related and thus not associated with a sugar reward, are scarce. In this study, we use thermoregulation in bumblebees as experimental system. Bumblebees are able to actively regulate the temperature of their brood by either incubating (warming) or fanning (cooling). We address the question whether fanning bumblebee workers assess their own task efficiency (cooling of the brood) and whether task efficiency modulates individual fanning behavior. We present a new setup that allows measuring and manipulating the cooling efficiency of individual workers. We show that indeed the immediate fanning response is modulated based on the impact of fanning behavior on brood temperature, indicating that workers assess and respond to their own task efficiency.

PP-BB-11

Living in a 3D world: Depth perception in nocturnal hunting spiders investigated with Virtual Reality technique

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Cupiennius salei is a nocturnal hunting spider that serves as important model system in neurobiology, developmental biology and bioengineering. Equipped with highly adapted eyes, vision is very likely to play an important role in their life. Previous experiments confirm that vision is important in behavioral contexts like hunting and navigation and can be used for object discrimination. Neither of the four eye pairs shows binocular overlap, making stereopsis an unlikely mechanism for sensing distances. *C. salei* shows zig-zag-like walks that induce motion cues that potentially serve as depth cues. Our results from depth discrimination experiments suggest that self-induced motion parallax in combination with a structured background allows discrimination of objects placed a different distances. To overcome limitations of the real world arena setup and avoid potential influence of other depth cues we designed a Virtual Reality (VR) setup. The spider walks on top of an actively driven sphere that compensates for its movement. Further, a virtual environment is projected around the spider onto a circular screen (360° horizontal & 50° vertical field-of-view). The projection is updated in real time to create a real VR in which the spider can move freely. The SpiderVR allows to separate potential depth cues (e.g. absolute and relative size differences, retinal expansion, motion parallax) and test their relevance independently. The experiments confirm that motion parallax is used by the spiders to discriminate distance in their environment.

PP-BB-12

One more or less matters in nestmate recognition of ants

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In ants, discrimination between colony members (nestmates) and members from a foreign colony (non-nestmates) is of fundamental importance to protect the colony's resources from being exploited. The discrimination is based on many low-volatile chemical components on the ants' body (CHCs). Through frequent exchanges of CHCs between nestmates, the colony odor is uniformed. The current concept, describing the process of nestmate recognition is a label-template matching, in which the colony odors (labels) are compared to a neuronal representation of the own colony odor (template). Mismatches between label and template cause aggressive responses. Importantly, colony odors change over time, which requires template adjustment. We manipulate colony odors by adding one or two CHCs to subcolonies, and we keep one subcolony without manipulation, as reference. Using GC-MS, we verify our treatments of adding component(s) to the CHC profile. In behavioral experiments, we test how ants react to each other, after receiving different treatments. Ants with added components in their CHC profile do not only accept their nestmates, but they also still accept (do not respond aggressively) ants from the reference subcolony. Thus, the old label still contains valid nestmate cues for several days, as has been shown previously. Our experimental design also allows testing if a missing component of the currently valid label (two components added) elicits an aggressive response. This indeed is the case, and it rules out that label-template matching can be incomplete with missing components of the label being of little importance (inclusion theory). Our results strongly indicate that colony odors are recognized rather as entities than as the sum of single components.

PP-BB-13 - Do honey bees share food equally in cages?

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Caged honey bees (Apis mellifera) are used to investigate pesticide toxicity. We estimated the distribution of sugar solution within groups of caged honey bees under standard in vitro laboratory conditions using ^{14}C polyethylene glycol as a marker to analyze consumption of each bee after group feeding. We evaluated the impact of different experimental setups varying in number of bees, age, origin of bees, duration of experiment, the amount of applied sugar solution and the influence of pesticide in sugar solution on the feeding and food sharing behavior. We found that labelled sugar solution was unequally distributed in bees in 36 of 135 investigated cages (Kolmogorov-Smirnov, $p<0.05$). As equality parameter, we calculated an intake ratio by dividing the intake of the 90th percentile bee by the intake of the 10th percentile bee. By doing so, we trimmed the distribution to the inner 80% to eliminate outliers. These intake ratios ranged from 1.3 to 94.8 in 133 cages, 8.8 on average, further supporting an unequal distribution of food among caged bees. Additionally, we investigated the food sharing behavior (trophallaxis) of caged honey bees by itself. Therefore, starved and marked bees were added to the cages in a ratio of 10:5 or 20:20 after the initial set of bees consumed all the labelled sugar solution. The transmission of this labelled food by trophallaxis within 48 hours to added bees was 26.3% (10:5) or 45.1% (20:20) of the initial sugar solution. Imidacloprid in median lethal dose in the sugar solution reduced this post-feeding food transmission to 27.1%. Our results show that differences in food intake exist within caged bees that may lead to biased results in toxicity tests. A more natural setting for caged bee experiments may reduce this bias.

PP-BB-14

Comparison of two slave-making ant species *Polyergus rufescens* and *Formica sanguinea* concerning their pupae-acceptance and the behaviour of their slaves

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The two European ant species *Polygergus rufescens* and *Formica sanguinea* enslave other ants of the subgenus *Serviformica*. *P. rufescens* is an obligatory slave-maker, whose workers are unable to breed pupae or to eat by themselves. In contrast to that, *F. sanguinea* is a facultative slave-making ant. To investigate differences in behaviour of these two species, we relocated pupae (5 replicates a' 10 pupae per group) and observed behaviour of eclosed slaves (n = 20 focal observations per group). The comparison of *P. rufescens* and *F. sanguinea* concerning their pupal acceptance shows that *P. rufescens* is able to distinguish between different host species: fewer pupae from the other slavemaker, *F. sanguinea* were accepted, than from *Formica fusca* or *Formica lusatica,* their natural host species (p<0.01, Mann-Whitney). In contrast, *F. sanguinea* did not differentiate between the pupae of *P. rufescens*, *F. fusca* and *F. lusatica* (p>0.05). Focal observations of *P. rufescens, F. fusca* and *F. lusatica* eclosed in the nest of *P. rufescens* and observations of *F. sanguinea, F. fusca*, *F. lusatica* and *P. rufescens* in the nest of *F. sanguinea* demonstrate, that *P. rufescens* is a completely useless slave. They show less and shorter breeding behaviour (p<0.01, Mann-Whitney) but more and longer ducking down, a submissive behaviour, than other enslaved ant species (p<0.01). Pupae of *F. sanguinea* did not eclose in the nest of *P. rufescens*. Our experiments suggest, that the obligatory slave-maker *P. rufescens* is better adapted to enslave other ants than the facultative slave-maker *F. sanguinea*, because *P. rufescens* is able to distinguish between different host species and is completely useless as a slave itself.

PP-BB-15

Trinidadian guppies differ consistently in their following tendencies towards a biomimetic robot

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In recent years, simple biomimetic robots have been increasingly used in behavioral research to investigate animal social behavior, like mate choice or collective movement. In my presentation, I will outline (a) the Robofish system developed at the Freie Universität Berlin in cooperation with the Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB), (b) recent advances in the acceptance of Robofish by live Trinidadian guppies, and (c) experiments on leadership using the Robofish. Our results indicate that realistic eye dummies and natural motion patterns drastically improve the Robofish acceptance. Experiments using the Robofish as a leader to guide single guppies as well as small groups (2 and 4 live individuals) further show that individuals differ consistently in their tendency to follow the Robofish. These differences also correlate with differences in the tendency to follow live guppy leaders. However, behavioral types of the tested guppies (i.e., their boldness, activity and sociability) did not predict their following behavior. These results have strong implications for the study of social organization of animal groups and especially leadership phenomena.

OP-DB-IT-01 - Sex, brains and spawning behavior: Investigating molecular regulation of sexual differentiation in a slowly-evolving model.

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Sexual reproduction is essential for the survival and propagation of most organisms on earth. Yet in these animals, we know very little about the molecular mechanisms that regulate sexual dimorphisms. The genetic mechanisms that govern sexual differentiation of the reproductive system have been explored for a few classical molecular model systems. However, we still know relatively little about the molecular pathways that determine sexual dimorphisms in somatic tissues, particularly in the brain, and how these relate to the control of male and female behaviours that are required for successful reproduction. We are exploring the marine polychaete *Platynereis dumerilii* as a new, genetically tractable model system to study how sexual dimorphisms important for reproduction have evolved. *P. dumerilii* are particularly suited to addressing this question as they are slowly-evolving compared to conventional molecular models (eg *D. melanogaster* and *C. elegans*) and are thus likely retain molecular and physiological pathways comparable to both vertebrates and invertebrates. Males and females develop as separate individuals in *P. dumerilii*, yet there are no discernable sex chromosomes in this species and sexually mature worms do not develop discrete gonads typical of other reproductive systems. Nonetheless, males and females display distinct sexual dimorphisms from the level of germline differentiation, to epitoke morphology and spawning behaviours. We take advantage of molecular and functional tools established in *P. dumerilii* to identify and study molecular pathways that regulate sexual dimorphism in the brain as worms undergo sexual maturation. To investigate the molecular differences between sexes, we have conducted transcriptomic profiling of heads during sexual maturation. These data revealed around 500 transcripts differentially expressed between males and female heads. To complement this molecular approach, we are also establishing quantitative assays to characterize sex-specific behaviours. Our aim is to combine these techniques with the recently established functional tools in *Platynereis* to study how sexually dimorphic molecular and neuronal pathways regulate physiological and behavioural functions *in vivo*.

OP-DB-IT-02 - The Wnt morphogenetic field: Ligand transport, advection, and signaling

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After secretion, developmental signals known as morphogens must travel relatively long distances to form a concentration gradient that the responding tissue uses to acquire positional information. The role of morphogen transport and endocytic trafficking in this process is the subject of intense debate. Wnt proteins regulate developmental processes, tissue regeneration and stem cell maintenance. It has been postulated that Wnt/β-catenin signalling form concentration gradients across responsive tissues and act as morphogens. However, little is known about the transport mechanism for these lipid-modified signalling proteins in vertebrates. Here we show that Wnt8a is transported on short, actin-based filopodia to contact responding cells and activate signalling during neural plate formation in zebrafish. Cdc42/N-Wasp regulates the formation of these Wnt-positive filopodia. Enhanced formation of filopodia increases the effective signalling range of Wnt by facilitating spreading. Consistently, reduction in filopodia leads to a restricted distribution of the ligand and a limited signalling range. Using a simulation, we provide evidence that such a short-range transport system for Wnt has long-range signalling function. After contact by Wnt/β-catenin positive filopodia, a multi-protein complex at the plasma membrane assembles clustering membrane-bound receptors and intracellular signal transducers into the so-called Lrp6-signalosome. Our imaging studies in live zebrafish embryos show that the signalosome is a highly dynamic structure which is continuously assembled and disassembled by a Dvl2-mediated endocytic process. We show that this endocytic process is not only essential for ligand-receptor internalization but also for signaling. We conclude that a filopodia-based transport system for Wnt and subsequent endocytosis is important for Wnt/β-catenin signaling and controls anteroposterior patterning of the neural plate during vertebrate gastrulation.

OP-DB-01

Expression of "segment polarity genes" in brachiopod larvae reveals convergent similarities to protostome segments and deuterostome brain boundaries

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The evolution of animal segmentation is a long standing topic in evolutionary biology. Developmental studies revealed that segmentation mechanisms are diverse and complex, but can share striking molecular similarities. Whether these similarities represent convergent evolution or the inheritance of segmentation mechanisms from the bilaterian ancestor is still debated. Because most studies focus in organisms considered to be "truly segmented" it remains unclear what the common "segmentation genes" are doing in other groups. In order to address this issue and expand the comparative data on segmentation we use the brachiopod larvae as a showcase for investigating "segment polarity genes" in the segmented mesoderm and ectoderm of two species. Our results on the expression of *en*, *wnt1* and the Hedgehog pathway reveal that *hedgehog* is unrelated to any developmental boundaries, and that the ectodermal boundary between the apical and mantle lobes is demarcated by the adjacent expression of *en* and *wnt1* strikingly similar to the parasegment boundaries of arthropods. We further investigated factors known to regulate *en* expression during the establishment of boundaries in the neuroectoderm of vertebrates. We found that *pax6*, *pax258* and *en* expression correlate spatially and temporally with the apical/mantle boundary in a similar manner as observed in the di/mesencephalon boundary of the vertebrate brain. Our results suggest that the molecular profile at the apical/mantle boundary is more similar to the vertebrate brain than to the arthropod segments. Our finding that the adjacent expression of *en*/*wnt1* can occur in a non-metameric boundary suggests that these genes might have an ancient role in boundary formation not connected to segmentation.

OP-DB-02

Analyzing the Pair Rule Gene Network in the Spider *Parasteatoda tepidariorum*

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Pair rule genes are part of the *Drosophila* segmentation gene cascade. They divide the developing embryo into the first metameric units. Their complementary expression patterns, characterized by a series of seven stripes, and loss-of-function phenotypes occur in a two-segment periodicity. The pair rule genes can be divided into primary (activated by gap genes) and secondary (activated by the primary) pair rule genes. These expression patterns are somewhat conserved within the holometabolous insects but outside this group divergence in expression and function is rapidly progressing. However, the division of pair rule genes into primary and secondary ones seem to be conserved based on the timing of expression. We have analyzed the expression of the pair rule gene orthologues *fushi-tarazu* (*ftz*), *runt*, *even-skipped* (*eve*), *pairberry* (*pby*), *sloppy-paired* (*slp*) and hairy (*h*) in the growth zone of the spider *Parasteatoda tepidariorum.* We confirm a division into primary and secondary pair rule genes. Furthermore, partly fluorescent double-in situ hybridization shows the relative expression of these genes to each other, revealing differences in the fine tuning of these genes compared with other arthropods. We have established a reference system, based on the expression of the segment polarity gene *hedgehog* (*hh*), which allows the comparison of expression patterns across embryos of the same developmental stage. Analysis of fluorescent in situ hybridization with confocal imaging can be used to distinguish ectodermal and mesodermal expression of pair-rule genes in the growth zone of the spider. This shows that pair rule gene segmentation mainly acts in the ectodermal layer. Finally, we perform functional analysis of *Parasteatoda* pair rule genes using RNA interference (RNAi) and CRISPR/Cas9 genome editing.

OP-DB-03 - Investigating the role of embryonic appendage patterning genes in the postembryonic development of the male pedipalp of the spider *Parasteatoda tepidariorum*

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The genetic factors that control size and shape during animal development are partially known in a few model species, but the evolutionary modifications of these mechanisms that have resulted in novel morphologies and body plans remain largely unknown. Using the male pedipalp of the spider *Parasteatoda tepidariorum* as a model, we investigate the genetic factors that determine the morphology of this complex copulatory organ. This copulatory organ is an evolutionary novelty that only exists in spiders (so-called autapomorphy). Especially interesting is the fact that the shape of the male pedipalp in spiders is species specific and thus directly links developmental genetic mechanisms with mechanisms of species recognition and speciation. In addition, the species specific morphology of the pedipalp forms only during postembryonic development within a single molt. Thus, the development of the male pedipalp represents a form of metamorphosis. Which genes regulate this postembryonic developmental process? And how do they control the specification of the species specific morphology? Recently, we discovered that a gene that has an essential role in distal appendage formation during embryonic development, namely the gene *Distal-less*, is required for distal development during the metamorphosis of the male pedipalp as well. Genes that play a role during embryonic appendage development may thus reprise this role also later during postembryonic development. We want to investigate this hypothesis further using additional appendage patterning genes already identified in *P. tepidariorum*. The project comprises two aspects: first, all Hox genes expressed in the embryonic pedipalp segment will be investigated as to their expression and function during pedipalp metamorphosis. Hox genes determine the identity of body segments in arthropods and therefore may play a role in the specification of pedipalp identity during metamorphosis. Second, we will investigate selected embryonic appendage axis patterning genes. This includes the mentioned *Distal-less* gene, but also additional genes that have been identified so far that are expressed in the distal, medial and proximal portion of the appendages. The results will for the first time provide important insight into the genetic control of postembryonic development of the male pedipalp in spiders. The data will also form the basis for comparative studies in additional spider species in order to link changes in the developmental genetic mechanisms with evolutionary alterations of species specific morphology.

OP-DB-04 - Adhesive organs of a marine flatworm as a new model system for post-embryonic organogenesis

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Regeneration has fascinated researchers for more than hundred years, but still a lot of questions remain. One problem to overcome is the limited number of valuable model systems for post-embryonic organogenesis. The adhesive organs of the marine flatworm *Macrostomum lignano* are a useful model system for *de novo* organ regeneration. *M. lignano* exhibits approximately 130 adhesive organs, to attach and stabilize itself to the substrate. In a previous study we described the morphology of these organs on ultra-structural level. One adhesive organ consists of solely three interacting cells, two secretory cells and one modified epidermal cell. When amputated the organs regenerate completely within 9 days. Using cell type specific lectin- and antibody staining, as well as transmission electron microscopy, we analyzed the morphology of the adhesive organs during different regeneration stages. We have generated an RNAseq dataset at different time points of tail regeneration and currently we identify and characterize transcripts involved in the differentiation of the adhesive system. Our findings contribute to a better understanding of organogenesis in flatworms and enable further molecular investigations of cell-fate decisions during regeneration.Supported by the Austrian Science Fund: [P 25404-B25]. BL is a recipient of a DOC Fellowship of the Austrian Academy of Sciences

OP-DB-05

Actin dynamics and the formation of animal shape in *Hydra*

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Bending of 2D cell sheets is a fundamental morphogenetic mechanism in creating body shape during metazoan development. Much of our current knowledge about tissue bending comes from embryonic development in bilaterian model organisms, while asexual reproduction and regeneration particularly in lower metazoans have been neglected. Tissue bending is generally based on spatially and temporally coordinated cellular activities such as cell shape changes and cell motility, and the actin cytoskeleton has been shown to be the most important and dynamic player controlling shape and motility of animal cells. Here, we have analysed dynamic actin-based processes *in vivo* during asexual bud evagination in the simple metazoan *Hydra*. We created transgenic *Hydra* strains stably expressing Lifeact-GFP proteins in ectodermal and endodermal epitheliomuscular cells, and we also used conventional phalloidin-staining on fixed specimens. By combining these techniques, we were able to track actin dynamics at an almost molecular resolution. We found that bending is initiated by a group of endodermal epitheliomuscular cells, which decrease their apical-basal dimension and reorganise their basal myonemes in circular arrangement. We propose that contractility of these endodermal myonemes participates in producing the momentum to bend the endodermal towards the ectodermal tissue layer. Convergent tissue movement in both epithelial layers towards the centre of evagination then leads to elongation and extension of the bud along its new body axis. Movement into the bud is associated with lateral intercalation of epithelial cells and extensive reorganisation of the actin cytoskeleton. Basal myonemes in both layers detach from the mesoglea and rearrange in distinct patterns to attain proper polarity according to the bud's new body axis. Remodelling of apical septate junctions in the ectodermal layer occurs in an arrangement that resembles the remodelling of adherens junctions during bilaterian convergent-extension movements. The work presented here aims at providing a framework of bud morphogenesis underlying future molecular studies and at extending the analysis of shape creating processes beyond embryonic tissues of model bilaterians.

OP-DB-06 - Something to die for - Inhibition of the p53-Mdm2 interaction increases programmed cell death in the placozoon *Trichoplax adhaerens*

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Trichoplax adhaerens is the only species in the phylum Placozoa and its position in the Tree of Life is controversially discussed. Even though it is the simplest living animal, consisting of only two cell layers and five cell types with no nerve-, muscle- or sensory cells, the genome exhibits a rich component of regulatory genes. The identification of gene homologs of the human p53 and Mdm2 in *Trichoplax* was a big surprise and raises the question whether the network undertakes the same functions in the most primitive metazoan organism as it does in higher animals. Here, we describe inhibition experiments on the p53/Mdm2 interaction in *Trichoplax adhaerens* by applying the inhibitors nutlin-3 and roscovitine. Both inhibitors had a strong impact on the animals' survival by significantly increasing programmed cell death. Treatment with roscovitine decreased cell proliferation, which is likely reducible to its function as cyclin-dependent kinase inhibitor. Obvious phenotypic abnormalities have been observed during long-term application of both inhibitors and either treatment is highly lethal in *T. adhaerens*. Additionally, p53 gene knockdown experiments were performed with morpholino antisense nucleotides. The decrease in body size and reproduction underlines the importance of p53 for the organism's integrity. The findings of this study suggest a conserved role of the p53/Mdm2 network for programmed cell death since the origin of the Metazoa and advocate the deployment of Placozoa as a model for p53, apoptosis, and possibly cancer research.

OP-DB-07

Role of nuclear lamin protein in non-senescent Hydra

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Unlimited lifespan of the basal metazoan *Hydra* has long attracted researcher's attention. While indefinite self-renewal capacity of stem cells in *Hydra* is recognized fundamental for its non-senescence, the underlying molecular mechanisms have been poorly explored. The nuclear envelope intermediate filament proteins of the lamin family play a major role in maintaining stem-cell activity and controlling lifespan in vertebrates. Age-related decrease in lamin B expression promotes cellular senescence and causes organism ageing. Moreover, mutations affecting either structure of lamin proteins or their expression level are proved to cause diverse degenerative diseases (laminopathies) and premature ageing phenotypes. Presence of multiple lamin genes and splice variants in higher vertebrates and complex network of their interactions hamper the elucidation of lamin functions in vertebrates. A single lamin protein (HyLMN) is coded in the genome of *Hydra*, providing a unique possibility for deep *in vivo* functional analysis of the gene. Expression analysis indicated that HyLMN protein is present in virtually all *Hydra* cells, while transcription of *hyLMN* gene is restricted to stem cells only. Functional analysis by transgenesis revealed that overexpression of HyLMN results in uneven distribution of lamin in the nuclear envelope, and gravely affects nuclear morphology. Surprisingly, the abnormal structure of nuclear lamina does not affect transcriptional profile and mitotic activity of Hydra stem cells. These findings point to an extraordinary independence of *Hydra* stem cells from nuclear envelope architecture. We propose that this may be one of the mechanisms underlying the unlimited self-renewal capacity of *Hydra* stem cells.

PP-DB-01

WNT/b-Catenin target genes in *Hydra* patterning and regeneration

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The Wnt/b-Catenin pathway plays a crucial role in developmental and regenerative processes and shows high conservation of structure and function of its signaling components. In cnidarians, Wnt/b-Catenin signaling acts in the formation of a head/blastoporal organizer, establishing positional information along the body axis of cnidarian polyps. How this positional information affects cell behavior is largely unknown. In a systematic expression profiling of Wnt/b-catenin target genes, we identified a candidate list of 10 putative direct target genes of this pathway. Whole mount *in situ* hybridizations showed spatial expression patterns in the hypostome, in the tentacles, or in an apical gradient in the body column - areas that most likely represent the presence of secreted Wnt proteins. To uncover direct binding of Tcf/b-catenin to the enhancer regions, CHIP analyses are performed using an α-*Hydra*Tcf antibody confirming that the candidates are regulated directly. Expression of target genes is affected by Alsterpaullone-treatment and in b-Catenin transgenic polyps. Notably, all target gene candidates show significant transcriptional up-regulation restricted to the regenerating tip within the first hours during head regeneration. The regenerating tip is known to exhibit an equivalent activation of b-Catenin itself starting within the first hour after onset of regeneration. Hence all candidate target genes seem to be directly controlled by b-Catenin also in regenerating tissues. In order to test b-Catenin and its target genes on a more functional level, we have started to apply newly available pharmacological inhibitors directed against nuclear b-Catenin activity, and preliminary results show clear inhibitory effects on head regeneration.

PP-DB-02

Molecular characterization of highly derived *MYC3* and *MYC4* protooncogenes in *Hydra*

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Myc proteins arose at the basis of metazoan evolution. They show high oncogenic potential and execute crucial functions in cell-proliferation, apoptosis, development, and metabolism. While members of most animal phyla exhibit one *myc* gene, this gene family diversified for so far unknown reasons in vertebrates and cnidarians. *Hydra* encodes four *myc* genes. *Hymyc1* and *Hymyc2* have been well described. The corresponding proteins are similar in structure and function when compared with vertebrate c-Myc. Their expression dynamics in the *Hydra* polyp indicate that they act in controlling cell proliferation and stemness. Here we have focussed on the characterization of *Hymyc3* and *Hymyc4.* Molecular phylogenetic trees show that these two *myc* genes are the result of a rather recent gene duplication event. They encode proteins with highly derived N-terminal parts that show no Myc boxes. Their C-terminal DNA binding domains are, in contrast, well conserved. Whole mount *in situ* hybridizations revealed *hymyc3* as interstitial stem cell marker; it is specifically expressed in interstitial stem cells (1s+2s) and in very few nematoblast nests. Heat shock in A10 polyps completely eliminates *hymyc3*-positive stem cells within 48 hr. *hymyc4* seems to be expressed at a very low level throughout the endoderm, with no occurrence in interstitial cells. We currently study, to what extent these two derived *myc* genes are regulated by canonical Wnt signaling. Overall, functional aspects of *myc*-genes in *Hydra* are poorly understood at present, but have the potential to contribute to a more detailed understanding of stem cell decision making.

PP-DB-03

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

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While the general bauplan of an arthropod appendage is highly conserved differences in how they are formed during embryogenesis differ between species. In the fruit fly *Drosophila*, the leg originates from the imaginal disc that is internalized within the larval body and everts only during pupation. At the contrary, embryos of *Tribolium* and vertebrates display everted limb buds and cell proliferation and cell shape changes contribute to their distal outgrowth. To date, the initial decision of invagination vs. evagination of the limb primordia is not yet understood at the molecular level.

To analyse this crucial aspect of early appendage development we describe here in *Tribolium* the functional analysis of candidate genes with an inverted appendage knock-down phenotype. The gene *Tc-flipflop* (*Tc-ff*) was identified in the genome-wide RNAi screen iBeetle. *Tc-flipflop*^{RNAi} results in inverted but otherwise fully developed legs forming inside the larval thorax rather than growing outwards. This phenotype becomes apparent already in early embryogenesis during limb bud formation. *Tc-ff* codes for a novel, 136 amino acid long protein and no obvious homolog was found so far in another sequenced genome. Intriguingly, *Tc-RhoGEF2*-RNAi resulted in a phenotype similar to that of *Tc-ff*, indicating the involvement of Rho associated signalling in the early evaginating limb bud. We will further analyse the function of *Tc-flipflop* and other candidate genes at both, the cellular and the molecular level in order to better understand the decision between evagination vs. invagination.

PP-DB-04

The role of Blow during *Drosophila* myoblast fusion and its regulation

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During *Drosophila* myogenesis two different types of myoblasts the founder cells (fc) and fusion-competent myoblasts (fcm) fuse to form the larval body wall musculature. The recognition and adhesion of the myoblasts leads to a dynamic reorganisation of the actin cytoskeleton in both myoblast types. This reorganisation is essential for the progression of fusion. Actin polymerisation on the site of cell-cell contact is mediated by the evolutionary conserved Arp2/3 complex which leads to the formation of a thin actin layer in fcs and a dense actin focus in fcms. The nucleation promoting factors Scar and Wasp are both responsible for the activation of the complex during fusion. Wasp is only required in fcms, but Scar is expressed in both cell types.

The fcm-specific protein Blow has been implicated to play a role during Scar and Wasp dependent Arp2/3 activation (Schröter et al., 2004, Jin et al., 2011). Ultrastructural analysis exhibit that *scar* and *wasp* mutants stop fusion during membrane breakdown whereas *blow* mutants stop prior to membrane breakdown when electron-dense vesicles are recruited to the membrane at the site of cell-cell contact. Since the function of Blow remains unclear we performed a yeast-two-hybrid screen to identify new potential interacting partner. Here we present the expression pattern of first potential interacting partners and preliminary interactional analyses.

PP-DB-05

Kette and WASP act antagonistically during F-actin formation in fusion competent myoblasts

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The formation of skeletal muscles depends on intercellular cell-cell fusion composed of mutual recognition and adhesion between myoblasts resulting in membrane fusion. In *Drosophila* two types of myoblasts, the so called founder cells (FCs) and fusion competent myoblasts (FCMs) fuse to form a mature muscle (reviewed in Abmayr and Pavlath, 2013). Both cell types show different shapes and behaviors during the fusion process especially in formation of F-actin at the site of fusion. While FCs show a rather thin actin sheath a thick actin focus can be observed in FCMs, indicating a difference in their regulation of generation. Essential for their formation is the F-actin nucleating Arp2/3 complex. Extensive studies on this Arp2/3 based actin polymerization during myoblast fusion have shown that the activation of the Arp2/3 complex depends on the nucleation promoting factor (NPF) SCAR (WAVE) in FCs and on the activation of both NPFs SCAR and WASP (Wiskott-Aldrich syndrome protein) in FCMs. The activity of SCAR is controlled by the SCAR complex which consists of 4 proteins including Kette (Hem-2/Nap-1). The loss of *kette* results in severe myoblast fusion defects in homozygous null mutant embryos. Recently, we generated *kette wasp* double mutants (Schäfer et al. 2007). Homozygous *kette wasp* double mutant embryos display a *kette*-like phenotype. However we observed a suppression of the *kette* mutant phenotype when the *wasp* gene dosage was reduced. This suggests an antagonizing effect of Kette on the activity of the WASP pathway. Here we present first genetic experiments to determine the coordination of *scar* and *wasp* dependent Arp2/3 activation in FCMs.

PP-DB-06

Macrostomum lignano - head regeneration through gene silencing

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There is a great variability in the regeneration capacity of animals, some can regenerate all body parts, such as cnidarians and several flatworms, while many others are unable to regenerate more complex structures, such as most mammals. In triclad flatworms regeneration research has been carried out for many centuries. Most species of these animals can regenerate a whole body from small pieces. Previous studies have shown that some regeneration deficient triclad species are able to regenerate a head from posterior pieces through silencing of β-catenin. β-catenin plays an important role in the canonical Wnt-signaling pathway and it is suggested that this pathway is taking part in the anterior-posterior regeneration blastema polarity. Here we use the basally branching flatworm *Macrostomum lignano* as an organism to study and rescue head regeneration in a regeneration deficient flatworm that is phylogenetically distant from the triclads. If head regeneration can also be rescued in *M. lignano* through silencing of β-catenin, this would imply that the pathway leading to head regeneration is conserved within the rhabditophoran flatworms and has been independently and repeatedly lost in several flatworm groups.

OP-E-IT-01

Predators and their prey -a phenotypic approach

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A fundamental approach in understanding complex biological diversity is to study the interaction of individuals and their environments. Predators represent a constant threat for organisms in almost all habitats, structuring occurrence and abundance of prey communities. Only recently, however, has the impact of predators in generating phenotypic diversity been acknowledged. This is surprising considering the plethora of defensive traits prey has evolved, with characteristics and expression of traits differing along fine-scaled predation gradients. Freshwater habitats, which typically vary in top-predator assemblages, offer a great opportunity to study the interaction of predators with their prey and their impact on phenotypic evolution. Here, I summarise antagonistic and relaxed selection by vertebrate and invertebrate top-predators causing phenotypic trait diversification in morphology, behaviour and physiology using a suite of dragonflies. I highlight that studying predator-prey interaction and trait diversification will benefit from an integrated approach focusing on multiple trait relationships. Understanding multiple rather than just single trait changes will enhance our understanding of phenotypic evolution as well as how networks of traits mediate trophic interactions, community structures and food web dynamics.

OP-E-IT-02

Arthropods on fungi: from patterns to chemical and molecular mechanisms

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Feeding on fungi is wide-spread among arthropods. Yet, fungi differ in the benefit they provide to animals. A wide-spread assumption is that fungi vary in palatability because of differences in their chemical anti-grazer defence arsenal. This assumption, however, is only little supported by experimental evidence. We use a combination of organismic, biochemical, and molecular genetic approaches to test for the involvement of mechanisms regulating toxin-formation in the defence of fungi against arthropod. I will present data showing how far we got with identifying causal links between fungal toxin formation and animals responses. I will outline strategies that may help animals circumventing highly efficient fungal chemical defences and give first insights into how third party interactions can substantially alter arthropod-fungus interrelationships.

OP-E-01

Predator Evasion in Zooplankton Is Supressed by Polyunsaturated Fatty Acid Limitation

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Herbivorous zooplankton avoids size-selective predation by vertical migration to the deep, cold water refuge. As adaptation to low temperatures in planktonic poikilotherms depends on essential dietary lipids, the availability of these lipids often limits growth and reproduction of zooplankton. We hypothesized that limiting essential lipids may affect habitat preferences and predator avoidance behaviour in planktonic poikilotherms. We used a liposome supplementation technique to enrich the green alga *Scenedesmus obliquus* and the cyanobacterium *Synecchococcus elongatus* with the essential lipids cholesterol and eicosapentaenoic acid (EPA), and an indoor system with a stratified water column (plankton organ) to test whether the absence of these selected dietary lipids constrains predator avoidance (habitat preferences) in four species of the pelagic freshwater grazer *Daphnia* (a keystone genus in ponds and lakes). We found that the capability of avoiding fish predation through habitat shift to the deeper and colder environment was suppressed in *Daphnia* unless the diet was supplemented with EPA; however, the availability of cholesterol did not affect habitat preferences of the tested taxa. Thus the outcome of predator-prey interactions between zooplankton species as well as their ability to access a predator-free refuge depends upon food quality (i.e. the amount of an essential fatty acid). Our results suggest that biochemical food quality limitation, a bottom-up factor, may affect the top-down control of herbivorous zooplankton.

OP-E-02

CASCADING EFFECTS OF BIODIVERSITY LOSS IN FRESHWATER PLANKTON

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Anthropogenically induced environmental changes (e.g. global warming, eutrophication) are ranked among the major drivers of biodiversity loss in different types of ecosystems. In aquatic ecosystems, herbivorous zooplankton feeds directly on phytoplankton (primary producers). Thus, changes in the biodiversity of phytoplankton might alter the zooplankton community structure. While there have been numerous laboratory experiments that examined the impact of biodiversity on ecosystem functioning and community dynamics, it is not known whether the patterns observed at small scales also occur in complex natural communities. To examine such patterns in "wild nature", we conducted large-scale experiments in three Bavarian lakes along a trophic gradient (oligotrophic to eutrophic). We manipulated the natural phytoplankton communities of the lakes through manipulation of the water column stratification at different frequencies. We first hypothesized that the disturbance of the water column stratification leads to a loss of stress sensitive phytoplankton species and thus changes the biodiversity of the natural phytoplankton community. As a consequence, the zooplankton community composition could also change due to trophic cascades. Our results show that disturbance altered not only phytoplankton community composition (determined as changes in the pigment composition of the algal community), but also affected the consumer trophic level (microcrustacean zooplankton) through an alteration of the relative dominance of cladoceran and copepod microcustaceans.

OP-E-03

Consumer species richness and nutrients determine producer diversity

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Although the benefits of biodiversity are well documented, little is known regarding the mechanisms controlling it. Due to human activities, freshwater ecosystems suffer from an excessive input of phosphorus. Most studies show a negative effect of eutrophication on the biodiversity of primary producers, but how a phosphorus gradient affects biodiversity is less well understood. Yet biodiversity is not controlled by resource availability alone. Recent studies have pointed out both top-down and bottom-up control as important factors in determining biodiversity, with trophic cascades being the most extensively studied top down effect. How biodiversity on one trophic level might affect biodiversity on underlying trophic levels has not been systematically investigated to date. Studies that focus on only one factor, such as eutrophication, could be misleading since it is likely that interactions between different control mechanisms of biodiversity occur. We conducted a lab experiment with an aquatic model food web consisting of benthic algae and herbivorous invertebrates to investigate how biodiversity of primary producers is controlled. Our data demonstrate (1) a unimodal relationship of producer diversity with increasing amounts of phosphorus, (2) a positive linear relationship between producer diversity and consumer species richness, and (3) interactive effects between phosphorus loading and consumer species richness that shape primary producer diversity. We conclude that eutrophication reduces primary producer diversity and further dampens the positive effect of consumer species richness on primary producer diversity.

OP-E-04 - Translocated pike trigger a tapeworm epidemic in Arctic charr

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In 2005, half a century after introducing the final host Northern pike (*Esox lucius*) into Lake Grundlsee in Austria, a sudden massive infection with the pike tapeworm *Triaenophorus crassus* was noticed in the population of the second intermediate host Arctic charr (*Salvelinus umbla*). Within two years the prevalence of the cestode in medium sized Arctic charr increased to almost 100% and the abundance reached a maximum of 55 cysts per fish, leading to the closure of the fishery. The occurrence of a suitable copepod as first intermediate host and a large pike population, that served as reservoir for *T. crassus* with up to 687 cestodes per fish, facilitated the outbreak. In an effort to contain the epidemic and to develop strategies for similar lakes throughout the area of distribution of *T. crassus*, a total of 1671 pike were removed by gill and fyke netting, electro and spear fishing between 2008 and 2013. Infection rates within the three hosts as well as efficiencies of the different catch methods were assessed. The prevalence of *T. crassus* in Arctic charr decreased to 60% and the maximum abundance to 16 cysts in 2013. All four catch methods were costly with EUR 37-371 to catch a single fish, but fyke netting coupled with electro fishing turned out to be the most practicable strategy to reduce the pike stock. However, it will be impossible to completely eradicate pike and its parasite in the lake.

OP-E-05 - From myth to reason - a potential spawning area of tropical eels in the western South Pacific

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Freshwater eels (Genus *Anguilla*) are major ecological components across the islands of the western South Pacific region and have been important mythical creatures for human societies there. Yet, very little is known about their biology. These catadromous eels live most of their lives in freshwater or estuaries before they finally migrate to offshore marine spawning areas. Their leaf-shaped larvae (leptocephali) drift with currents to their freshwater or coastal habitats. After two years of tagging silver eels (giant mottled eel - *Anguilla marmorata*, Polynesian long-finned eel - *A. megastoma*, Polynesian short-finned eel - *A. obscura*) from Vanuatu with pop-up satellite archival transmitters (PSATs), a potential spawning area (460 x 250 km; 8-12°S, 170-175°E) has been discovered in the western South Pacific at the border of the South Equatorial Current and the South Equatorial Counter Current. Our genetic studies showed that *A. marmorata* and *A. megastoma* hybridize and thus spawn in the same area. A salinity maximum at the eels' upper nighttime migration depths (150 m) was discovered and may serve as a landmark to help eels locate the spawning area. Today, the efforts to understand the long-distance oceanic migrations and spawning ecology of eels are no longer just driven by pure scientific curiosity but also by the necessity to cope with the potential collapse of eel stocks. Some populations have shown alarming declines, and the European eel is now classified as "critically endangered" in the IUCN Red List.

OP-E-06

Effects of dim artificial light at night on rodent behavior and physiology

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Light functions as an important zeitgeber in many animal species which use this external stimulus to adapt to predictable environmental changes throughout the day and the season. The increasing spread of artificial light at night was found to have strong negative effects on ecosystems. This so called light pollution can lead for example to alterations in activity, body condition and reproduction of animals. In this study, the manifold impacts of chronic dim artificial light at night were investigated in the Bank Vole (*Myodes glareolus*). Animals were subjected to night lighting or lived under natural dark-light conditions for seven months in outdoor enclosures while it was investigated how light pollution might change their survival, body mass, chronic stress level, activity or space use. Results suggest that these bank voles were not differing in their physiology but in their space use including home range, activity and distance covered during the day. Voles subjected to light at night showed increased activity before sunrise in comparison to those living under natural light conditions. Additionally, they covered comparably larger distances and had larger home range areas during new moon. These observations indicate that already very low intensities of artificial light at night can alter the behavior of small mammals but might not be sufficient to have a lasting negative impact on the condition of these animals.

OP-E-07

Beyond species recognition: nutritional state, age, body size and parasite load affect long distance sex pheromone communication in the burying beetle *Nicrophorus vespilloides*

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Long range sex pheromones have been identified and studied in various groups of insects, primarily in moths, butterflies, bees and beetles. According to fundamental paradigm was the assumption that sex attractants serve solely as species recognition signals. However, especially when they are produced by males, the evolution of heightened condition dependence might be expected and long range sex pheromones might therefore also inform about a signaler's quality. Using a combination of chemical analyses, video observations and field experiments we provide a comprehensive study about the role of a male's long range sex pheromone in female mate choice by manipulating a males' condition. We show that the emission of the long distance sex pheromone of the burying beetle *Nicrophorus vespilloides* has a surprisingly high information content and reliably reflects the actual nutritional state, age, body size, and parasite load - key determinants of an individual condition. Both, the quantity as well as the ratio of the pheromone components were affected whereas the time invested in pheromone emission was largely unaffected by a male's condition. Moreover, the pheromonal differences caused by the variation in condition affected the attractiveness of the males in the field. Males in better nutritional condition, of older age, larger body size and bearing less parasites were more attractive. So far it was unknown that a single pheromone is influenced by so many determinants of an individual's condition and more importantly affects significantly the attractiveness of a male in the field. Our study provides good evidence that long range sex pheromones contain information beyond species and are reliable indicator of a male's quality.

OP-E-08

Local adaptation in phoretic mites

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Much of the phenotypic and genotypic variation we can observe within species is thought to be generated and maintained by environmental variation. In particular local adaptation of populations to their specific habitats generates diversity. We study mites of the genus *Poecilochirus* as a model for local adaptation. It has long been known that the mites vary in development time between species, and we found this trait to vary within species as well. The mites are phoretic on burying beetles, and development time is a trait that is adapted to the beetle hosts. Variation in this trait has fitness consequences, and we were able to affect the trait by artificial selection. However, development is a process heavily influenced by temperature, and we found evidence for counter-gradient variation in this trait, with trait variation across populations compensating the effects of temperature variation between habitats. Such close links of a single trait to both the abiotic environment and host traits offer interesting opportunities to study the dynamics of local adaptation in a meaningful ecological context.

OP-E-09

Life cycle and Development of the spotted wing Drosophila, *Drosophila suzukii*

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Drosophila suzukii, which is commonly called spotted wing drosophila (SWD), is an invasive pest to many small soft and stone fruits. It is native to Asia, but has widely spread out in the last few years and has also become established in Germany since 2011. Especially in the year 2014, SWD was responsible for crop failure mainly in cherries and blackberries up to 70% in some places. The females have saw-like ovipositors and are able to lay eggs inside of different fruits, e.g. strawberry, raspberry, blueberry, cherry, plums and also grapes. The eggs hatch between one and two days later and the larvae feed inside the fruit. Within a few days, the fruit collapses. 5-7 days after hatching the larvae pupate. The whole development cycle lasts about 10-14 days, depending on the temperature and the host fruit. The film gives an overview on the life cycle and development of *Drosophila suzukii.*

OP-E-10

Preferred oviposition substrate of the mountain fly *Drosophila nigrosparsa* (Diptera: Drosophilidae)

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The survival of insect larvae often depends on the female's choice of oviposition substrate, and thus, this choice is an essential part of a species' ecology. Especially species with narrow substrate preferences may suffer from changes in substrate availability triggered by, for example, climate change. The preferred oviposition substrate is known for a handful drosophilids but is still unknown for many species, especially for those from higher elevations. In this study, we investigated the oviposition-substrate preference of the montane-alpine fly *Drosophila nigrosparsa* in multiple-choice and rearing experiments using natural substrates in the laboratory. The flies preferred ovipositing on mushrooms (> 93% of eggs); additionally, a few eggs were laid on berries, but none on other substrates such as cow faeces, rotten plant material, and soil. When no mushrooms were present, *D. nigrosparsa* reduced egg-laying from more than 700 eggs/day to 29 eggs/day. We infer that *D. nigrosparsa* is a mushroom breeder with some variation in oviposition site choice. The flies favoured some mushrooms more than others (e.g., *Inocybe*: 36% of eggs, *Tricholoma*: 1%), but they were not specialised on a single fungal taxon. Although it is unclear if and how climate change will affect *D. nigrosparsa*, we suggest that this species will not be threatened by oviposition substrate limitations because of the broad altitudinal distribution of the mushrooms considered here, even if the flies will have to shift upwards to withstand increasing temperatures.

OP-E-11

Food quality induces plasticity in oral and intestinal morphology in larval amphibians

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Phenotypic plasticity is the ability of a genotype to exhibit a wide range of different phenotypes in response to variation in the environment. Morphological, physiological and behavioral characteristics can be plastic. Environmental variation concerns both biotic and abiotic components of the environment including food quality and quantity. Quantity induced phenotypic plasticity has been widely documented in anuran larvae, but studies examining the impact of food quality are rare. We examined whether, and to what degree, tadpoles of the common frog (*Rana temporaria*) show phenotypic plasticity of the oral apparatus and intestine morphology when raised on either pure algae (i.e., low nitrogen content) or animal (i.e., *Daphnia*; high nitrogen content) diet. Oral morphology was plastic only in one variable (number of absolute number of teeth) of the oral apparatus. However, intestinal morphology was greatly plastic. Tadpoles that fed on plant food developed significantly longer guts and larger larval stomachs than tadpoles that were raised on an animal diet. Conditions such as food availability and food quality in the habitats of tadpoles are known to change either very quickly (e.g., due to pond desiccation or eutrophication) or on a long term due to global change. This poses a challenge for larval amphibians. The ability of a species to respond plastically to changing conditions in the environment, as this study shows for *Rana temporaria*, indicates that this species can cope with these new conditions.

PP-E-01

Pathogen sharing among managed and wild bees in apple orchards of Kirgizstan and Georgia

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In the face of biodiversity decline and the loss of pollination service in many countries, understanding the forces driving these negative trends is an important task. Besides habitat fragmentation and the liberal use pesticides that have been identified as major drivers for the loss of insect pollinators, the importance of emerging pathogens has come more and more clearly to the fore. For honey bees, multiple viruses and other parasitic organisms have been suggested to play an important role in colony loss. Yet, little is known about the importance of such diseases for wild pollinators, and the impact of infected, managed honey bees on wild bee populations. Here, we address this question by studying the prevalence of 10 common bee viruses in populations of wild and managed bees at three locations: Georgia, Kyrgyzstan and Germany. We found viruses in wild and managed bee populations, with several viruses being shared between both, suggesting inter-species transfer of pathogens. Though our data cannot be used to demonstrate the directionality of pathogen transmission, they do highlight how viruses may infect and may be transmitted by multiple members of the same guild of flower visitors.

PP-E-02

Macroinvertebrate biodiversity in Icelandic freshwater springs

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Freshwater springs are ecotones between surface and subsurface water habitats and have potential to house a diverse and highly-specialized invertebrate fauna. In Iceland, an abundance of cold and thermal springs can be found, which makes the country a perfect place to study temperature influences on stygobiont and crenobiont macroinvertebrates. The aim of the study is to analyze community composition in Icelandic freshwater springs at the surface-subsurface water interface and assess temporal, environmental, and spatial influences on those. About 30 warm and cold freshwater springs all over Iceland have been sampled using a combination of a modified electric fishing gear and manual pumping. Since the water temperature for each spring is seasonally and annually stable, community composition is expected to be similar all year round. For a biogeographical approach, springs both within and outside the volcanic active zone in Iceland will be compared in order to assess whether spring type (limnocrene or rheocrene) or geographical distribution have greater influence on macroinvertebrate composition. Additionally, food web analyses will reveal whether primary producers are a limiting factor in spring habitats. So far, Chironomidae, Copepoda, Cladocera, and Hydracarina (Acari) seem to be the most abundant invertebrate taxa in Icelandic freshwater springs.

PP-E-03

From the laboratory into the field: a new field test to evaluate heat tolerance of *Drosophila* species under seminatural conditions

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Currently, climate change is affecting many organisms, and thus the thermal biology of species has increasingly become the focus of research. Patterns of heat tolerance have been investigated extensively in the laboratory. However, these experiments have often been criticised due to a lack of ecological relevance in nature. We have established a new field method to evaluate heat tolerance of different species, populations, or strains of *Drosophila* flies under field conditions. We tested for heat tolerance by measuring the ability of flies in reaching a food source. One half of a wooden cage covered with mosquito net provided shadow and protection from heat, whereas the other was sunlight-exposed. Individuals were released at the protected end; at the exposed end, a bait was placed, reachable only by passing the heated part of the cage. We hypothesised that more heat-tolerant individuals will reach the food source at a higher temperature in the field than less tolerant ones. To distinguish different groups easily, individuals were marked with fluorescent powder. By using our field cage, release of alien individuals into a natural population is avoided, an important aspect for conservation and long-time monitoring, and smaller numbers of individuals are needed than for release-recapture approaches. The new method can also be applied to various other insects and to investigate issues like the heat tolerance of heat-selected strains in the field.

PP-E-04

Effects of inter-row management intensity on wild bees in Austrian, Spanish, French and Romanian vineyards

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Traditionally managed vineyards have increased landscape complexity (e.g. stone walls, fruit trees, hedges or loess walls), provide habitats for thermophilous species and ecosystem services (ES). Intensive management like frequent tilling and/or high input of pesticides and use of machinery have resulted in the degradation of landscape structures and ecological communities with detrimental impacts on biodiversity and ES. In agricultural systems wild bees enhance ES like the provision of biodiversity and pollination. They depend on floral resources and suitable nesting habitats, both being influenced by management practices at the field and landscape scale. In the BiodivERsaA project “VineDivers”, we study how different management intensities and landscape complexity affects above- and below-ground biodiversity (vegetation, pollinators, soil biota) and the consequences for ES. This study investigates the effects of management intensity in vineyard inter-rows on wild bee diversity and abundance in Austria, Spain, France and Romania. In 2015 each country sampled wild bees in 16 vineyards of three different management intensities using a semi-quantitative transect method. Management intensity differs in tillage frequency from high frequency tillage systems resulting in bare soil, to temporary vegetation cover and no tillage in permanent vegetation cover systems. We will discuss first results of the bee survey in relation to management intensity and ES in vineyards.

PP-E-05

Fitness consequences of the endogenous clock of *Drosophila melanogaster*: impact of day length

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Due to the rotation of the earth around its own axis organisms experience daily changes in the environment with a rhythm of about 24 hours. Therefore, most organisms adjust their lives with a circadian rhythm to the environment. This adjustment should result in a fitness advantage. For the synchronization to the environment one of the most important Zeitgeber is light. The endogenous clock of wild type *Drosophila melanogaster* CantonS (CS) has a free-running period of 24.15 +/- 0.07h. To verify our working hypothesis - the endogenous clock of *Drosophila melanogaster* implies a fitness advantage - we used the experimental design as follows: we performed a competition assay with CS wild type flies against the well described *period* (*per*) mutant per^{S}, per^{L} and per^{01}. Due to the fact that per^{01} lacks the clock function it is arrhythmic under constant conditions. The per^{S} mutant flies have a free-running period of about 19 hours and per^{L} of about 29 hours. The experiments were conducted under T-cycles of 24 hours (T= period of Zeitgeber) according to the free running period of the wild type flies and T-cycles of 19 and 29 h according to the free-running period of per^{S} and per^{L} as well as constant light to disturb the circadian rhythm of CS as per^{01} lacks a functional endogenous clock. Another set of the competition assay experiments was performed outdoors to have natural like changes in light, temperature and humidity. For the competition experiments we used the following pairings: CS x per^{S}, CS x per^{L} and CS x per^{01} and recorded the locomotor activity of male flies of every third generation to discriminate the genotypes and calculate the genotype distribution in those mixed populations. Additionally, the locomotor activity of heterozygous female flies was recorded and the free-running period was calculated because the different strains mate in the course of the experiments. Since there are also heterozygous females present we tested the heterozygous as well as the homozygous females for mating preferences.

PP-E-06

Conservation genetics of the Northern river terrapin (*Batagur baska*) breeding project

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The highly endangered Northern river terrapin *Batagur baska* was once spread over Eastern India, Bangladesh, Thailand and Cambodia. Nowadays the distribution is restricted to regions in Bangladesh and Myanmar. Overall there are just 20 wild animals confirmed. In response to this extreme decimation a rescue program was started from the Vienna zoo and the Turtle Survival Alliance (TSA) in 2010. First random breeding attempts in 2012 and 2013 resulted in 84 juveniles. For further species conservation breeding by choice must take place to conserve the broad genetic variance. Therefore we genotyped all known individuals of *B. baska* with 13 polymorphic microsatellites to investigate the relationships among the remaining individuals.

PP-E-07

Bioluminescence in the open waters of Gullmarfjord, Sweden

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Bioluminescent events were recorded with photomultiplier tubes in underwater housings for several days, during different seasons, and at different depths in the open waters of Gullmarfjord, Sweden. Several bioluminescent groups are known to inhabit the fjord (e.g. krill, copepods, dinoflagellates). While stimulated bioluminescence is quite commonly used to examine the water column, not much is known about the ecological relevance of bioluminescence in the life history of marine organisms. Reviews about marine bioluminescence propose several different probable uses of the light, but actual experiments examining these hypotheses are rare. Therefore, in a first attempt, we tried to record unstimulated naturally occurring bioluminescent events, which worked out nicely. Almost 74.000 events were recorded and categorized. Possible future work might try to relate bioluminescent events to actual behaviors of organisms in the open water.

PP-E-08

Caution! There´re oribatid mites on bark beetles!

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Bark beetles (Scolytinae), a highly diverse subfamily of weevils with worldwide distribution, are well-known by everyone - not because of their ecological roles in natural plant communities and large-scale biomes but rather due to their significant damages in agriculture and forestry. Besides their well-known associations with all major groups of terrestrial plants, symbiotic associations of bark beetles have received less attention. However, such associations often do have an important role for the success of the beetles. Typical associates are symbiotic fungi, bacteria, nematodes and also mites. There are numerous documented examples that mites, more precisely phoretic species, are involved in complex symbiotic interactions, e.g. beetle-mite-fungus, suggesting that mites´ phoresy on beetles is not just a means of transport. Most phoretic species on beetles belong to the orders Mesostigmata (Parasitiformes) and Trombidiformes (Acariformes) and are thus the most frequent residents in the galleries of bark beetles and accordingly on the beetles themselves. In this work, however, we are focusing on another acariform group, the Oribatida (order Sarcoptiformes). Oribatid mites are a diverse group that can be found in all types of ecosystems. Little is known about their dispersal ability, though it is generally assumed that oribatid mites are weak dispersers, although there are some records of phoresy on other arthropods and birds. So far, phoresy on bark beetles could be shown for a few oribatid species only. And this is the focus of the present study. Using mites extracted from galleries and pheromone traps, “real” phoretic and non-phoretic behavior should be identified.

PP-E-09

An approach for a multi-temporal post classification analysis of Landsat imagery to reconstruct changes in forest land cover exemplified on Bulgaria

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Forests are under continuous threat across the world. To protect forests and their associated biodiversity, careful monitoring of changes in forest cover is vital. Forests in Eastern Europe are among the oldest and most diverse on the continent, yet are increasingly being logged. To detect forest land cover change in Bulgaria, we used Landsat imagery from 1984 until 2011. Eight landcover maps at xx m resolution were created using supervised classification and a prior definition of forest. For post-classification analysis several approaches were pursued. (1) The comparison of the absolute area values for forest from each map suggests a continuous afforestation process, consistent with observations by the Food and Agriculture Organization (FAO) of the United Nations. (2) A pixel-by-pixel comparison as change detection method for a bi-temporal analysis between subsequent years suggests a possible deforestation period in the nineties. To further examine the dynamics of forest land cover change a multi-temporal change detection was implemented. (3) We developed algorithms that extract and reclassify relevant information on landcover to generate a map on forest cover changes of Bulgaria. (3a) Results suggest that only 18,906 km² of forest detected in 2011 is persistent forest originating from 1984 and earlier. (3b) This loosely fits results suggesting that 17,665km² of forest detected in 1984 still existed in 2011. This however leaves about 30% of (old growth) forest that was lost over these 27 years, though in net values the forested area increased over approximately 148%. In conclusion, although the data published by the FAO concurs with the data resulting from a comparison of absolute values, implementing this newly developed approach for a multi-temporal change detection revealed a far more complex dynamic between de- and afforestation.

PP-E-10

The invasive freshwater jellyfish *Craspedacusta sowerbii* - occult polyps and conspicuous medusae

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The rising introduction of non-native species into new ecosystems is a consequence of increased human mobility. The freshwater jellyfish *Craspedacusta sowerbii* is one example of a recently globally distributed species with original source populations in China. First reports in Germany are from 1905, today the species is widespread in standing and slow-flowing waters. *C. sowerbii* has a metagenetic life cycle, including a tiny sessile polyp and a conspicuous free-swimming medusa, both feeding on zooplankton. As gelatinous predator the medusa occupies a specific ecological niche and the introduction of this species created a new functional guild within freshwater plankton communities. Although mass occurrences of medusae have been recorded and effects on aquatic food web dynamics are likely, the consequences of *C. sowerbii* being introduced to aquatic systems has not been analyzed yet. Field mesocosm experiments will be designed to identify the trophic position of medusae, the cascading effects down to phytoplankton, and pelagic-benthic fluxes of energy and organic matter mediated by jellyfish. In laboratory experiments food selectivity, assimilation and ingestion efficiencies of medusae and polyps will be determined, in order to evalute competitiveness. To test for population structure and evolutionary dynamics, genetic and sexual diversity will be quantified using molecular markers in field samples. Evidence for multiple introductions and the association between genotype and sex will be identified by genetic analyses. Combined analyses of the genetic diversity and the ecological function of this species will allow a better understanding of cause and effect relationships within aquatic food webs exposed to invasions.

PP-E-11

Landscape genetics of house sparrows (*Passer domesticus*) in Romania and Bulgaria.

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Human influences such as climate change, overhunting, land use change, habitat fragmentation and pollution threaten biodiversity. One way for species to respond to ongoing changes is adapting to new conditions. For successful adaptations, species need a high evolutionary adaptive potential, which is maximized by protecting intraspecific genetic variation. Consequently, a conservation strategy where the current level of genetic diversity is identified, mapped, and maintained is needed. A novel approach was developed to integrate genetic and morphological dissimilarities and environmental variation in order to map the intraspecific variation of species in various landscapes and environments. One such project is conducted in Bulgaria and Romania with 12 different target species. Within this study the intraspecific genetic variation of the house sparrow (*Passer domesticus*) was identified and combined with environmental variables. With the calculation of pairwise genetic distances (Fst) between several sparrow populations and correlating this with a set of environmental variables and geographic distances in generalized dissimilarity models (GDM), the intraspecific genetic variation of the house sparrow could be mapped. We assessed (i) whether the genetic structure of the study species is maintained by the environment; (ii) how areas with a high genetic diversity are comparable to already existing protected areas and (iii) how the results can be used for conservation prioritization of areas. The results show that environmental variables best described the intraspecific variation of the house sparrow. Areas with high genetic diversity are located along an elevation gradient. Furthermore, an additional unique genetic pattern in the black sea region was identified. A comparison with already existing protected areas showed that areas containing high levels of genetic diversity are only partially protected or not at all. These results stress the importance of implementing genetic diversity in conservation prioritization, directly protecting the current biodiversity and maximizing the adaptive potential of species for a better preparation for upcoming changes.

PP-E-12

Tetradecyl acetate: A new compound of aphid cornicle secretions and its potential role

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After mechanical stimulation, aphids often release sticky secretions from their cornicles to defend themselves against predators. In many species cornicle secretions often contain volatile constituents serving as alarm pheromones. A widespread volatile among aphid species is the sesquiterpene (E)-ß-farnesene (EFB), but other sesqui- and monoterpene compounds have been additionally described. Nevertheless, chemical communication in aphid colonies still deserves further investigations because many aphid species are still chemically unexplored and complete chemical profiles of most species are missing. In this study we used gas chromatography-mass spectrometry to study volatiles of aphids that were collected in different natural habitats in Austria, Hungary and Italy (N=35 samples). In several samples we found tetradecyl actetate that is known to act as a sex pheromone in some moth species, but has not been described in aphids so far. With the exception of EBF this molecule was the second most common substance in all probes. It was either present as the only component or occurred together with EBF and smaller monoterpenes. Surprisingly, it often exceeded the relative abundance of all other components. Future studies will shed light on the behavioral relevance of this molecule.

PP-E-13

Simulating effects of heat periods on different life stages in a tropical butterfly

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Climate change, especially increases in extreme weather events such as heat waves, has the potential to strongly affect biodiversity and poses a significant challenge to all natural systems on Earth. Their effects though are poorly understood due to a lack of empirical data. Therefore, we here explored the sensitivity of a tropical ectotherm, which are in general believed to have a low warming tolerance, to experimentally simulated heat periods of 24 hours across seven different life stages. We simulated five different heat periods of 36°C, 37°C, 38°C, 39°C and 40°C. Increasing temperatures had strong effects on the survival of all life stages in the butterfly *Bicyclus anynana.* In larvae mortality rates increased from 2-3% at 36°C to 100% at 40°C. In contrast, eggs (52%), hatchlings (24%) and adults (15%) suffered substantial mortality at 36°C already, while pupae were most heat resistant (61% mortality at 40°C). Thus, survival rates varied between different life stages in reaction to high temperatures. Heat periods substantially reduced survival even in this plastic and widespread butterfly, exemplifying the potentially dramatic impact of extreme weather events on biodiversity. Furthermore our results underline the importance of the developmental stage and the timing of extreme weather events on the survival of insects.

OP-EB-IT-01

Some evolutionary and immunological perspectives on a highly diversified insect gene

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Dscam1 (*Down syndrome cell adhesion molecule 1*) is a complex gene that has evolved dual functions in insect and crustacean pathogen defence and neuronal guidance. The complexity of the *Dscam1* gene lies within its extreme variability: due to the expansion of some exons and mutually exclusive alternative splicing, tens of thousands of different isoforms can be produced from one gene. I will first present an analysis of the evolutionary history of the *Dscam* gene family where, amongst other aspects, we examined the evolution of the alternatively spliced exons, to attempt to decipher how many exons of each exon cluster were present in the most recent common ancestor and how these clusters evolved across insect and crustacean species. Second, it has been proposed that the diverse *Dscam1* isoforms may be involved in the recognition of diverse parasite epitopes, although evidence to support this is sparse. We have taken an integrative approach to examine the effects of *Dscam* in various fitness-related contexts. First we tested whether general *Dscam* expression is affected by bacterial immune challenge; second whether *Dscam* alternative splicing patterns are affected by bacteria exposure; and third, whether there is a life-history cost to *Dscam* knockdown. We found no short-term modulation of *Dscam1* after bacteria exposure; RNAi-mediated *Dscam1* knockdown did not affect survival after bacteria exposure, and contrary to previous findings, we did not find evidence of changes in alternative splicing patterns after bacteria infection and subsequent RNA sequencing. However, *Dscam1* knockdown in larvae resulted in adult locomotion defects, as well as severely reduced fecundity. We suggest that *Dscam1* does not always play a straightforward role in immunity, but strongly influences behaviour and fecundity and we hope we have taken a step towards understanding more about the role of this intriguing gene in an integrative context.

OP-EB-IT-02

Anuran hybridization and sex chromosome evolution in space and time

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Reproductive isolation (RI) is expected to accumulate with divergence time but the time taken to speciate may vary between organisms. In anurans, lab-crosses can still produce viable hybrids >20 My after separation but speciation speed in closely related lineages under natural conditions is poorly studied. Heteromorphic sex chromosomes (SC; e.g. mammals, birds) have key roles in driving RI. However, most amphibians exhibit indistinguishable (homomorphic) SC, whose evolutionary significance is not well known. Phylogeography of Palearctic tree frogs (*Hyla arborea* group) and green toads (*Bufo viridis* subgroup) allows dating and identification of secondary contacts. In four tree frog and all diploid green toad species, we established homologous, homomorphic, occasionally recombining XY-SC. Using transcriptome-based microsatellites, we study introgression in hybrid zones of differently diverged lineages. Introgression at autosomes should be greater than on SC, as expected from Haldane's rule, stating that in interspecies crosses the heterogametic sex (XY-♂♂ ZW-♀♀) suffers greater fitness depressions than the homogametic (XX, ZZ); shown in many species but all with heteromorphic SC. Indeed, genome-wide vs. linkage-group-specific hybrid index in a tree frog hybrid zone (div.-time 5 My, moderate RI) revealed stronger autosomal than sex-linked introgression. However, in two green toad zones of younger divergence, we observe no difference (2.6 My; strong RI) between both marker types or even more sex-linked than autosomal introgression (1.9 My; weak RI), possibly pointing to unknown evolutionary features of homomorphic SC in early speciation. If confirmed, our findings might have implications on the recognized anuran biodiversity.

OP-EB-01

Does increasing offspring genetic diversity influence their resistance to infection?

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It has been suggested that polyandry allows females to increase offspring genetic diversity and reduce the prevalence and susceptibility of their offspring to infectious diseases. We tested this hypothesis in wild-derived house mice *(Mus musculus)* by experimentally infecting the offspring from 15 single and 15 multiple sired litters with two different strains of a mouse pathogen (*Salmonella Typhimurium)* and comparing their ability to control infection. We found high variation in individual pathogen loads and significant differences among families, suggesting genetic effects on *Salmonella* resistance, but we found no difference in prevalence or pathogen loads between single versus multiple sired litters. We found a significant sex difference in pathogen loads, but surprisingly, males were more resistant than females. Also, pathogen load was correlated with weight loss during infection, though only for females, indicating that susceptibility to infection had more harmful health consequences for females than males. To our knowledge, our findings provide the first evidence for sex-dependent resistance to *Salmonella* infection in house mice. Our results do not support the hypothesis that multiple sired litters are more resistant to infection; however, they do not necessarily rule out this hypothesis. For example, studies that evaluate this hypothesis using a wide diversity of pathogens and parasites might find positive results, as expected from bet-hedging models. Increasing the number of sires per litter might also provide different results (previous positive evidence with bees had up to 10 sires per brood), but such tests would not be ecologically relevant to mice or other vertebrates that have only two sires per litter.

OP-EB-02

Speciation under gene flow? The case of *Mauremys caspica* and *M. rivulata*

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The stripe-necked terrapins *Mauremys caspica* and *M. rivulata* are a sister species occupying a similar ecological niches and occurring in more or less mutually exclusive parapatric distribution ranges. The ranges of the two species are forming a narrow contact zone over hundreds of kilometres. We used 13 quickly evolving microsatellite loci and five nuclear genes for gaining insights in gene flow and hybridization of 13 populations of *M. caspica* and 18 populations of *M. rivulata* from the contact zone and compared these to randomly chosen individuals from the whole distribution range of each species.

OP-EB-03

Taxonomy, phylogeography and genetic differentiation of the eastern and western green lizard *Lacerta viridis* and *L. bilineata*

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The taxonomy and hence biogeography of the closely related lacertid lizards *Lacerta viridis* and *L. bilineata* is very controversial. These two taxa do not show obvious morphological differences and their genetic distance is low when compared to their congeners. Although hybrids occur, it is unclear whether they produce viable offspring. In order to assess their taxonomic status and phylgeographic patterns, we analysed the sequence differences at two nuclear (*recombination activating gene 1*, *β-fibrinogen intron 7*) and two mitochondrial (*cytochrome b*, 16S-rDNA) markers from samples collected over a wide distribution range. The phylogenetic analysis of the concatenated data revealed three distinct clades, *L. bilineata* clade 1, *L. bilineata* clade 2, and *L. viridis* and a paraphyletic relationship of *L. bilineata*. Phylogeographic analyses of the mitochondrial markers revealed three distinct networks reflecting the pleistocene refugia in the Appennins, southeastern Balkans and southwestern Balkans. In all three networks we detected a south to north gradient of genetic diversity decrease, reflecting the northwards post-glacial expansion. In order to investigate the mechanisms of speciation between *L. viridis* and *L. bilineata*, we sequenced and assembled the complete genomes of both taxa using Illumina- and PacBio-Next Generation Sequencing technology. According to suppressed-recombination models of chromosomal speciation, genetic divergence can quickly accumulate within regions of low recombination, such as in chromosomal rearrangements. Our ultimate goal is to test this theory by searching evidence for accumulated divergence within chromosomal rearrangements.

OP-EB-04

Gaining new insights into speciation processes in rock-dwelling land snails (*Montenegrina*, Clausiliidae, Gastropoda, Pulmonata)

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Rock-dwelling gastropods usually live on isolated rocky outcrops and have a low dispersal activity which results in a patchy distribution. This led to the assumption that they evolve mainly by allopatric speciation and that co-occurring taxa are in secondary contact. Our study organism *Montenegrina* has a very restricted distribution range in the Balkan Peninsula and is with its 88 described taxa one of the taxon-richest genera of rock-dwelling gastropods. We know several taxon-pairs (subspecies) that occur parapatrically but are easily distinguishable by their morphology (e.g. strongly ribbed vs. completely smooth) and a few taxon-pairs differ even exclusively in their ribbing. As our first phylogenetic results show a low genetic diversity between these taxon-pairs we hypothesise that they could be in the first phase of a parapatric speciation. To test this we reconstructed the phylogeny of this genus with multi-locus molecular analyses and combine this with a morphometric and ecological data. Furthermore, we will asses gene flow and depict population genetic structures with the help of microsatellite markers, which were established for the first time in clausiliids. Eventually, this extensive study should help to answer fundamental questions of speciation in this highly diverse rock-dwelling land snail.

OP-EB-05

Resource dependence of exocrine secretions - A challenge for chemotaxonomy?

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Many terrestrial arthropods produce exocrine defensive secretions. These are often blends of multiple compounds from various chemical classes. The composition has been assumed to be species-specific in many cases - hence, such chemical profiles are more and more used as a source of information for species delineation (=chemotaxonomy) and phylogenetic inference (=chemosystematics). Oribatid mites (Acari, Oribatida) produce blends of hydrocarbons, terpenes, aromatics and alkaloids in a pair of so-called oil glands, and the chemical profiles of these secretions have been used for large-scale phylogenies and taxonomy for more than twenty years now. However, the biological mechanisms behind the highly conserved species-specific chemical profiles have not been studied. Are they under genetic control or the result of specific feeding habits and/or symbiotic bacteria? To answer this question, *Archegozetes longisetosus*, a parthenogenetic model oribatid mite producing a complex blend of hydrocarbons, terpenes and aromatics, was reared on different resources, strongly differing in nutritional/chemical composition. Chemical profiles of oil-gland secretions were analyzed in individual adults after feeding exclusively on each of the resources for at least one generation (larva, three nymphal stages, adult). The absolute quality of secretions (i.e. which compounds were present) was identical in all treatments. However, absolute and relative quantities (i.e. how much secretions were produced as well as their relative composition) were significantly affected by resources. Regarding chemotaxonomy/chemosystematics, multivariate analyses of quantitative chemical profile data should hence be treated with some caution. However, when given the choice for feeding on available resources in nature, species-specific food-preferences probably lead to reliable quantitative profiles.

OP-EB-06

Mating, longevity and immunity in ant males

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The interrelation between reproduction and longevity is one of the most studied life history trade-offs, predicting a lifespan reduction cost caused by reproduction for both sexes. A notable exception to this rule are female reproductives (queens) of social Hymenoptera, which may outlive the non-reproductive workers for decades. On the contrary, males of social Hymenoptera are usually short-lived. Mating typically occurs in unobservable mating flights and hence, data on male longevity and / or reproductive success are difficult to obtain. In the ant genus *Cardiocondyla*, wingless males mate inside their maternal nest with young virgin queens, stay lifelong in the colony, and reach extraordinary long lifespans. Different to other social Hymenopteran males, their spermatogenesis continues throughout their lives and they therefore possess an “unlimited” sperm supply. *C. obscurior* therefore provides an optimal study system to investigate the classic trade-off between longevity and reproduction as well as immunity, which is further predicted to be a costly life history trait. We here compare longevity, sperm quality and quantity, reproductive success, and immunocompetence of virgin *C. obscurior* males to males having mated with a low or high number of virgin queens.

OP-EB-07

Epimerization of chiral hydroxylactones by short chain dehydrogenases/reductases during sex pheromone diversification in *Nasonia*

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Newly evolved species depend on novel channels of sexual communication to avoid costly mismating with closely related species. In organisms relying on pheromones, speciation is often accompanied by a diversification of the chemical signals. The underlying genetic and biochemical mechanisms, however, are only poorly understood. Males of the parasitic wasp *Nasonia vitripennis* (*Nv*) have evolved (4*R*,5*R*)-5-hydroxy-4-decanolide (*RR*) as an extra pheromone component to attract conspecific females while (4*R*,5*S*)-5-hydroxy-4-decanolide (*RS*) is used by all *Nasonia* species. An array of three genes coding for short-chain dehydrogenases/reductases (SDRs) is correlated with the ability of *Nv* to produce *RR* [1]. Here we show by functional expression that all SDRs from *Nv* as wells as *N. giraulti*, a species with only *RS* in the pheromone, are capable of epimerising *RS* into *RR* and vice versa with (4*R*)-5-oxo-4-decanolide (ODL) occurring as an intermediate. The product ratios are influenced by the amino acid sequences of the SDRs and the availability of NAD$^+$/NADH as co-factors. Gene and protein expression analyses revealed that the SDR genes are expressed in the abdomens of males of either species. Both *Nv* and *Ng* males are able to reduce ^{13}C-labelled ODL *in vivo* to both *RR* and *RS*. These results suggest that the oxidation of *RS* to ODL, presumably controlled by the NAD$^+$/NADH status of the abdominal pheromone gland, is the critical step responsible for the exclusive formation of *RR* in *Nv*.

OP-EB-08

Not tonight darling - a female pheromone mediating sexual abstinence in males ensures concerted parental care

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Brood caring animals are always confronted with the reproductive dilemma when to invest resources into the current brood and when in sexual activity and the development of new offspring. In many species females are physiologically restrained from producing further young during the period of offspring feeding. In mammals including humans, this temporary infertility is caused by hormones such as prolactin being secreted during lactation and repressing ovulation. However, whether such a temporary infertility is a general principle of brood caring animals and how this dilemma is resolved in other species such as insects is only poorly understood. Females of the burying beetle *Nicrophorus vespilloides*, an insect exhibiting elaborate biparental care, also show a temporary infertility during the time of offspring tending. In the present study we show that this period of intensive brood care and intermitted oviposition is associated with high juvenile hormone III levels and accompanied by the emission of large amounts of the volatile methyl geranate. We were able to mimic the suppressive effect of JH III on ovarian activity by the application of a synthetic JH analogue. Stable isotope labelling experiments revealed that JH and methyl geranate share a common biosynthetic pathway. This physiological link between the hormone and the volatile suggests that methyl geranate is a reliable signal communicating the reproductive status of the female to the male partner. In fact, treatment of females with synthetic methyl geranate inhibited male copulation. Hence, our study illustrates how a physiological interplay between hormone and pheromone system guarantees that both parents draw their attention towards the existing young as long as they are needy.

OP-EB-09

Caste- and function-specific odor bouquets and the evolution of fertility signals in sweat bees

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Chemical communication systems are a major precondition for the evolution of insect sociality. Queen recognition by the means of so-called fertility signals has been shown to occur in many social insects, however not yet in primitively eusocial halictine bees. Several studies indicate that substances occurring in the Dufour's gland as well as on the cuticle surface of halictine bees may function as fertility or dominance signals. In order to offer new insights into the evolution of sociality, the major aim of this study was to characterize such fertility or dominance signals in the primitively eusocial halictine bee *Lasioglossum malachurum* and the socially polymorphic species *Halictus rubicundus*. We analyzed population-, caste- or function-specific odor bouquets and characterized substances correlating with the ovary development of different females. Moreover we examined if differences in the odor bouquets play a role in dominance interactions. While non-breeding females of social and solitary *H. rubicundus* populations were in part similar, breeding queens of social nests showed a unique odor bouquet distinct from all other groups indicating the occurrence of a queen-specific fertility signal in social populations. The separation of functional female groups, castes and populations were due to different relative proportions of macrocyclic lactones, n-alkanes and n-alkenes which also correlated with the ovary development. Therefore, these substances may have a key function as fertility signals whereas its behavioral function should be investigated.

OP-EB-10

Major urinary protein (MUP) profiles show dynamic changes rather than individual 'barcode' signatures

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Male house mice produce large quantities of major urinary proteins (MUPs), which bind and transport volatile pheromones to urinary scent marks. It has been suggested that MUP isoform profiles are highly polymorphic and provide a unique signature that mediates individual and kin recognition (barcode hypothesis). This hypothesis assumes that MUP profiles show high inter-individual variability and high intra-individual consistency, and we conducted the first study to test these assumptions. We analyzed urinary MUP profiles of 66 wild-caught house mice (Mus musculus musculus) from 8 populations using isoelectric focusing. We found that MUP profiles were not individually unique, and the variation depended on the type of isoform. Most proteins (the major isoforms) were surprisingly monomorphic, but the smaller ones were variable and therefore candidates for individual barcodes. To test this hypothesis, we examined changes in 58 mice over time, and found that individual MUP profiles were surprisingly dynamic and the minor isoforms showed the most fluctuation. Thus, most MUP isoforms were monomorphic, and though we found minor isoforms that were variable among individuals, they showed dynamic changes over time within mice. Nevertheless, we found more similarities in MUP profiles between siblings than non-siblings. Our findings challenge the hypothesis that MUPs contain individual signatures, though it is feasible that they mediate kin recognition in house mice.

OP-EB-11

High complexity of protein composition in nuptial gifts of bushcrickets

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Differential investment of the sexes into mating and reproduction leads to unbalanced costs and benefits in bushcrickets (Lehmann 2012). In many species nuptial gifts are transferred during courtship and mating. Nuptial gifts are materials provided by a donor to a recipient during courtship or copulation in order to improve donor fitness (Lewis et al. 2014). Bushcrickets transfer spermatophores as nuptial gifts which are divided into the spermatophylax and the ampulla. Spermatophores are oral gifts (taken in through the digestive system) - as well as genital "gifts" (absorbed through the reproductive tract). While bushcricket spermatophores are endogenous manufactured by the males this might give them the chance to include manipulative substances. The candy maker hypothesis argue it might be cheap to produce and tasting sweet to exploit the gustatory response of females. In contrast, if the spermatophore is used by males to transfer manipulative substances, we expect a high number of diverse proteins for different functions in both the ampulla and the spermatophylax.

Proteomic analysis using 2 dimensional gel electrophoresis (2DE) coupled with mass fingerprinting (MS/MS MALDI-TOF) separated the protein composition of spermatophylax und ampulla with high resolution and detected several hundred different protein spots in both compartments. Furthermore the majority of protein spots differed between the two parts. The high number of different proteins refutes the candy maker hypothesis. The first protein identification revealed a number of unknown proteins as well. I conclude, that bushcricket spermatophores contain a protein cocktail which, due to its high variability between the compartments, seems to be under sexual selection.

OP-EB-12

Costs of mating in females are accompanied by whole organismal functional decline

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Multiple mating can inflict substantial costs on females in a large number of taxa. For some taxa we gain a first understanding of the male traits causing these costs. In *Drosophila melanogaster* the ejaculatory protein sex peptide, amongst other seminal fluid proteins transferred by males at mating, is one such agent contributing to the cost of mating in females. Strikingly though we have no clear understanding of how these costs arise and how they affect female non-reproductive biological functions. Here we tested for functional senescence in females experiencing either no, intermediate or high costs of mating by varying exposure to males. We measured female motor function as well as starvation resistance as an index for metabolic state under these different male exposure conditions repeatedly over their entire lifespan. We show that females experiencing high male exposure indeed lose organismal functionality faster than females under reduced male exposure regimes. We further asked whether sex peptide might be causal in accelerating the rate of deterioration in organismal function. Our results demonstrate that higher costs of mating lead to age-related reduced performance in a range of organismal functions, not just reproductive traits, and as such cause extensive global senescence in the whole body.

OP-EB-13

Linking avian sperm form to function: How morphology predicts velocity of coal, great and blue tit spermatozoa

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Despite their common task, avian spermatozoa come in endless forms and it is a challenge to understand the evolution and maintenance of diversity in sperm morphology between and within species. Assessing how sperm form relates to sperm function may be the key to discovering selective pressures that have shaped such variation in birds, in particular when variance in male fitness is strongly determined during postcopulatory processes. Empirical data relating avian sperm form to function are scarce, however, and the results obtained so far appear inconsistent across lineages. To better understand the differential functional morphology of spermatozoa in different groups of birds, we here used computer-assisted sperm analysis (CASA) to examine how sperm velocity is influenced by sperm morphology in a large sample of blue, coal and great tits, three socially monogamous passerine birds with contrasting levels of extra-pair mating.

OP-EB-14

An adult morphology of the Marginated tortoise follows the Charnov-Bull theoretical model

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An adaptive significance of environmental sex determination in animals is widely debated from a perspective of the Charnov-Bull theoretical model. This model predicts that selection favours environmental sex determination (ESD) when environmentally induced phenotypes of sexes differently affect their fitness. However, almost all studies aimed to test the model focused on an association between temperature-induced hatchling morphology and sex-specific survival, while lifetime fitness of sexes is largely unknown. Hence, here I tested relationship between environmental factors and morphological traits in 51 free living adults of the Marginated tortoise which is known to reproduce via ESD. Environmental factors was summarized as monthly mean temperature and precipitation over 50 years, while size and shape of tortoise's plastron was quantified by 2D geometric morphometrics. It was found that the plastron size of sexes is linked with different and independent environmental sources. Contrary to males, females did not show relationship between plastron shape with both temperature and precipitation. Moreover, association between size and shape was not significant in females, while it was in males. Therefore, sexes likely have differential (heterogeneous) causes for the overall morphology which in turn may affect physiological, behavioral and life-history traits and finally lifetime fitness. In the framework of Charnov-Bull model, an association between adult morphology (quantified as size and shape) and environmental factors is pioneering to my knowledge. While it may give an additional perspective to influence of ESD on the morphological variation, it remains open whether this pattern can be extrapolated to other animals with ESD.

OP-EB-15

Personality and individual quality in a pulsed resource consumer, the wild boar (*Sus scrofa*)

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There is increasing evidence that animal personalities are linked to different life history strategies but our knowledge of those links in large mammals is still sparse. Here we investigated if animal personality is affecting reproductive success in female wild boar (*Sus scrofa*) and whether this effect is influenced by environmental conditions (i.e., food availability). Our results show that under good food conditions less explorative individuals had a higher reproductive success whereas under less favourable food conditions there seemed to be a slight advantage for more explorative individuals. Further, we show that juvenile body mass was another important factor affecting adult reproductive success and that there were no long-term costs of reproduction. We conclude that individual quality of female wild boars is determined already early in life and that different personalities in wild boar populations might be maintained by antagonistic selection pressures on personality traits depending on food availability in this pulsed resource consumer.

OP-EB-16

Short and long-term consequences of predator-induced phenotypic plasticity in a cichlid fish

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Phenotypic plasticity allows individuals to adjust their phenotype in order to optimally respond to their environment, for example to predation. These modifications can comprise both behavior and morphology. However, plastic modifications are also supposed to be costly and little is known about the long-term consequences of a plastic response. Here, we report results of a study on perpetual effects of antipredator phenotypic plasticity in the West African river cichlid fish *Pelvicachromis taeniatus*. Predation risk was simulated by exposing fish to conspecific alarm cues. In aquatic animals, chemical alarm cues are passively released by injured individuals during a predation event. We used a split-clutch rearing design and exposed fish continuously since fry stage to either conspecific alarm cues or control treatments for a time period of 2 years. During this time, we continuously assessed their morphology and behavior in different experiments ranging from shoaling experiments in juveniles to mate choice experiments in adult fish. Our results may allow inferences about the fitness consequences of plastic antipredator defenses by considering the force of both natural and sexual selection.

OP-EB-17

Habitat structure and the phenotypic diversity of the African cichlid fish *Tropheus moorii*

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In the East African rift Lake Tanganyika, the endemic cichlid *Tropheus moorii* exhibits an extremely high level of geographic color pattern variation. Genetic differentiation in *T. moorii* is strong, even across short geographic distances as long as populations are separated by at least a minor habitat barrier, and certainly helps to maintain color pattern differentiation among the allopatric populations. In the history of the species, however, the distribution of the stenotopic, littoral rock dweller has repeatedly been disturbed by lake level fluctuations and associated shoreline changes, causing secondary contact between previously isolated color variants. Incomplete reproductive isolation among color variants in experimental situations suggests that extant variants would not persist as independent taxa in secondary contact. Previous periods of secondary contact left signatures of introgression in many of the extant populations. In one well investigated case, locally restricted hybridization in secondary contact ~100,000 year BP gave rise to a novel hybrid color variant, which is currently separated from its parental lineages by geographic barriers in the lake but not by assortative mating preferences in experimental contact. Hence, whereas hybridization induced by punctuated paleolimnological events contributed to phenotypic variation, persistent habitat fragmentation remains indispensable for the preservation of the renowned color pattern diversity in *T. moorii*.

OP-EB-18

The ever asked question: Species or subspecies? -High genetic differences between *Orthetrum coerulescens* and *Orthetrum (coerulescnes) anceps* (Odonata, Libellulide).

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Correct species identification and characterization is the crucial fundament for every conservational effort. Though Europe is the cradle of Odonate systematics many uncertainties remain concerning species status and nomenclature, while the potential of adding molecular methods is still not taken into full consideration. One of many examples are the the libellulid dragonfly species *Orthetrum coerulescens* (Fabricius) and *Orthetrum anceps* (Schneider). Here, the subspecies status was recently established solely based on morphological characters. In the presented study, 100 individuals of *Orthetrum coerulescens ssp. coerulescens* and *anceps* (= former *O. anceps*) from nine study sites in Europe were analyzed for the mitochondrial gene fragments ND1, CO1 and 16S rDNA which are well established markers in Odonate genetic research. Additionally, the phylogenetic relationship between both forms was studied by comparison to a set of four "true" European species of the genus. Three genetic clusters with high genetic distances (>7% for ND1&CO1, >3.7% for 16S) seperate *O.coerulescens coerulescens* from whole Europe and *O.coerulescens anceps* from Cyprus. Those clusters are also highly supported by the phylogeny. The third group contains individuals from Italy, Sardinia and Hungary that are again highly distinct from Cypriote individuals, but close to western populations described as *O.coerulescens coerulescens*. Based on these results returning to a good species status between both forms is strongly recommended. Especially, as *O.coeruelescens coerulescens* is endangered in Germany and northern Europe whereas *O.coerulescens anceps* is listed as least concern in Eastern Europe. Uniting both forms in a single taxa could lead to inappropriate management strategies.

OP-EB-19

Cooperation under the bark: The evolution of microbial symbioses and sociality in ambrosia beetles

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Sociality and fungiculture independently evolved multiple times in wood-boring weevils, the so called ambrosia beetles. Interestingly, these lineages vary in ploidy levels (haplodiploidy vs. diploidy) and mating systems (inbreeding vs. outbreeding), which makes them ideal models for testing the importance of these factors for social evolution. Here I present some data on our focal species, *Xyleborinus saxesenii*, which demonstrate the potential of ambrosia beetles for studies on microbial symbioses and social evolution. This species is facultatively eusocial, i.e. given optimal conditions many females decide to delay dispersal from the mother's nest and help to rear their siblings. Exceptional for social insects also larvae and males help in the natal nest. Sociality apparently evolved only in weevils nutritionally associated with fungi. Fungal yields are probably higher in socially maintained nests, but to be sure we need to study the mechanisms of fungiculture using molecular methods. Pyrosequencing of microbial communities associated with dispersing *X. saxesenii* females, nest material and wood revealed several symbiotic fungi and bacteria. I present preliminary data on the role of some of the major fungal and bacterial players and how they interact with each other. Understanding the techniques of fungiculture will reveal why these beetles became social.

OP-EB-20

Social immunisation in ant societies

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Social insects (bees, wasps, ants and termites) protect their colony from disease outbreaks by health care of pathogen-exposed group members. While these sanitary actions reduce the risk of infection of the exposed individuals, they bear the risk for helpers to contract the disease themselves. By studying the invasive garden ant and its natural fungal pathogen *Metarhizium*, we found that the majority of the previously healthy workers indeed pick up the infection from their diseased nestmates. Interestingly, however, this pathogen transfer by social contact typically only results in low-level infections that do not kill the helpers but instead reduce their susceptibility to the pathogen upon secondary challenge due to increased immune gene expression. We study (i) how broadly this social immunisation protects ant workers against pathogenic threats, and (ii) how the acquired protection affects sanitary behaviours of these "socially immunised" individuals in the colony.

OP-EB-21

The queens, the workers, and the grim reaper: aging and reproduction in social insects

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Why organisms age and die and why they do so at very different paces are still major puzzles in evolutionary biology. Perennial social insects (honey bees, ants, termites) provide suitable systems to tackle this fundamental problem. In particular ants are characterized by an extraordinarily long lifespan of their reproductive females (queens), which may live tens or hundreds of times longer than non-social insects of similar body size. Furthermore, while many animals show the well-known trade-off between longevity and reproductive success, highly fertile ant queens by far outlive their non-reproductive nestmates, i.e., the trade-off appears to be reversed. We combined experimental manipulations of colony structure and queen fecundity, functional genomics, and analyses of the proteome of seminal fluid to shed light on the proximate bases of the apparent reversal of the fecundity/longevity trade-off in the ant *Cardiocondyla obscurior*. This species is an ideal model system because its queens are relatively short-lived (< 1 year), colonies are small (< 100 workers) and can be kept in the lab in large numbers, sexuals mate readily under controlled conditions, and the genome has recently been fully sequenced. The results of our studies indicate that both mating and egg laying prolong queen life span. Furthermore, highly fecund queens live longer than queens with a lower egg laying rate, and individual life span and fecundity react flexibly to the queen's social environment without any changes in external mortality risks. Preliminary functional genomic analyses reveal fundamental differences between the age-specific patterns of gene expression between *Cardiocondyl*a queens and solitary insects. Studies on the proximate and ultimate causes of life span variation in *C. obscurior* might yield important insights into the evolution of aging and age-specific fecundity in social insects.

OP-EB-22

A negleted early barrier: Learning of chemical host cues drives ecological divergence during speciation processes in a parasitoid wasps

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Ecological speciation, i.e. speciation via the evolution of ecotypes that are separated into different ecological niches, is considered an important mode of speciation in herbivorous and parasitoid insects. However, the mechanism behind the first step of separation, the switch of individuals into new niches, is unclear. One longstanding hypothesis, which was never tested, is that early learning of chemical host cues causes new ecological preferences, leading to a switch into a new niche within one generation. Here we show that a host switch occurred within a parasitoid wasp, associated the splitting into separate lineages during speciation. This host switch was most likely enabled by the ability for early learning (i.e. learning during larval development and after emergence from the host substrate) of chemical host cues in one of the lineages. The parasitoid wasp *Lariophagus distinguendus* (Chalcidoidea) consists of two genetically distinct lineages, which are reproductively isolated and have to be considered different species. One species has an innate preference for chemical cues from drugstore beetle larvae, which can not be altered by experience. Our data indicate that this was also true for the common ancestor of both species. In contrast, the second species is mostly found on *Sitophilus* weevils as hosts and changes its preference for chemical host cues by early experience. Therefore, a host switch must have occurred in the second species, which must have been enabled by early learning of host cues. Because early learning is a widespread mechanism in insects, it might have facilitated ecological divergence and associated speciation in this megadiverse group.

OP-EB-23

The evolution of an antimicrobial brood protection mechanism: Comparative morphology of the postpharyngeal gland in the Philanthinae (Hymenoptera, Crabronidae)

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Many Hymenoptera provision their offspring with highly nutritive resources. To ward off fungal infestation of the larval food, these species need antimicrobial strategies. Females of the philanthine wasps *Philanthus triangulum* and *Trachypus elongatus* embalm the surface of their prey, paralyzed bees, with a secretion from a complex postpharyngeal gland (PPG). This coating, consisting mainly of unsaturated hydrocarbons, reduces the accumulation of water on the prey's surface, thus rendering it unfavorable for fungal growth. Since the PPG has long been thought to be restricted to ants, where it is mainly involved in the generation of the colony odor, both the occurrence of a complex PPG, and its function in antimicrobial brood protection in solitary wasps are unusual. To investigate the evolution of both traits in philanthine wasps, we examined 26 species from six genera, representing all three tribes of the subfamily Philanthinae (Hymenoptera, Crabronidae). Comparative analyses, using light-microscopy and 3D-reconstructions, revealed pronounced morphological differences in the PPGs among the different tribes. While all members of the tribe Philanthini have complex PPGs, the studied species of the two more basal tribes possess comparatively simple glands. Moreover, we have clear evidence that females of another *Philanthus* species, *Philanthus gibbosus*, also possessing large PPGs, embalm their prey. Since prey embalming seems to require large, complex PPGs, we propose that both traits have evolved in and are restricted to the tribe Philanthini.

OP-EB-24

Genetic diversity in the *ex situ* population of the Northern Bald Ibis - Choosing suitable individuals for a reintroduction

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The Northern Bald Ibis, *Geronticus eremita* (Linnaeus, 1758), is a critically endangered bird species belonging to the family of Threskiornithidae. Until the 17th century the Northern Bald Ibis had its breeding grounds in the European Alps and the subalpine regions across Europe. Furthermore, the species had and partly still has its geographic range in Northern Africa and the Middle East. Due to hunting and the loss of suitable habitats, the Northern Bald Ibis became regionally extinct in Europe. In January 2014, the EU-LIFE+ Project "Reason for Hope - Reintroduction of Northern Bald Ibis in Europe" started, aiming at sustainable reintroduction of the Northern Bald Ibis as a migratory bird in Europe. As part of this project, we genotype the ex situ population as well as the last in situ population in Morocco and some ancient samples form the near-extinct Syrian population. For the genetic analysis, a set of primer pairs for 15 microsatellite loci was developed for the Northern Bald Ibis. We compared the genetic diversity within and between the genetic clusters identified in the ex situ population. In addition, we analyse the mitochondrial DNA using the gene ND5 as well as the nuclear genes KIAA, SACS and TTN. DNA sequencing is used to clarify if the species *Geronticus eremita* is subdivided into two genetic lineages (eastern and western lineage) as proposed by a former study. Based on the results, the origin of the zoo individuals will be clarified and a genetically diverse set of individuals will be chosen for reintroduction.

OP-EB-25

The value of spatio-temporal population genetic analyses, as exemplified by two case studies

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Most population genetic analyses are performed across different spatial scales without incorporating a temporal aspect. However, when including temporal samples into population genetic studies, inferences about the stability of observed patterns can be drawn. Spatio-temporal population genetic analyses further allow estimating effective population sizes, demographic trends and the potential for drift in a population. Here I present two examples to demonstrate the value of spatio-temporal analyses: 1) the pre- and post-fragmentation population structure and demographics of an endemic forest bird in Kenya, and 2) the effective population sizes and demographics of a microendemic and a widespread species of Lake Malawi cichlid fish. In both systems, spatio-temporal sampling was applied to address hypotheses regarding the demographics and population structure, which otherwise could not be resolved. We found small effective population sizes in both systems. In the birds fragmentation has resulted in source-sink dynamics between the remaining habitat patches. In the cichlids analyses revealed some evidence that drift may be a considerable force in driving the evolution of microendemics. Yet, allele frequency shifts were limited across ecological time frames.

OP-EB-26

A mitogenomic view on intercontinental dispersal in gray wolves (*Canis lupus*)

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Gray wolves (*Canis lupus*) have a very wide native distribution across the entire Holarctic. The fossil record indicates that the species evolved in Eurasia in the early Pleistocene, and then colonized North America in the mid Pleistocene. Previous phylogeographic studies found polyphyly of North American wolves within the diversity of Eurasian wolves with mitochondrial markers, but the support on deep branches was low and genomic data has suggested monophyly of the North American wolves. Here we analyze 105 whole mitochondrial genomes from the main clade of gray wolves by means of Bayesian coalescent analyses and within an approximate Bayesian computation framework to test for the number of times wolves colonized North America from Eurasia, and date colonization(s). We find that the mitogenomes of all living wolves in North America, including Mexican wolves, derive from a single colonization event from Eurasia that expanded its range into southern North America before the Cordillerian and Laurentide ice sheets fused in the Last Glacial Maximum, approximately 23KYA. This is more recent than expected based on the fossil record, suggesting that there were earlier colonizations that left no descendents.

OP-EB-27

Genetic and morphological divergence in Baltic postglacial common goby (*Pomatoschistus microps*) populations

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Divergent natural selection can cause adaptation of populations using different habitats - especially with a lack of barriers - while gene flow between such adapted populations acts as homogenising force and erodes population differentiation. However, even on a small spatial scale distinct genetic structuring of marine populations may exist. We used eight microsatellites to investigate population divergence on a small spatial scale between eleven populations of common gobies (*Pomatoschistus microps*) in the Baltic Sea but also considered a wider geographic range and included additional populations. The Baltic Sea is characterised by a steep decrease in salinity from the west to the east. Therefore, another goal of this study was to investigate how such an environmental gradient possibly acts as a natural barrier preventing gene flow between populations. To distinguish between natural selection and neutral processes like genetic drift causing population differentiation we used body shape of Baltic *P. microps* as phenotypic trait to perform a P_{ST} - F_{ST} comparison. Our molecular results (Nei's Da) show a clear genetic differentiation between Mediterranean, Atlantic, North Sea and Baltic populations, whereby eastern Baltic populations (low salinity) form a monophyletic group within the Baltic cluster. P_{ST}-F_{ST} comparison revealed natural selection favoring different phenotypes in different populations driving population differentiation of common gobies in the Baltic Sea. We discuss phenotypic and genetic patterns in relation to our complementary site-specific demographic and ecological field data.

OP-EB-28

Population genetic structure of the coconut crab *Birgus latro* (Decapoda: Anomura: Coenobitidae) from Christmas Island in the Indian Ocean

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The coconut crab *Birgus latro* has suffered from population declines up to complete extirpations on many islands throughout its wide range in the tropical Indo-Pacific, mostly as a consequence of overharvesting, habitat loss, predation by introduced alien species and road mortality. Due to a lack of data, the species has been classified as "data deficient" by the IUCN. With the objective to enhance scientific knowledge on the species' ecology and give scientific advice for future conservation strategies, we assessed the genetic population structure of *B. latro* on Christmas Island, Indian Ocean (area » 135km^2), which is reported to harbour the largest population of this species. For the population genetic structure analysis we used seven polymorphic microsatellite markers. We sampled adult individuals at five different locations (≙ subpopulations), with 20 individuals per location. The results of the genetic structuring analyses do not suggest an obvious population subdivision: Global and pairwise F_{ST} values were low; Bayesian methods and a principal component analysis did not reveal any population sub-structuring. Genetic diversity was comparatively high and similar for both sexes. However, consistently lower values for observed in relation to expected heterozygosity, and high values of F_{IS} suggest an inbreeding system of mating. We did not detect a population genetic signature of sex-biased dispersal. With approx. 492, the effective population size of the total population was low, but the population has most likely not experienced a recent genetic bottleneck. In conclusion, the population of *B. latro* on Christmas Island is in urgent need of protection measures, but may so far be considered as a single management unit.

OP-EB-29 - Evolution of thermogenic adipose tissue in mammals

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Brown adipose tissue (BAT) is a unique evolutionary outcome enabling adaptive thermoregulation in eutherian mammals. BAT releases energy as heat, in contrast to energy-storing white adipose tissue (WAT). Heat production is catalysed by the BAT-specific mitochondrial uncoupling protein 1 (UCP1). Recently, the molecular signature of a third adipocyte type expressing UCP1, termed the beige or brite (brown-in-white) cell, was characterized in rodents and humans. However, the physiological role, the contribution to systemic thermoregulation and the evolutionary origins of the beige/brite cell are unknown. In marsupials, which diverged from eutherian mammals about 140 MYA, we identified expression of UCP1 in adipose tissue of 'brownish' appearance, but noradrenaline did not trigger the classical adaptive excitation of thermogenesis. We have determined UCP1 gene expression levels during juvenile development of the grey short-tailed opossum, *Monodelphis domestica* and found the emergence of UCP1 in three different adipose tissue depots that coincides with a shift of fat storage from the liver towards distinct anatomical adipose tissue sites. Despite progressive increases in UCP1 levels, histological analysis identified no significant remodelling into typical multilocular lipid droplets of BAT. To determine the molecular identity of UCP1-positive adipocytes in marsupials for cellular classification and functional implications, we performed RNA sequencing of the interscapular adipose tissue and characterized global gene program changes associating with UCP1 gene expression. We annotated gene products to the respective modern eutherian orthologs to answer the question which pathways were already wiring UCP1 biology in adipocytes about 140 million years ago.

OP-EB-30

One inversion to rule them all: the genomic basis of mating strategies in the ruff

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Characterising genomic structures that produce complex phenotypic variation within a species are important to understand how behavioural and morphological diversity has evolved and is maintained. The ruff *Philomachus pugnax* is a model system of sexual selection where males follow one of three genetically determined mating strategies: most ruff males are dark ornamented aggressive “Independents” that fight for territories on a lek. In contrast, light ornamented “Satellite” and unornamented female mimic “Faeder” males are non-aggressive and pursue opportunistic matings on leks. We used a combination of whole genome sequencing and RAD sequencing to characterise the genomic basis of this stable polymorphism. We describe an autosomal 4.4 Mb inversion located on chromosome 11, which is shared by Faeders and Satellites. The inverted haplotypes are homozygous lethal since one of the breakpoints disrupts the *Centromere N* gene, which is essential for centromere assembly during mitosis. Therefore recombination between haplotypes is suppressed. Within the inversion we found 125 predicted genes of which 80% differ between the three morphs. Five of these genes are involved in steroid metabolism including *Estradiol 17-beta-dehydrogenase 2*, which converts bioactive androgen and modulates aggressive behaviour. Other genes with unique rearrangments such as *Melanocortin receptor-1* and *1-Phosphatidylinositol 4,5-bisphosphate phosphodiesterase γ-2* may explain the pale ornaments in Satellites and the lack of ornaments in Faeders. We conclude that the inversion enabled the evolution of divergent haplotypes that led to multiple alternative reproductive morphs.

PP-EB-01

Inferring reproductive mechanisms of extinct organisms: Examples from dictyopteran insects

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Modern representatives of cockroaches and praying mantises deposit their eggs in a kind of egg package, a quite robust case, the so-called ‘ootheca’. This characteristic is one of the most remarkable apomorphies of Dictyoptera (s. str). This specific reproductive strategy, involving more parental investment than the deposition of single eggs, might be one reason for the relatively large evolutionary success of this insect group. Despite the robustness of the oothecae, fossil examples have been found very rarely. Only five specimens are known so far in the literature, additional specimens are presented here. Assuredly, more specimens exist, but it might be challenging to identify fossil oothecae. The oldest definitive cockroach oothecae were discovered in the Cretaceous Crato Formation, Brazil (115 mya), and it seems likely that the origin of this reproductive strategy can be allocated near this time period. The deposition of eggs in an ootheca can be considered as a simple type of brood care. The ability to produce oothecae is presumably linked with the reduction of the ovipositor, up to an ovipositor completely covered by abdominal sternites. Therefore, several dictyopteran species are also able to protect their descendants by retaining the ootheca attached to the abdomen until the time of hatching of the nymphs. Beside this, several species of Blattodea exhibit a wider range of further brood care, which can be mirrored in the developmental condition of the hatchlings. In consequence, the morphology of early nymphs and of the ovipositor of females as well as the presence of oothecae facilitate to infer details about the degree of brood care and in general about the reproductive strategies in dictyopteran insects.

PP-EB-02

Coevolution in action: effect of simultaneous exposure to two parasites on the host's external & internal immune defence

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Every organism is a potential host to a multitude of natural enemies existing in the environment such as parasites. Hosts and parasites in their close associations can exert a variety of selection pressures on one another. A likely result of such interactions is coevolution marked by reciprocal genetic changes in the host and the parasite. We performed experimental coevolution under standard laboratory conditions using the red flour beetle *Tribolium castaneum* as the host and two parasites; the general entomopathogenic fungus *Beauveria bassiana* and coleopteran specific bacterium *Bacillus thuringiensis*. Four treatments were performed with seven replicate beetle lines per treatment: (i) control (ii) parasite adaptation (iii) host adaptation and (iv) coevolution. Each set of four treatments was conducted under fast and slow host developmental regimes. Barring control, *B. bassiana* and *B. thuringiensis* were present in the environment in all the treatments. The entire experiment was conducted for eight host generations. In addition to having an innate immune defense *T. castaneum* is also able to condition its environment via external defense secretions in the form of volatile Quinone compounds. It has been shown in *T. castaneum* that external immunity is compromised upon *B. bassiana* infection and internal immune activity increases upon *B. thuringiensis* infection. Phenoloxidase activity and Quinone secretions of adult beetles were measured as a proxy for internal and external immune defence respectively at fixed time points during the entire experiment. Here we present the results on the effects of two parasites on the host's immune defense in the context of experimental host-parasite coevolution.

PP-EB-03

Testes degeneration in ant males

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In males of social Hymenoptera, testes degenerate after adult emergence. Mating is normally a short episode on the wing, and hence, the sperm supply can be expected to be sufficient to inseminate all available females. This is different in the ant *Cardiocondyla obscurior*, where mating takes place in the nest and sexuals are produced regularly. Therefore, males are able to mate with a large number of female sexuals. This has led to the evolution of an environmentally induced male diphenism. Wingless males stay lifelong in the nest and fight with eclosing rivals to monopolize all virgin queens in the colony. As an adaptation, their testes do not degenerate and spermatogenesis continuous throughout their lives. Winged males represent the "normal" ant males. They are produced as disperser morph under stressful conditions, and, as typical for ant males, their testes degenerate a few days after emergence. However, winged males of *C. obscurior* mate also within the nest before they leave it after several days, and it has been shown that the timing of dispersal depends on the availability of virgin queens and competitors inside of the colony. Here, we investigate whether - in accordance with the behavioral plasticity - the timing of testis degeneration in winged *C. obscurior* males is similarly flexible, dependent on their mating opportunities. We compare the occurrence of germline stem cells and the degree of testes degeneration of winged males of different chronological ages with and without access to virgin queens and queen pupae.

PP-EB-04

Does sexual dichromatism predict sex-biased opsin expression in cichlid fishes?

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Cichlid fishes are one of the most diverse and colorful animal families on earth. This color diversity is complemented by a highly complex visual system. Cichlids typically exhibit a trichromatic vision based on seven different cone opsin genes, each with distinct light sensitivities. Natural selection has driven the divergence in visual systems among cichlids inhabiting different photic environments. This resulted in the differential expression of opsin genes which in turn influenced reproductive isolation based on body coloration. Yet, it is unclear if sexual selection has directly affected the evolution of the visual system. R. Fisher's *´Run-Away Theory*´ predicts that sexual selection favors the evolution of colorful males if female preference for these colors gets genetically correlated. This could result in the coevolution of sex-related dichromatism and dimorphism in the visual system. In this study we tested if sexual dimorphism in visual systems is correlated to differences in nuptial body coloration. We used RT-qPCR to investigate differences in cone opsin gene expression between the sexes across multiple cichlid species. Our analysis included several monochromatic and dichromatic species from both, the old and new world cichlid clades. As expected, we identified differences in opsin expression levels among investigated species. However, sexual dimorphism in opsin expression patterns seemed to be restricted to only some dichromatic species. We conclude that the evolution of sex-biased opsin gene expression may be affected by additional factors, such as breeding mode, territorial behavior and male-male interactions. In fact, we found first evidence that sexual dichromatism affects opsin pseudogenization rates.

PP-EB-05

Role of endosymbionts as isolating barrier for *Nasonia* strains from different host habitats

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Due to the fact, that their genomes are sequenced, the jewel wasp *Nasonia vitripennis*, a parasitoid of fly pupae, and the congeneric species *N. giraulti*, *N. longicornis* and *N. oneida* are increasingly used as model organisms to study mechanisms of speciation. To analyse early phases of separation, we compared different isolating barriers with two different strains of one population of *N. vitripennis,* collected either from bird nests or from carcasses in the field. Here we report on the role of endosymbiotic bacteria causing cytoplasmic incompatibility (CI), and sexual isolation. Mating experiments revealed that females from the strain collected on carcasses do not produce female offspring when mated to males collected from bird nests. In contrast, female offspring is produced in the reciprocal cross and when both strains have been treated with antibiotics. Thus, there is unidirectional isolation between the two strains, which can be rescued by antibiotics. This strongly indicates the presence of cytoplasmic incompatibility (CI) caused by endosymbiotic bacteria.We hypothesized that females from the carcass strain avoid copulations with males from the nest strain because this results in mortality of female offspring. Therefore, we observed mating behaviour of females and males from the two strains which have been treated with antibiotics or not. Interestingly, females mated in all cases, indicating that they are not able to discriminate between suitable and unsuitable males. Thus, our strains of *N. vitripennis* from one population but two different habitats are isolated by CI due to endosymbionts, but not due to sexual isolation.

PP-EB-06

Coping with host plant toxins - Adaptive strategies of milkweed bugs

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Milkweed species (*Asclepias*) contain toxic cardenolides as an anti-herbivore defense. The specialized herbivorous bug *Oncopeltus fasciatus* is nonetheless able to feed on milkweeds because it evolved striking physiological and morphological adaptations to deal with these toxins. Owing to a highly insensitive Na,K-ATPase the bugs are able to assimilate large concentrations of cardenolides in their body without suffering toxic effects. Furthermore, ingested cardenolides are taken up and sequestered in specialized storage compartments in the thoracic region. Upon encounter with a predator a defense fluid enriched with ingested cardenolides is released from special releasing sites at the lateral margins of the thorax. The bugs thus not only cope with the chemical defense of their host plants, but also employ it for their own defense against predators. To study the molecular mechanisms which enable cardenolide sequestration in *O. fasciatus* we are focusing on two gene families, ABC transporters and organic anion-transporting polypeptides (Oatps). Both are potential efflux or influx carriers and have been shown to transport cardenolides in vertebrates and are involved in the adaptations of herbivores to host plant toxins. Thus, these carriers are good candidates to mediate cardenolide sequestration in *O. fasciatus*. A search of the transcriptome of *O. fasciatus* revealed two sequences each with similarity to members of the ABC-B and ABC-C subfamily. ABC-B and ABC-C genes showed expression in various tissues of bugs fed on *Asclepias*. By qPCR we are currently quantifying gene expression to further elucidate a potential role of these carriers in cardenolide sequestration and to identify candidates for RNAi knock-down experiments.

PP-EB-07

Chromosomes of the *Lariophagus distinguendus* complex

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The parasitoid wasp *Lariophagus distinguendus* (Förster 1841) has been shown to consist of two distinct types that differ in their host preference, are found in different habitats and are reproductively isolated under natural conditions. One type parasitizes the granary weevil *Sitophilus granarius* in grain stores, the other is found in pantries using the drugstore beetle *Stegobium paniceum* as a host. Thorough morphological analyses based on numerous characters showed no clear differences. A chromosomal analysis revealed that the type parasitizing *St. paniceum* has a single set of six chromosomes whereas the type using *S. granarius* as hosts has five chromosomes. This clearly demonstrates that the two types are in fact different species. This agrees with the results of a molecular analysis, showing a clear separation between the types. Certain circumstances allow hybridization of the *Lariophagus* species. A chromosomal analysis of the hybrids showed that the female hybrids each possessed eleven chromosomes, whereas in hybrid males only sets of five chromosomes occurred. This indicates that chromosomal rearrangements contribute to reproductive isolation in *Lariophagus.*

PP-EB-08

Mapping genes of life-history traits in a wild bird population

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Understanding evolutionary change obviously requires knowledge of genetic variation in traits that are under selection. Over the last decade quantitative genetic analyses in wild, pedigreed populations have contributed to this by estimating genetic (co)variation in many traits, which has helped us to understand why (or why not) and how traits can respond to selection. Identifying the genes underlying these traits will further advance our understanding of evolutionary processes in natural populations, e.g. because it would allow us to directly track genetic changes and thereby disentangling phenotypically plastic from genetic changes. The necessary genomic resources for gene mapping have only been available for species that are closely related to domesticated species but the recent technological advances allow us now to develop the necessary resources also in 'ecological model species'. Making use of the recently assembled great tit genome and a 500k SNP chip developed for this species we here explored the genomic basis of seasonal breeding time and clutch size in a wild great tit (*Parus major*) population. We genotyped about 2500 individuals from our long-term study population with known phenotypes and identified genomic regions related to these traits using a genome-wide association study.

PP-EB-09

Evidence for a chemical arms race: chemical mimicry in the cuckoo wasp genus *Hedychrum*

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Mimicking cuticular hydrocarbons (CHC) is a strategy of various parasites that allows exploiting resources of their hosts inconspicuously. There are two alternative sub-strategies to mimic the hosts' CHC profile: the parasite acquires the CHCs directly from their host; or the parasite evolves the ability to produce a CHC profile similar to the host by altering its own CHC biosynthesis. In the latter case, an arms race is expected to take place between host and parasite. Evidence for the latter taking place in nature is scarce, however. To investigate a chemical arms race between hosts and parasites, we compared the CHC profiles of cuckoo wasps of the genus *Hedychrum* and their hosts, digger wasps of the subfamily Philanthinae. Within these hosts, one group uses a highly specific CHC mixture for preserving its prey. These hosts exhibit the same largely uniform CHC composition also on their own cuticle. Due to the dual function of CHCs in this group of hosts, the hosts' CHC profiles are expected to be under stabilizing selection, providing cuckoo wasps an easy model to mimic. The CHC profiles of these cuckoo wasps indeed match those of their hosts. In a second group of hosts, CHCs are not used for prey preservation. The CHC profiles of these hosts differ much more from each other and are highly species-specific. Chemical mimicry by cuckoo wasps parasitizing this last group of hosts is far less precise. We therefore hypothesize that the conspicuous interspecific CHC differences among hosts is likely the result of these hosts evading chemical mimicry of their cuckoo wasps.

PP-EB-10

Does sessility simplify nervous systems? A case study in Annelida

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Ascidian tunicates are a prominent example for a strict correlation between simplification of the nervous system and sessility (Benito-Gutièrrez & Arendt 2009). A few authors recently regarded this correlation as a causal relation assuming that sessility results in simplified nervous systems (Northcutt 2013). Vagile animals are accordingly expected to have a more complex neuroanatomy. Annelids are ideal to test these assumptions. Recent phylogenomic analyses show that sessility is an ancestral trait, maintained in the basal most branching tubicolous annelids, like in oweniids. According to these analyses certain higher annelid taxa, like sabellids, secondarily returned to sessility. By comparing the brain structures of these taxa, one would expect (1) that the brain structure of vagile species is more complex than that of sessile species and (2) that secondary sessility simplifies the brains structure, probably in such way that it is similar to primarily sessile species in terms of character reversals. We therefore generated complete series of Azan-stained histological sections of the brain of 35 annelid species from different subgroups. We used aligned stacks to reconstruct the anatomy of the central nervous systems and to infer the evolution of this organ system based on recently published molecular phylogenies. We can show that the brain of vagile species turned out to be highly complex, while basally branching sessile groups possess a simple basiepidermal, ring-like brain. In contrast to our expectation secondarily sessile species possess a brain that is far more complex than that in basally branching taxa. This result advises caution about interpreting observed correlations as examples for general rules or causal relations.

PP-EB-11

Signalling strategies in the bushcricket *Poecilimon ampliatus* (Orthoptera: Tettigoniidae)

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Males of most buscrickets taxa use acoustic signals to attract conspecific females for mating. In most cases, males sing in choruses, with several simultaneous rivals. Those songs seem to be honest signals, allowing females to choose the male with superior quality. Therefore, song traits are probably under sexual selection. In previous studies on the unidirectional communicating species *Poecilimon zimmeri* (Tettigoniidae: Phaneropterinae), females preferred the heavier of two competing males (Lehmann & Lehmann 2008), which transfer the bigger nuptial gift during mating (Lehmann & Lehmann 2009). Using the congeneric bushcricket species *Poecilimon ampliatus*, we investigated condition-dependent signalling in males, measuring several song characters: a) duty cycle (amount of song produced per time unit), b) singing rate (verses/min) c) verse duration and d) pause duration. During song competition heavier males surpassed their 100 mg lighter rivals in emission of acoustic signals. Heavier males produced songs with significantly longer verses at higher duty cycles. These individuals were especially capable of speeding up their acoustic production at closer distances. In contrast, singing rate was similar between lighter and heavier males; verse duration was only slightly increased in the later ones. We can infer that male body weight and singing distance affect the male's investment in song production. In *P. ampliatus*, verse duration and duty cycle seem to be important clues to signal a males' quality. Giving the strong song competition in this species, we expect important consequences for male calling strategies in natural choruses.

PP-EB-12

A potential role for sexual selection in the divergence of Tropical Pacific honeyeaters (*Myzomela*)

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The relative roles of neutral and selective processes in divergence are of key interest in evolutionary biology. Due to the many large and small islands, the Indopacific area constitutes an ideal natural laboratory to study the different modes of diversification. It is a biotically extremely rich region, and as a result is designated as several distinct biodiversity hotspots. It was suggested that the islands of the Pacific are a likely source of biodiversity, rather than a sink of species that originated on the mainland, as has long been the established hypothesis. We use landscape genetic approaches to study the potential roles of drift, natural selection, and sexual selection to study the divergence among island and mainland species of sexually dimorphic honeyeaters, *Myzomela sp.* We found that males exhibit distinct differences between islands in plumage coloration and song, but not in other, fitness-related morphological traits. Females did not show divergence in any morphological traits between islands. Neither environmental heterogeneity nor oceanic barriers explained the observed divergence in plumage coloration and song. These results suggest that sexual selection is a potential factor in maintaining and deepening population differentiation. Sequence and microsatellite data indicate that these populations either very recently diverged or experience ongoing gene flow, and planned coalescence-based analyses will be useful in distinguishing these two hypotheses. The role of sexual selection in population divergence will be further evaluated using mate choice experiments.

PP-EB-13

Oribatid chemosystematics revisited: “Brachypyline Compounds”

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Oribatid mites (Acari) represent a group of more than 10.000 species, and the majority of these possesses characteristic oil glands in the hysterosoma (“glandulate Oribatida”). Oil glands are known to produce taxon-specific multicomponent secretions, allowing chemosystematic studies within the Oribatida sensu lato (i.e. including Astigmata). So far, investigations focused on so-called “Astigmata-compounds” - a set of oxygenated monoterpenes and aromatics that characterize both lower glandulate Oribatida (i.e. Mixonomata, Desmonomata) and Astigmata. By contrast, virtually nothing is known about the oil gland chemistry of higher Oribatida (Brachypylina): these, however, constitute the largest oribatid taxon. We here provide first evidence for the possibly basal oil gland chemistry of higher Oribatida: In detail, an array of homo- and sesquiterpenes was found in both basal brachypylines but also in a few lower Oribatida. We thus propose the existence of a second chemical lineage within Oribatida that evolved from “early” astigmatid compounds-bearing groups, bridging the chemical gap between lower oribatids and basal brachypylines. Compounds characterizing this lineage are referred to as “brachypyline compounds”. The addition of this second chemical lineage to currently available chemical data allows the generation of a much more comprehensive, logically explainable and consistent model to explain the evolution of oil gland secretion chemistry in the Oribatida.

PP-EB-14

The role of acoustic tracheal design on directional hearing in crickets

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Sound localization is an important task for mate finding. In crickets, however, this is challenging because the wavelength of the carrier frequency of calling songs strongly exceeds the cricket's body size and therefore produces no significant diffraction for the establishment of interaural intensity differences (IIDs). Their excellent localization ability is achieved by a modified system of trachea connecting the tympana of both ears via an external sound entrance. Sound transmitted within the connecting trachea between both ears has to pass a thin membrane (septum) in the midline of an acoustic vesicle. Crossing of the septum induces phase delays within a narrow range of species-specific calling frequencies resulting in tuned directionality and IIDs. In a comparative approach including 50 ensiferan species, we found a high morphological variation in acoustic tracheal types, both with respect to design and relative size. In species that are characterized by loss of acoustic signaling, we show a strong reduction of the acoustic trachea. We also studied the property of acoustic tracheal design for providing peripheral directionality and binaural cues used for sound localization. The amount of IIDs and the match between frequency sensitivity and directional tuning (which is expected to be important for optimal performance for the task to detect and to localize mating signals) seem positively correlated to the relative acoustic vesicle size. However, unfavorable large wavelengths of species with low carrier song frequencies are not related to relative acoustic vesicle size, suggesting that species-specific calling frequencies are not crucial evolutionary constrains with respect to vesicle and septum size.

PP-EB-15

When morphology meets genes: divergence between western and eastern subclades of Hermann's tortoise in the Balkans

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Quantification of morphological and genetic divergence among populations is fundamental to the understanding of microevolutionary processes. Congruence between morphological and molecular data is often seen as an evidence for species delimitation. However, early stage of differentiation between populations is usually characterized by complex and/or incongruent relationship between morphological and genetic variation which in turn may impede taxonomical assessment, biodiversity estimation and conservation strategies. Here we quantified and compared pattern of genetic and morphological diversity of the eastern clade of Herman's tortoise (*Testudo hermanni boettgeri*) which inhabits the Balkan Peninsula. Populations of the taxon are prone to the illegal harvesting, transloacations and habitat degradation while its taxonomical status was widely debated and still unresolved. Therefore, we studied phylogeographic structure based on cytochrome b mitochondrial DNA of 48 individuals and morphological diversity of shell shape of 469 individuals using 2D geometric morphometrics. Molecular data showed that western group (populations along the Adriatic coast) represents divergent evolutionary unit compared to the eastern group (Central and Southern Balkans). Likewise, based on shell shape variation, 90% of individuals were correctly classified to eastern and western groups. Analysis of morphological disparity suggests that shell morphology is developmentally more canalized in the western group, which is further corroborated with tendency for greater integration of shell parts. Furthermore, magnitude and direction of sexual shape dimorphism is differently affected in western and eastern groups. Therefore, consistent pattern of shell shape canalization between sexes and differential pattern of sexual dimorphism between eastern and western groups suggest that sexual selection may play driving role of morphological divergence. These findings will be discussed from taxonomical perspective as well.

PP-EB-16

Contrasting phylogeographic patterns in the Red Sea collector urchin *Tripneustes gratilla* based on mitochondrial vs. nuclear marker genes

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Tripneustes gratilla is one of the most widespread Indopacific shallow-water echinoids. As in populations from the Red Sea *T. gratilla* is morphologically well differentiated compared to populations in other parts of the species' range, a separate subspecies was proposed for the Red Sea population: *T. gratilla elatensis*. Earlier phylogeographic studies based on mtDNA demonstrated a lack of phylogenetic structure for *T. gratilla* and haplotype sharing was observed between widely distant regions. Here we present first genetic data for *T. g. elatensis* from the Red Sea, which so far has not been included in phylogeographic studies on *Tripneustes*. Phylogeographic reconstruction was based on two marker sequences (mitochondrial *COI* gene, nuclear *Bindin* gene) analysed in samples from widely distant populations. In contrast to the expectations based on the apparent morphological differences, Red Sea *Tripneustes* are not differentiated from Indian Ocean populations and share haplotypes with specimens from both the Philippines and East Africa. *Bindin* sequences, however, show a different pattern: three clades were found, comprising 1) Red Sea, 2) Indomalayan (Philippines, Guam, Papua New Guinea), and 3) mixed Indo-West-Pacific samples. High levels of differentiation in *Bindin* sequences among these clades suggest ancient radiation, greatly contrasting the COI data. This apparent mismatch of mitochondrial and nuclear DNA data implies a mitochondrial capture event in the recent past. Independent morphological evidence lends support to this, since in-depth investigations indicate that the differentiation of *T. g. elatensis* is not restricted solely to minor difference in corona proportions and coloration, but is also observed in lantern morphology and tubefeet spicules.

OP-M-IT-01 - Moving fluids for live - a sponge perspective

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Sessile filter feeding animals, including sponges (Porifera), rely on efficient fluid transport systems to keep energy expenditure for water processing low. As a consequence of the sponge canal system complexity only limited data on flow velocities and transport rates are available. This restricts our understanding of this central anatomical structure and related physiological processes, functional morophological principles and ecology. Obtaining experimental measurements from internal parts of the canal system is almost impossible for most species. Therefore data are mainly based on theoretical assumptions. This is linked to the limited availability of detailed morphometric and quantitative data on canal system architecture. Here I discuss experimental and *in silico* results on flow studies in marine and fresh water sponges. Canal system models based on SR-µCT data allowed for the setup of finite element models to study flow inside the aquiferous system and the influence of specific canal system elements (bypasses and cellular structures). In order to calibrate the model and verify results flow velocity measurements by particle tracking velocimetry have been performed. Observed flow velocities in canal segments of diverse hierarchical orders differ from predictions based on the classical hierarchical model of flow for sponges which reported much higher and faster increasing flow velocities towards the osculum. This is a consequence of the aquiferous system architecture which displays a compensating increase in available canal volume. With the ability to actively change canal diameters and aperture openings in the canal system sponges are most likely able to fine tune internal flow velocities and perfusion rates of specific areas of their body.

OP-M-IT-02

Prey capture systems in newts (salamandrids): Does behavioral plasticity trigger morphological alterations?

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Newts exhibit a remarkable form of behavioral plasticity where adults seasonally change between an aquatic and a terrestrial life. These seasonal habitat changes alter functional demands on the whole organism as physics are strikingly different between water and air. Recently it was shown that the prey capture mechanism in newts changes from suction feeding in water to lingual prehension on land. However, suction feeding and lingual prehension demand different and to a large degree conflicting functional-morphological adaptations to the feeding system. Accordingly, it was hypothesized that the habitat shifts in newts trigger morphological changes in the feeding system to account for different structural requirements. Specifically, changes were expected in the musculoskeletal system, the lingual mucosa and the labial lobes. While the musculoskeletal system of the prey capture apparatus seems not to be subject of major changes across habitat shifts, significant alterations were detected in labial lobe design and lingual mucosa morphology. Labial lobes are skin folds that occlude the gaping mouth laterally and grow when newts change to the aquatic stage but are degenerated when newts become terrestrial again. Similarly, the lingual epithelium is thin and has a smooth surface with few mucous cells in the aquatic stage but grows thicker, increases the number of mucous cells and gains special papillae as newts become terrestrial. This study shows that labial lobes facilitate directional water flow during suction feeding but are useless on land while the appearance of filiform papillae and the augmentation of mucous cells increase adhesive potential when the tongue is used to capture prey in the terrestrial stage.

OP-M-01

The feeding apparatus of chelicerates - far from 'primitive'

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Chelicerates are often treated as the 'primitive' branch of the euarthropod tree. This seems based on the morphology of the feeding apparatus: it appears much less specialised in chelicerates. In extreme views chelicerates have been interpreted to have somehow missed to develop proper mouthparts. Such assumptions base on a profound misunderstanding of character evolution within euarthropods. Also, the morphologies of the feeding apparatuses of fossil chelicerates are simply not taken into account. Both these factors are coupled. The inclusion especially of fossil marine chelicerates shows clearly that the short and seemingly simple ('primitive') feeding apparatus of land-living chelicerates is indeed highly specialised. I present here the feeding apparatuses of different chelicerates: 1) early forms, 2) xiphosurans, 3) sea scorpions, and 4) early arachnids. In early forms of the chelicerate lineage the feeding apparatus appears still rather unspecialised. Like in the ground pattern of euarthropods all legs are incorporated into the feeding apparatus. But also here some forms already possess further specialised legs. In xiphosurans the feeding apparatus is shortened to only the prosomal appendages. Sea scorpions have fairly complex feeding apparatuses, into which also all prosomal legs are incorporated. The last prosomal appendage pair is connected medially and forms a functional lower lip. This structure guides the second-last appendage pair, which is mandible-like. All legs possess numerous spines and hairs and thus do not differ significantly in this aspect from the armature of the mouthparts of crustaceans. In arachnids, the feeding apparatus is even shorter, however, not in all forms restricted to the most anterior area.

OP-M-02

The “very hungry caterpillar“: a 150 million years old parasitic isopod and the functional morphology of its extant relatives

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Parasites are known from all habitats and among most major groups of animals. Due to their influence on food webs, ecosystems and evolutionary development, they are ecological and economical important. However, the fossil record of parasitism is very rare, especially the direct evidence of parasites on hosts. We describe 150 million years old fossil fishes from the famous Solnhofen lithographic limestones, on which isopods are attached. Up to three isopods sit on one of the fishes, all close to the vertical or ventral fins. Morphology of the fossil isopods and their position on the fishes are similar to modern cymothoid isopods, which also are parasitic on fishes. With this, the fossils represent a case of direct indication of parasitism in extinct organisms. Additionally, we reconstructed the functional morphology of the modern counterparts of the fossils, *Nerocila*-like cymothoid isopods. These where documented with micro-CT and autofluorescence imaging. The mouth parts show strong modifications to form a mouth cone which facilitates sucking. Also the trunk appendages are strongly modified. The elongate scimitar-shaped distal parts of these appendages grab into the rays of the fins, prohibiting an easy removal of the isopod from the host. Deep lesions occur when successfully actively removing the isopods. Our discovery represents the first direct fossil record of a cymothoid isopod parasitizing on fishes. It also supports that *Nerocila*-like isopods are at least 150 million years old. Lastly, we have now a better understanding of the functional morphology of the extant forms facilitating also an identification of possible isolated fossil parasitic isopods in the future.

OP-M-03

Cribellar thread production in spiders: an example for processing fibres

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Spider silk has been intensively investigated during the last decades, especially with respect to mechanical properties, which are of high interest for technical applications. However, not only the mechanical properties of spider silk are amazing: Cribellar spiders have the capability of processing up to three different types of silk to one functional capture thread. Involved in this assembly is a comb-like structure on the metatarsus of the fourth leg, called calamistrum. This processing is nearly unstudied, mainly due to the small scale of the involved fibres, its complex arrangement and the occurring difficulties studying nocturnal and very small animals. Nevertheless, the importance of resolving the mechanism behind the production has not only been emphasised by the biological side, but is also interesting for a technical reproduction. Analysing the threads structure, we found nano-scale fibres organized as a mat, enclosing two parallel larger fibres and forming the typical puffy structure of cribellate threads. Mat and larger fibres are punctiform connected to each other between two puffs, presumably by the action of the median spinnerets. However, this connection does not lead to the typical puffy shape of a cribellate thread, exclusively. Removing the calamistrum, we found a functional capture thread still being produced, but the puffy shape of the thread was lost. Therefore, the calamistrum is not necessary for the extraction nor combination of fibres, but for further processing of the nano-scale fibres. Using the data from *Uloborus plumipes* we were able to develop a model of the cribellate thread production. Our model is probably universally valid, as it visually matches the production process in other cribellar spiders

OP-M-04

Ptychoidy done differently - insights into the Protoplophoridae (Enarthronota, Oribatida, Acari)

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Oribatida (Acari, Arachnida) developed a number of different defensive mechanisms supposedly based on the relatively low quality of their food resulting in slow movement, prolonged generation time and a reduced reproductive potential. The most complex mechanical defensive mechanism is ptychoidy, where the animals can retract their legs and mouthparts into a secondary cavity in the idiosoma and encapsulate by deflecting the prodorsum. Despite its complexity, ptychoidy evolved three times independently, once each in Ptyctima, Mesoplophoridae and Protoplophoridae. Ptychoidy is well studied in Ptyctima, but so far no investigations have dealt with the morphology and function of ptychoidy in the other two groups. We used synchrotron X-ray microtomography (SRµCT), scanning electron microscopy and high-speed videography to investigate the morphological and functional characteristics of ptychoidy in the protoplophorid mite *Prototritia major* JACOT. *P. major* shows yet another mechanism for the accommodation of volume changes associated with ptychoidy. Ecptychosis, the process of re-opening starts with the paired pleuraspis sliding dorso-laterad on rails on the unpaired pygidium thereby revealing anal and genital valves. Subsequently, the unity of those plates is telescopically retracted into the pronotaspis. Against all expectations we could not find muscles directly connecting pronotaspis and pygidium leading to the retraction of the plates, but suspect one of the muscles responsible for the sliding mechanism to perform this task as well. To gain insights in the evolution of ptychoidy in Protoplophoridae, we will compare our findings in *P. major* to the non-ptychoid Sphaerochthoniidae, the sister group of Protoplophoridae.

OP-M-05

Functional morphology of the tracheal system of *Galeodes granti* (Chelicerata:Solifugae)

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Camel spiders (Chelicerata: Solifugae) are active predators (Punzo, 1998) with a high metabolic rate (Lighton et al., 2001). As opposed to other large and active chelicerates, e.g. scorpions, camel spiders rely for gas exchange solely on their tracheal system. In contrast to other tracheate chelicerates, the camel spider‘s tracheal system is complex (Kaestner, 1931). Its complexity is close to the tracheal system of insects with its wide network of connected tubules (Wigglesworth, 1931; Meyer, 1989). This complexity and the high demand for oxygen during activity require an efficient system for oxygen delivery to the demand organs, e.g. musculature, gut. To understand the functional design of the respiratory system (and to provide data for a broader comparison), we studied the detailed anatomy of the tracheal system using micro-CT imaging in combination with 3D-reconstruction as well as light and transmission electron microscopy. We could confirm Kaestner's (1931) description of the tracheal system's gross morphology. In addition, we were able to show new features such as tracheal sacks in the chelicerae as well as the extent of tracheae for the entire length of the legs, an indication for weight reduction in these large animals. On the other hand, we were also able to collect data on the terminal tracheae branches. We could show, that the tracheae of camel spiders reach into the epithelium of organs like the midgut diverticula as well as the sarcoplasmatic reticulum of the striated musculature of the chelicerae and legs. The acquired results provide comparative morphological data for the study of evolution of tracheal systems in chelicerates and give evidence of a parallel evolution of complex tracheal systems in chelicerates and insects.

OP-M-06

The key role of X-ray microCT in morphological imaging pipelines

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During the last ten years, 3D imaging and visualization techniques became increasingly important to several disciplines in biomedical research including descriptive, comparative, and functional animal morphology. This methodological shift brought new and fascinating opportunities for investigating different levels of structural organization at different optical resolutions. Today, microscopic x-ray computed tomography (microCT) occupies a key role in many morphological imaging pipelines. This is mainly because microCT (1) yields isotropic 3D images, (2) can be applied to a range of sample sizes, (3) images very dense samples, and (4) is relatively robust to imaging artefacts. Further, microCT gives fully quantitative images, allowing to measure both geometry and density. Because microCT, like any other imaging technique, is limited by certain physical parameters, it is often necessary to correlate microCT to other imaging techniques. Such multi-modal imaging pipelines often significantly broaden the amount of information obtained. In my talk I will discuss the role of microCT imaging in morphology and present methodological developments that have the potential to further extend the role of microCT in morphological research.

OP-M-07

Copulatory courtship by bushcricket genital titillators revealed by functional morphology, µCT scanning for 3D reconstruction and female sense structures

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Most genitalia are hidden inside the body that's why only few morpho-functional studies on animal genitalia have been made so far. We studied the titillators, paired genital structures of the male phallus in bushcrickets. The presence of titillators in several bushcricket taxa has been described for a long time. However, their exact function during mating is still unknown. We used a combination of several independent, yet complementary, techniques to investigate morpho-functional aspects of titillators in the bushcricket *Metrioptera roeselii* (Hagenbach, 1822). Couples were flash-frozen and analyzed by X-ray micro-computed tomography (µCT) to visualize the interaction of male and female genitalis during copulation. Moreover, video footage of copulating pairs showed rhythmical tapping of the titillators on a softened structure of the female's subgenital plate. Those movements did not harm the female's genitals, which showed no sclerotized genital counter-structure to the titillators. Scanning electron microscopy and histological sections reveal the female subgenital plate to be covered with sensory cells at the interaction zone between the male's titillator and the female genital chamber. Due to the non-damaging function of the titillators, the lack of a genital counterparts and the presence of sensory receptors on the female's subgenital plate, we propose a copulatory courtship function of bushcricket titillators, likely subject to sexual selection by female choice.

OP-M-08

The neuromuscular system of *Pycnophyes kielensis* (Kinorhyncha: Homalorhagida). Are kinorhynchs segmented?

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Kinorhynchs are ecdysozoan animals with a phylogenetic position close to priapulids and loriciferans. The musculature and the nervous system of the homalorhagid kinorhynch *Pycnophyes kielensis* was investigated by use of immunohistochemistry, confocal laser scanning microscopy, and 3D reconstruction software. The trunk musculature consists of paired ventral and dorsal longitudinal muscles as well as dorso-ventral muscles in segments 2-10. The gut musculature shows no signs of segmentation. The serotonergic nervous system comprises a brain that consists of a neuropil ring around the pharyngeal bulb, behind the introvert. Associated to this ring are somata extending anteriorly and posteriorly. A ventral nerve cord runs in anterior-posterior direction and has associated serotonergic somata in each zonite. The stained nervous system conforms to the typical cycloneuralian brain that is characterized by an equally thick circumpharyngal nerve and found in kinorhynchs, nematodes, nematomorphs, priapulids, and loriciferans. It is concluded that kinorhynchs are not truly segmented and that their segmented appearance evolved independently from other segmented animal groups.

OP-M-09

Neuromuscular development in Patellogastropoda (Gastropoda: Mollusca) and its importance in the reconstruction of ancestral gastropod bodyplan features

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Although limpets (Patellogastrpoda) have been extensively used in ecological investigations knowledge on their organogenesis including the nervous and muscle system is limited to few investigations. This is particularly surprising, because the basal branching position of Patellogastropoda within Gastropoda renders them of prime importance for evolutionary questions. Here, the development of the nervous (serotonin, FMRFamide) and muscular (F-actin) system in *Lottia* cf. *kogamogai* is analysed by fluorescence labelling in conjunction with confocal laser scanning microscopy. In trochophore larvae, first serotonin-like immunoreactivity (lir) appears in the apical organ and in the prototroch nerve ring. The arrangement and number of the serotonin-lir cells in the apical organ (three flask-shaped, two round cells) is strikingly similar to those in putatively derived gastropods. First FMRFamide-lir appears in veliger larvae in the *anlagen* of the future adult nervous system including the cerebral- and pedal ganglia. As in other gastropods, the larvae of this limpet shows one main and one accessory retractor as well as a pedal retractor and a prototroch muscle ring. Of these, only the pedal retractor persists until after metamorphosis and contributes to the adult shell musculature. We found a hitherto undescribed, paired muscular system that inserts at the base of the foot and runs towards the base of the tentacles. An apical organ with flask-shaped cells as well as one main and one accessory retractor muscle is commonly found among gastropod larvae, and thereby might have been part of their common ancestor.

OP-M-10

Neuroplasticity in a Jumping Spider

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Behavioral plasticity is usually associated with neuroplasticity, as changes in brain anatomy can be necessary for an organism to cope with changes in the environment. In some hymenopteran species, volume changes in specific brain areas have been found that are linked to learning, experience and formation of memory. Jumping spiders are known for a wide array of complex behaviors. Previous studies have shown that salticids possess extraordinary cognitive abilities including planning, learning and reversal learning. However, the underlying brain structures which enable them to exhibit such flexible behaviors are basically unknown. We explored the nervous system of the jumping spider *Marpissa muscosa* and compared the volumes of higher integrating brain structures of individuals that grew up in four different environments: (1) Wild-caught spiders, (2) spiders reared alone in a deprived setup, (3) spiders reared alone in an enriched setup, and (4) spiders reared in groups of several siblings. Our results demonstrate that neuroplasticity occurs in spiders and that brain structures in *Marpissa muscosa* plastically respond to the environment the individual is confronted with.

PP-M-01

Early nymphal development of the praying mantis *Hierodula* cf. *grandis*

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Mantodeans are solitary, predatory representatives of Neoptera. The group Mantodea includes about 2,300 species worldwide, with a main distribution in the tropics. The probably most notable characteristics of these insects is a pair of very prominent raptorial appendages. Morphological changes during nymphal development is a rather understudied field of entomology, and this applies also to mantodeans. Here we show aspects of the early nymphal development of the praying mantis *Hierodula* cf. *grandis* and its morphological changes during the early post-embryonic ontogenesis. All specimens were documented with up-to-date high-resolution imaging: 1) under cross-polarised light for overview, and 2) smaller structures, isolated heads, mouth parts and parts of the genital apparatus were documented with auto-fluorescence microscopy. Observed ontogenetic changes include: changes in body proportions; changes in the head proportions; changes in ratios of the appendage parts. These changes are likely coupled to changes of the life habits of the different stages. These new data are important because 1) ontogenetic characters have been proposed to have the potential to provide important characters for phylogenetic analysis, and 2) fossil mantodeans (mostly preserved in amber) are generally nymphal specimens; hence these are often difficult to interpret due to the lack of data about extant mantodean nymphs. With our study we aim at partly closing this gap of knowledge, offering the comparison also in a wider phylogenetic range and for the interpretation of fossil specimens.

PP-M-02

The female reproductive system of two sympatric heelwalkers (Insecta: Mantophasmatodea) - A comparison using µ-CT

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Insect reproductive systems are extremely divers in morphology and are often used to discriminate between species. For example, there are three different ovary types (panoistic, telotrophic-meroistic, polytrophic-meroistic), and the classification in one of these types is order specific. The insect order Mantophasmatodea was first described in 2002; extant species are found in South Africa, Namibia, Malawi and Tanzania. Most heelwalker taxa are distinguished by characteristics of cuticular structures in male and female postabdomen and genitalia. Non-cuticular structures were only rarely studied in Mantophasmatodea so far. To determine a species it is therefore necessary to macerate the specimen to gain access to the respective cuticular structures. With the aid of x-ray micro-computed-tomography (µ-CT), such irreversible maceration steps might no longer be necessary, if resolution was good enough to describe the system in detail. To investigate this question, we examined the female reproductive system of two South African heelwalker species, *Karoophasma biedouwense* and *Viridiphasma clanwilliamense*. Both species occur in sympatry and are not known to interbreed. We used µ-CT imaging and 3D rendering, supplemented by paraffin histology. We demonstrate that the ovary belongs to the panoistic type in both species, while the shape of the spermatheca differs between the two species. All the diagnostic taxonomic structures of the female genitalia can be depicted in their natural position within the abdomen.

PP-M-03

Wing development in 'hemimetabolous' insects and its twisted impact on phylogeny

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In modern insects there are two pairs of wings which arise laterally to the tergites of the mesothoracic and metathoracic segment. Throughout the ontogeny of 'hemimetabolous' insects the wings grow from little extensions (wing pads) to fully movable wings; this transformation appears rather stepwise with each moult. In early flying insects, known through 300 million years old fossils, the development of these wings is characterised by extreme gradualness, unparalleled in any modern form. Hence the ancestral type of wing development has become remodelled in the different lineages of modern insects. Such evolutionary changes can affect: 1) the direction or orientation of growth of the winglets also including 2) even differentiation by developing 'larval specialisations' or 3) heavily affect speed and timing of the development of the winglets. As a first step for a reconstruction of the evolutionary history of these specialisations it is necessary to clearly document the morphology of the nymphal instars of the species of interest. Remarkably the post-embryonic ontogeny of modern 'hemimetabolous' insects has rarely been documented in detail. Developmental characters have furthermore been proposed to have the potential to resolve the still controversial phylogeny of polyneopterans insects. Here we documented the wing development of the orthopteran *Schistocerca gregaria*. As known for many years orthopterans show a peculiar change in winglet morphology: the winglet becomes twisted from nymphal instar III to IV. We compare this specialisation to winglet specialisations of other polyneopterans and explore whether winglet characters can help to resolve the phylogeny of Polyneoptera.

PP-M-04

Functional morphology of giant mole crab larvae

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A defensive mechanism employed by arthropods of various groups is rolling up into a tight ball. Such defensive enrollment strategies are also found in certain larval stages as recently described in larvae of mantis shrimps. However, also larvae of other species exhibit a forward bending or curving of their pleon ('shrimp tail'), e.g., the giant zoea-type larvae of mole crabs (Hippidae; Anomala; Eucrustacea). These impressive giant larvae reach over 6 mm shield length. Additionally, the shield is equipped with long spines, one anterior (rostral spine), and a pair of postero-lateral ones. Together with the long and slender pleon they are outstretched more than 15mmlong. This makes them the largest known zoea-larva of all anomalan crustaceans. When they flex their pleon forward, they almost form a perfect ball; the posterior gap of the spherical shield is just broad enough to have the pleon segments fit in. The telson is large and lid-like and can cover most of the appendages, whichwould perfectly protect the entire body.For a better understanding of this mechanism, we provide a detailed description of an entire specimen of a giant hippidan larva, including all appendages. Based on the detailed observation, we discuss the possibilities of reconstructing behavioral aspects based on functional morphology for giant hippidan larvae. The observed larvae feature some similarities to larvae of Brachyura (true crabs). Also stomatopods are a good candidate group for functional comparisons, since some of their larvae strongly resemble the tightly enrolled body of the hippidan larvae when being enrolled. Additionally, we provide some clear indications for an unrecovered disparity among giant mole crabs larvae.

PP-M-05

Functional aspects and disparity of defense by means of expelling toxins in terrestrial arthropods

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Arthropods -- insects, crustaceans, myriapods, spiders and their relatives -- exhibit a variety of defensive strategies. Many terrestrial arthropods produce and expel toxic substances to defend themselves against threats. Here we present an overview about: 1) which groups pursue these strategies, 2) how these arthropods release the toxic substances, 3) where they secret them, and 4) which substances they produce. For 1) defense by means of expelling toxic substances occurs in different insect groups, in myriapods, and in different chelicerates. Interestingly, this type of defense can also be restricted to a certain ontogenetic phase. For 2) we can differentiate two ways how the toxic substances can be released: they are either sprayed or vaporized. For spraying, the animals either squeeze parts of their body with the aid of musculature and fire a liquid stream or an aerosol. Alternatively, a chemical reaction can be employed for accelerating the toxin. For vaporizing a droplet is extruded and passively vaporized. For 3) there seems to be a certain coupling to 2): spraying is usually performed on the head and the terminal end, while vaporizing seems to be restricted roughly to the lateral sides of the trunk. For 4) the toxic substances are mostly hydrocarbons such as formic acid or acetic acid. Also more complex mixtures are known, even explosive "cocktails". In many cases similar substances are used by species that are not closely related to each other. Apparently, producing toxic substances for defense represents a successful evolutionary strategy. This may also explain why this strategy evolved several times independently among terrestrial arthropods.

PP-M-06

Evolution of the ontogenetic development of wings: data from supposedly ‘primitive’ flying insects

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Flying insects have been considered to represent one of the most successful groups of metazoans. The most apparent character of a large majority of modern forms are two pairs of wings arising from the posterior two thoracic segments, enabling them to conquer the areal realm. These wings are only present in adults, but have to be developed stepwise during their nymphal or larval development. The presumably ‘original’ state of development in all insects seems to be a very gradual development as seen (though with alterations) in little derived “hemimetabolous” winged insects and also different fossil forms. Here we demonstrate that even though these groups are called ‘primitive’, their development is far from what is generally assumed to be the ‘original’, the ‘primitive’ state. Alteration from that ‘original’ developmental path can consist of different variations in heterchrony, e.g. altering different stages with regard to their temporal length in developing or pre-/postponing of certain stages. We focused on Palaeodictyoptera, Dictyoptera and extant cockroaches due to their presumably ‘primitive’, gradual development. In regards to wing development - the main focus of this work - it seems as if (in extant cockroaches) the wings do not develop evenly and continuously throughout all nymphal stages but to be accelerated in the later stages and show (logically) more rapid development of the wings in these stages. This seems to be paralleled in certain fossil forms. Therefore, we will try to put those findings in a phylogenetic framework.

PP-M-07

Comparative neuroanatomy of the accessory organ, a leg scolopidial sensory organ, in Ensifera (Insecta: Orthoptera)

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Large mechanosensitive organs are present in the legs of Orthoptera, especially in the femoral chordotonal organ and the subgenual organ complex, the latter containing important receptors for vibration and sound. Located in the posterior tibia of some orthopteroid insects, a scolopidial organ of few sensory neurons has been called the Nebenorgan (Mantophasmatodea, Blattaria) or accessory organ (Ensifera: Anostostomatidae, weta). Among Ensifera, the accessory organ has been described originally in bushcrickets (Tettigoniidae) but it was not identified in several tettigoniids in detailed anatomical studies. It appears to be entirely absent in crickets. We here cover the anatomy and distribution of the accessory organ in several Ensifera. In cave crickets (Rhaphidophoridae) and splay-footed crickets (Schizodactylidae), a separate cluster of few neurons is located posterior to the subgenual organ. The scolopidial sensilla are separated from the posterior subgenual organ, and are innervated by the legs main motor nerve. The organ is associated with a single campaniform sensillum in the cave cricket *Troglophilus neglectus*. In tettigoniids, a similar group of sensilla is present but in closer proximity to the posterior subgenual organ. However, the dendrites of these sensilla point in dorso-proximal direction, clearly different to the subgenual sensilla which point in distal direction. This supports the presence of an accessory organ. These results highlight that the accessory organ is present in diverse ensiferan taxa. The subgenual organ complex is thus rather elaborate in several groups and may contain up to four scolopidial organs in close proximity.

PP-M-08

Investigating the neuroanatomy of *Parhyale hawaiensis* in a combined approach

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The arthropod nervous system, especially the crustacean brain has caught attention by many scientists in the field of arthropod research. The past decade has also seen the emergence of the discipline of 'neurophylogeny' that is the synthesis of neurobiological questions and evolutionary aspects. These comparative data have yielded new insights into arthropod phylogeny. The amphipod *Parhyale hawaiensis* has been established as a model organism in arthropod developmental studies. However, despite these developmental, genetic, and molecular analyses, research on the architecture of the nervous system has been neglected. In order to gain insights into the architecture of the brain, we investigated *P. hawaiensis* in a multi-methodological approach using classical histology, immunohistochemical experiments in combination with confocal laser-scanning microscopy as well as X-ray micro-computed tomography. The syncerebrum shows a dorsoventral orientation and comprises the prominent neuropils of the central complex as well as the olfactory lobes composed of spherical olfactory glomeruli. The projection neuron tract forms a chiasm and innervates an unstructured neuropil in the lateral protocerebum which corresponds to the hemielipsoid bodies. Further details on distribution of cell somata and individual localizations of neuropeptides are presented.

PP-M-09

MicroCT Analysis as a tool for taxonomic research in Odonata

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For the identification of many dragonfly species, it is necessary to examine the secondary copulatory organ of the males. Dissecting out the genital ligula, however, entails the risk of damaging the specimen. This is especially problematic with old and thus frail specimens, such as type material. A method that allows the investigation of internal structures without the need for dissection would therefore be highly advantageous. The Micro-Computer Tomography Analysis (microCT) offers a non-dissipative way of visualizing and scrutinizing internal morphological characters. We tested the potential of microCT Analysis for investigating the genital ligula in Odonates.

PP-M-10

Cuticular microstructures turn black into velvet black in a stick insect

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The stick insect *Peruphasma schultei* stands out from other insects by its velvet-like, black cuticle. We tested whether the appearance of *P. schultei* is due to micro ornamentations of the cuticle, a phenomenon that has been recently described for the black of the Gaboon viper [1]. We found that the P. schultei cuticle is characterised by two different types of microstructures, tall elevations with a maximum size of 18 µm and small structures on tergites only with a height of 4 µm. Unlike the Gaboon viper, the P. schultei microstructures seem not to bear nanostructures. The microstructures scatter light evenly and independent of the viewing angle. They cause the velvety appearance of the cuticle, whereas pigments are responsible for the black colouration, as revealed by resin replicas of the cuticle. The combination of surface structures and pigments provide a very low reflectance of five percent at maximum. In addition, the tall surface structures contribute considerably to the water repellent properties of the cuticle, which shows high contact angels near 130°. Moreover, the velvet black cuticle has a higher heat absorption compared to the shiny black cuticle of a control species (*Anisomorpha paromalus*). We can hardly assess the selective benefit of the velvet black appearance yet, as there is only scarce information on the structure and the climatic conditions of the habitat of this species.

PP-M-11

Making the most of minute singletons: molecular data from SEM-samples in Solenogastres (Mollusca)

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Solenogastres is a small clade of worm-shaped molluscs. Most of the approx. 300 species inhabit the deep-sea and are described based on single findings. Specimens frequently only reach a few millimeters in body length, making subdivision for morphological and molecular studies impracticable. The present study explores different approaches to combine examination of entire individuals with scanning electron microscopy (SEM) with DNA barcoding to optimize the morphological information retrieved from single individuals prior to molecular analyses. We applied three different protocols of sample dehydration (via ethanol, HDMS, critical point drying via acetone) to our samples and sputter-coated all specimens with gold for SEM-examination using a LEO 1430 VP SEM (15kV). Subsequently, we performed three different DNA extraction methods (silica-based spin columns, CTAB and a quick-and-dirty approach by boiling in extraction buffer). We found no correlation between the method of dehydration of the samples for SEM and the measured DNA concentration, nor to the quality of the obtained COI-sequences. All compared DNA extraction methods successfully retrieved DNA from some samples, but spin-column extraction failed in 43 % of the tested samples. The quick-and-dirty approach yielded comparably high DNA concentrations, but COI could not be amplified successfully. The preliminary results of our study indicate that DNA extraction is unaffected by the different SEM-dehydration protocols. Comparing extraction methods the quick-and-dirty approach - successfully applied to SEM-samples in insects - failed on our molluscs and spin-column extraction seemed less efficient than CTAB, which yielded the best results based on our data.

PP-M-12

Intraspecific variability in the distribution of muscle fibre types in the masticatory muscles of the wolf (*Canis lupus* L. 1758) and domestic dog

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The anatomy and histology of the masticatory muscles, Mm. temporalis et masseter, is crucial for food intake and processing. The jaw adductors of carnivores are composed of masticatory muscle fibre type I and type IIM. Type I has an oxidative property, which is slow contracting and enduring, while type IIM is fast contracting and fatigues fast. Here we compare the muscle fibre type composition of the wolf and its domestic form, the dog. To this end, the intraspecific and regional distribution of the two fibre types was analysed in the jaw muscles of ten wolves (*Canis lupus*) from the German founding population of the Lausitz region. Muscle samples were taken at several locations within the muscles and histological sections were stained using an immunohistochemical protocol. While the average fibre distribution is comparable among all wolves, we found regional differences within and between the muscles of the wolves. On average, the masseter and temporalis muscle of wolves consist of 20±7 % type I and 80±10 % type IIM. Wolves have a higher proportion of type I fibres compared to domestic dogs which on average have 15 % and 14 % in the masseter muscle and temporalis muscle, respectively. We suggest that this is due to differences in predatory behaviour, i.e. wolves need persistent jaw closure to catch and kill wild prey. Future research is required to assess whether these findings are specific to the closely related German wolf population by including other European populations in the analysis.

PP-M-13 - Transition from marine to terrestrial life in 20 days - larval development and neurogenesis of the Giant Robber Crab *Birgus latro* (Linnaeus, 1767)

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The Giant Robber Crab *Birgus latro*, a representative of the hermit crabs (Anomala, Coenobitidae), is the largest living terrestrial arthropod on earth. It can reach an estimated age of up to 100 years and a weight of 4 kg. Nevertheless, ontogeny is *via* marine larvae and this cycle starts with the first Zoëa larva which has only a size of 2-3 mm in length. Across four marine pelagic larval stages (Zoëa 1-4), the marine benthic Glaucothoë (Megalopa) develops, an animal that enters an empty gastropod shell and moves onshore. This transition from a marine to a terrestrial lifestyle requires many physiological and morphological adaptations. We focus on the development of the olfactory system, including the first pair of antennae and the brain morphology. The olfactory receptive organs are the aesthetascs, simple setae, which are situated on the tip of the first antenna. They provide input into the 'deutocerebral chemosensory lobes', the primary olfactory processing centres in the brain. We examined a complete series of eight postembryonic stages, which comprised the first 96 days after hatching and included the marine as well as the terrestrial phase. The larval morphology was investigated by X-ray microcomputed tomography, scanning-electron microscopy as well as histochemical and immunohistochemical stainings. Our data revealed two phases of pronounced morphological changes of the first antennae and the brain. The first coincides with the molt from the fourth Zoëa to the marine Glaucothoë, and the second phase is associated with the subsequent molt to the terrestrial Glaucothoë. With our observations we are able to describe a complete transformation from a marine to a terrestrial "nose". This project is supported by the German Research Foundation (DFG: Ha 2540/13-1).

PP-M-14

Functional morphology of the tracheal system of *Galeodes granti* (Chelicerata:Solifugae)

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Camel spiders (Chelicerata: Solifugae) are active predators (Punzo, 1998) with a high metabolic rate (Lighton et al., 2001). As opposed to other large and active chelicerates, e.g. scorpions, camel spiders rely for gas exchange solely on their tracheal system. In contrast to other tracheate chelicerates, the camel spider‘s tracheal system is complex (Kaestner, 1931). Its complexity is close to the tracheal system of insects with its wide network of connected tubules (Wigglesworth, 1931; Meyer, 1989). This complexity and the high demand for oxygen during activity require an efficient system for oxygen delivery to the demand organs, e.g. musculature, gut. To understand the functional design of the respiratory system (and to provide data for a broader comparison), we studied the detailed anatomy of the tracheal system using micro-CT imaging in combination with 3D-reconstruction as well as light and transmission electron microscopy. We could confirm Kaestner's (1931) description of the tracheal system's gross morphology. In addition, we were able to show new features such as tracheal sacks in the chelicerae as well as the extent of tracheae for the entire length of the legs, an indication for weight reduction in these large animals. On the other hand, we were also able to collect data on the terminal tracheae branches. We could show, that the tracheae of camel spiders reach into the epithelium of organs like the midgut diverticula as well as the sarcoplasmatic reticulum of the striated musculature of the chelicerae and legs. The acquired results provide comparative morphological data for the study of evolution of tracheal systems in chelicerates and give evidence of a parallel evolution of complex tracheal systems in chelicerates and insects.

OP-NB-IT-01

Neurobiology of acoustic communication: Neural networks for singing and song pattern recognition in field crickets

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Male crickets use species-specific calling songs to attract females. By intracellular recordings in the CNS of singing males I identified key neurons of the central pattern generator circuit that drives the rhythmic activation of wing muscles for sound production. The pattern generating circuit is located in the anterior abdominal neuromers and comprises interneurons showing mutual inhibition and postinhibitory rebound (PIR). At the female side intracellular recordings revealed a small network of auditory brain neurons that recognizes the species-specific song pattern and exhibits properties fundamental to feature detection based on delay-line and coincidence-detection mechanism. An internal delay that matches the pulse period of the calling song is provided by a non-spiking neuron. Upon acoustic stimulation it receives inhibition that triggers PIR. Direct and delayed excitatory responses converge in a coincidence detector neuron, which responds best to the pulse pattern of the species-specific calling song. The output of the coincidence detector neuron is further processed by a feature detector neuron to suppress unselective responses and background activity. For effective communication, however, sender and the receiver need to be attuned to the same signal and generation and recognition of the song pattern are genetically coupled in crickets. Delayed excitation by PIR is crucial for song pattern recognition and also essential in the singing pattern generating network. Coupling at the level of membrane proteins (e.g. hyperpolarization-activated channels) that are controlled by the same genes seems to ensure concomitant changes of time constants in the networks for signal generation and recognition during speciation.

OP-NB-IT-02

Challenging vision in harbor seals

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Amongst the senses, vision is of paramount importance from a human perspective. In contrast, in marine mammals, the role of the visual system for underwater orientation is controversially discussed. Many authors speculated that vision cannot play a major role underwater due to low light levels that seem to dominate the visual environment of marine mammals. Low light levels are encountered at night but also when diving to deep waters even during the day when marine mammals experience perfect light conditions at the water surface to which they have to return for breathing. When diving, low light levels are caused by sunlight getting more and more absorbed and scattered with depth. Absorption and scattering is increased if particles are dissolved in the water which especially characterizes coastal waters or rivers. However, summing up latest vision research mainly in harbor seals, it becomes evident that their eyes have evolved specific adaptations to cope with these dim light conditions. And moreover, harbor seals can even benefit from dissolved particles in the context of motion vision and optic flow perception. Vision is also involved in estimating time intervals and distances, two fundamental aspects of orientation. On the basis of these experimental findings, the role of vision for underwater locomotion and orientation has to be rethought thorough fully.

OP-NB-01

Detection of impending vehicle collisions using an improved "locust eye algorithm"

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In hazardous traffic situations, a quick response of drivers to impending collisions can be lifesaving. Future car assistant systems will detect and respond to objects on a collision course by taking over the control of vehicles to prevent impending collisions. However in the field of computer vision, reliable detection and avoidance of collisions is a challenging task. Currently this task is realized by means of computationally demanding image processing techniques that are combined with radar and laser scanning systems permanently measuring the distance to all objects in the vicinity of a vehicle. Instead of absolute distance measurements, locusts and other flying insects are detecting impending collisions mainly by responding to a rapid increase in object size (object looming). Thus, bionic solutions of collision detectors may improve the speed and efficiency of technical collision avoidance by simultaneously lowering the costs associated with technical requirements. Recent neurophysiological experiments revealed a reliable response of collision detector neurons (DCMD) when locusts were exposed to playbacks of low-quality road movies containing impending collisions. The same movies were used to improve a numeric computer model that simulates motion processing steps known from locust eyes. One major improvement of this bionic collision detection algorithm compared to existing ones is its ability to detect objects approaching the vehicle from the side, whereas objects as part of the optic flow are ignored. This is achieved by evaluation of the activity of four "neuronal layers" with inherent motion directionality in a small region surrounding each receptor cell. If a certain amount of local motion trajectories point towards the center or bottom of the sensor, an object on a collision course is detected and a "warning state" is induced. This activates the processing of object looming in a region of selective attention that is defined by the speed and steering of the vehicle. After optimization of model parameters, objects on a collision course can be reliably detected in different road movies including hazardous traffic scenes. Using this model it is often possible to calculate a steering vector that would prevent an impending collision.

OP-NB-02

New anatomical and physiological insights in a collision sensing pathway in the locust *Locusta migratoria*

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The visual system in *Locusta migratoria* has provided an interesting ground for researchers over many years. A particular neuronal circuit in the *optic lobe* is a collision sensing one which, although investigated for almost three decades, still holds some secrets. In this rather simple neuronal pathway a key processing stage is assumed to be between Trans-medullary afferent neurons (AN) projecting from the second optical ganglion, the medulla, and the lobula giant movement detectors (LGMD 1 and 2) in the third optical ganglion (lobula). Previous work on the afferent cells by Rind and Simmons (1998, J. Comp. Neurol., 395) revealed a special synaptic arrangement of the ANs at the LGMDs that suggested lateral interactions between neighbouring ANs are important for collision sensing. Until now the origin of these ANs in the medulla and their input neurons are unknown. In a 4th instar of *L. migratoria* we traced a single afferent cell from its input synapse at the LGMD back to the medulla using the electron microscopic method of serial block face scanning electron microscopy (SBEM). Synaptic connections of the AN along the entire reconstruction revealed that there were output synapses in the medulla in addition to the output onto to the LGMD 1 and other neurons in the lobula. Further reconstruction work is under way to identify the input neurons in the medulla. For a complete understanding of how signals are processed in a neuronal circuit anatomical data alone is not enough, so complementary electrophysiological experiments were carried out. Their goal was to give new insight into the contribution of a single unit making up the compound eye, to the excitation pattern in the LGMD - precisely to see if the postulated lateral inhibition presynaptic at the LGMD works as models predict. Grant Sponsor: Land Steiermark, HTI:SMApp 2012.

OP-NB-03

Neural mechanisms for acoustic signal detection under strong masking in an insect.

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Males of the katydid *Mecopoda elongata* produce calling songs (chirps) for female attraction. These species specific, broad-band calls are strongly masked by signals of a competing, sympatric living Mecopoda species, where males produce continuous trills of high amplitude. The males of chirpers, however, detect their signal reliably under these noisy conditions, even when the trill is much louder. The spectral properties of the two calling songs are rather similar; however, only the chirp includes a narrow frequency band at 2 kHz. This small difference in spectral composition is exploited by the nervous system for response selectivity to chirps. By using intracellular recordings we identified auditory interneurons responding selectively to the chirp. Several types of interneurons revealed two basic neural mechanisms for chirp selectivity.

1. Selective tuning - Neurons respond only to the chirps, even at signal-to-noise ratios of -21 dB, as these neurons are sharply tuned to 2 kHz. Their dendritic arborisations overlap with the axonal terminations of low frequency receptors that reveal similar selective responses.

2. Novelty detection - Neurons are initially strongly excited by the high frequency of the trill but the response is followed by strong adaptation. Due to the longer chirp period the neurons do not adapt to the chirp and respond to its low frequency components that differ from the trill and represent a “novelty”.

OP-NB-04

The scorpion pectines and their primary neuropils: details of glomerular neuropil structure

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Primary chemosensory organs of scorpions are the pectines. They are located ventrally on the 2nd abdominal segment behind the walking legs. Depending on species, some 20,000 to 1,000,000 afferent neurons arise from a pectine. Afferent axons enter the main central nervous projection area, the (posterior) pectine neuropil, from the outside, and they terminate in glomerular structures reminiscent of the glomeruli in the olfactory lobes of other arthropod groups. However, there are also several idiosyncratic features, including very different sizes and shapes of the individual glomeruli. Most glomeruli are not globular but flattened to sausage-shaped, or even donut-shaped. These glomeruli are arranged in concentric layers, giving an onion-like structure to the pectine neuropils. Details of the neuropil structure were examined in *Euscorpius italicus* scorpions. In this species, the layers of glomeruli are about 20 to 30 micrometers thick, which is thus also the thickness of the glomeruli along their shortest axis. There are about 19 layers distinguishable, containing a total of roughly 140 glomeruli, in a pectine neuropil. There appear to be only small differences between genders, except that male pectine neuropils are often considerably larger, in keeping with the larger.

OP-NB-05

Timing of the peptide-orchestrated eclosion behaviour in *Drosophila melanogaster*

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Neuroendocrine peptide release is often rhythmic, potentially coupled to circadian oscillators in the brain. The neuronal mechanisms underlying clock-controlled release of neuropeptides is however only little understood. Eclosion in the fruit fly *Drosophila melanogaster* is a classic example for both: peptide-orchestrated and circadian-timed behaviour. It was shown that PDF-positive clock neurons are essentially for the rhythmic eclosion of flies, while the ecdysis behaviour itself is regulated via peptide hormone signalling. Therefore a yet unknown connection between the circadian pacemaker cells and the gated release of peptide hormones involved in eclosion must exist. In a behavioural screen we identified a new neuropeptide involved in eclosion timing: prothoracicotropic hormone (PTTH). PTTH was so far known to regulate ecdysone production. Ablating and electrical silencing of PTTH-positive neurons leads to arrhythmic eclosion under constant darkness. Furthermore, anatomical data suggest that PTTH signalling could be influenced by PDF-positive clock neurons. Our results suggest that PTTH is a key signal linking the central clock with a peripheral clock gating eclosion. Funded by the German Research Foundation (DFG), SFB 1047 “Insect timing”, Project B2.

OP-NB-06

Quantification of neurotransmitter from individual Drosophila cells

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Messenger molecules which are released from neurons play key roles in cell-cell communication in neuronal networks. The knowledge of their qualitative and quantitative chemical composition in individual cells is crucial for understanding behavioral pattern and physiological processes in organisms. Here, we are focusing on a strategy to quantify biogenic amines from individual cell using direct MALDI TOF MS analysis. However, the detection of biogenic amines by direct MALDI-TOF MS from such small sample sets has been challenging in analytical task so far. In a first experimental step, we develop and optimize a strategy for robust, stabile and reproducible measurements focusing first on synthetic octopamine by using on-plate chemical treatments to increase the detection limit up to 10^{-9} M which allows us to work on single cell level. First analyses of biological samples were focused on individual octopaminergic neurons of the ventral midline cluster (Vm neurons) from the subesophageal ganglion using a GAL4-TdC2, UAS-mCD8::GFP strain for cell identification. Individual V_m somata were manually dissected, transferred by a glass capillary on a MALDI sample plate and subsequent chemical treated. Only single isolated not damaged soma without microscopically apparent contaminations by other cells or axons were used. To quantify the level of OA in individual soma we added an internal standard to our native samples. For OA validation, we switched to the MS/MS mode of the MALDI instrument. Resulting fragmentation spectra revealed clear fragments to reconstruct the molecule by using MELTIN database. In a current project, we included behavioural assays to study the changes of OA level in flies under different conditions.

OP-NB-07 - Drosophila species living at different latitudes: is differential CRY and PDF expression within the circadian clock network important for adjusting locomotor activity to changing day length?

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The genus *Drosophila* contains over 2000 species that populate very different environments, from the equator to frigid zones. To survive in these diverse areas they must have evolved specific behaviors in order to avoid being exposed to midday heats at lower latitudes or morning chill at higher ones. We have collected *Drosophila* species from the wild and analyzed their locomotor activity under various environmental conditions in the lab. We found that species of lower latitudes show a bimodal activity pattern under light dark cycles, with a morning and an evening activity peak, and remain rhythmic under constant darkness while they become arrhythmic under constant light. Species of higher latitudes show instead a unimodal activity profile with a very prominent evening activity peak and adjust better to extremely long photoperiods or even constant light, conditions which are typical of their natural environment. These particular features of the locomotor activity of high and low latitudes species well correlate with the pattern of CRY (circadian photoreceptor) and PDF (neuropeptide involved in the clock output) expression in the brain. Low latitude species express both CRY and PDF in all ventral Lateral Neurons (small and large LNv) while species of higher show a reduced (if any) PDF expression in the small LNv (s-LNv, important for driving morning activity as well as sustaining rhythmicity under constant darkness) and no CRY expression in the large LNv (l-LNv). To confirm that differential CRY and PDF expression in the LNv of higher latitudes species compared to lower latitudes ones is directly responsible for their ability to better adjust to extremely long photoperiods, we used genetically manipulated *D. melanogaster*. When we mimic in *D. melanogaster* the typical CRY or PDF expression pattern of high latitude species we can shift also its behavior. In particular we find that PDF signaling from the l-LNv is necessary to properly time the evening activity peak under long days and that the absence of CRY from the same neurons can render even *D. melanogaster* rhythmic under constant light.

PP-NB-01 - Neurochemical characterization of a central pattern generator for vocalization

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Social communication is a trait shared among vertebrates including fishes. Vocal fishes are highly suited models to study vertebrate vocal circuits since the vocal neuronal network is likely conserved across vertebrates, but yet relatively simple. Toadfishes, a known vocal teleost order, exhibit a variety of social calls used by males to court females as well as by males and females during agnostic encounters. These vocalizations are shaped by a central pattern generator (CPG) in the caudal hindbrain consisting of three major nuclei: vocal prepacemaker nucleus (VPP), vocal pacemaker nucleus (VPN) and vocal motor nucleus (VMN). The motoneurons in turn innervate the sonic muscles attached to the swim bladder which produce the vocalization. While the anatomical and hierarchical organization of the CPG nuclei - VPP innervating VPN innervating VMN - is well investigated at a network and single neuron level [1], the transmitters involved in the interplay between the vocal nuclei and their role in shaping vocalization types has not been studied. Using immunohistochemical methods, we investigated the transmitter profile of the vocal CPG (VPP-VPN-VMN) in *Allenbatrachus grunniens.* In line with a previous electrophysiological study, we found extensive GABAergic innervation of the VMN [2]. Additionally, we demonstrate for the first time that VMN receives not only GABAergic inhibitory input but also a prominent glycinergic input. Both inputs presumably originated from small neurons positioned directly ventral to the VMN and ventrolateral to the VPN which are probably innervated by VPN neurons. The identification of the two inhibitory populations adds two additional, previously unidentified components to the vocal CPG whose functions need to be investigated. VMN also received glutamatergic input originating from neurons of the VPN. Among the vocal CPG, VMN's were the only cholinergic neurons as evidence by antibody labeling with ChAT, thereby confirming their motor signature. Our preliminary data show that vocalization in the toadfish CPG is controlled by a set of neurotransmitters that are well known for their excitatory (glutamate) or inhibitory (GABA and glycine) function. The functional consequence of the GABA-glycine inhibitory transmitter mix awaits electrophysiological investigation.

PP-NB-02 - Processing of polarized and chromatic light cues in the central complex of the desert locust

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Like other migratory insects, the desert locust likely uses a sky compass mechanism for spatial orientation. In the sky, several cues including direct sunlight, the polarization pattern of the sky and the chromatic and intensity gradient can be exploited for compass orientation. Previous work showed that the central complex in the locust brain holds a polarotopic internal representation of celestial *E*-vectors and may therefore act as an internal sky compass (Heinze and Homberg 2007, Science 315:995). To explore whether other celestial cues contribute to this internal compass, we examined whether polarization-sensitive (POL) neurons of the central complex receive additional input from the chromatic gradient of the sky. The intensity gradient of long wavelengths (green light) and the uniform distribution of short wavelengths (UV-light) across the sky lead to a chromatic gradient with highest intensity difference between long and short wavelengths near the sun and smallest difference in the antisolar hemisphere (Coemans et al. 1994, Vision Res 34:1461). We tested the responses of central-complex neurons to zenithal polarized light and a green and UV-light spot rotating at an elevation of 45° around the head of the animal. All POL-neurons were sensitive to the azimuth of the rotating unpolarized stimuli. In many neurons the azimuthal tunings to both light spots were in the same position or close to each other, favoring the intensity gradient of green light as the prominent unpolarized compass cue. The preferred position of the unpolarized light spots and the innervated slice of the protocerebral bridge (PB) were linearly correlated in certain columnar cell types, suggesting a topographic organization of solar azimuth positions in the PB.

PP-NB-03

Evidences of an acoustic fovea in the hearing of the bushcricket *Ancylecha fenestrata*

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Bushcrickets produce sounds to attract each other. In the species *Ancylecha fenestrata* (Ensifera - Tettigonioidea) both gender provide wing structures with different shape producing sound with different frequency spectra. We compared these song characteristics with the morphology and sound transduction characteristics of their hearing organ in the forelegs, called *crista acustica*. In comparison to other known bushcricket species*, A. fenestrata* possess an unusual high number of tonotopically arranged sensory cells in the *crista acustica;* 110-122 in males (n = 9) and 83-90 (n = 6) in females. In males and females the shape of the *crista acustica,* and especially the size of the supporting structures (cap cells), is tapering along the proximo-distal axis. In the medial region of the *crista acustica* this decrease of cap cells size is less prominent. Assuming that the size of the cap cells is essential for the generation of sound-induced responses, these regions with a constant area value might cause a disproportionate frequency representation in the *crista acustica*, which could be interpreted as an acoustic fovea. Mechanical and neuronal investigations of the frequency representation along the organ further support the finding of an acoustic fovea, which comprises the dominant frequency range (7-10 kHz) of the female call. We like to thank Berthold Hedwig and Stefan Schöneich for support on the electrophysiological recordings and Manfred Kössl for technical support, Markus Schaefer for photos and Marion Basoglu for her help to prepare the probes for the microtome. This work is supported by the DFG (NO 841/1-2).

PP-NB-04

Gating of auditory information in the bushcricket ear

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Bushcrickets have evolved highly sensitive tonotopically organized auditory organs (*crista acustica*, CA) allowing them to discriminate between conspecific calls and those of their predators by analyzing the frequency content of sound. However, the mechano-electrical transduction process and its tuning mechanisms remain unknown. To investigate the acoustic signal transduction, *in-vivo* experiments were carried out on bushcrickets of the tropical species *Mecopoda elongata* measuring the sound-induced mechanical tuning of CA motion and neuronal tuning of sensory cells. Sound-induced mechanical displacement of the CA was determined using laser Doppler Vibrometry. In general, mechanical frequency tuning curves (FTCs) of CA motion were broadly tuned. In a second step, the neuronal response of the CA was investigated by intracellular recordings of single cells. Surprisingly, neuronal FTCs were more sharply tuned ($BW_{10dB} < 1.1$ oct) than their corresponding mechanical FTC ($BW_{10dB} > 1.1$ oct). Thus, our data provide evidence for a filter mechanism that modifies sensory information already at the peripheral level. Further, only CA motions that were accompanied by a distinct phase delay seemed to evoke a neuronal response of sensory cells by providing a stimulus-relevant tilt of the sensory dendrite. Taken together, we conclude that the gating process in the bushcricket ear depends on a pronounced phase delay in the mechanics providing a leverage-like mechanism at the tip of the sensory cells. Funding: Jürgen Manchot Stiftung, DFG (NO 841/1-2) and Hanne and Torkel Weis-Fugh Fund.

PP-NB-05 - Compensatory tongue movements in the Amazon tree boa (*Corallus hortulanus*)

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To probe the environment, snakes cyclically protrude and retract the forked tongue to collect airborne and substrate-bound chemical compounds, which are transported to the vomero-nasal organ. For arboreal snakes that hunt in trees, directional information delivered by airborne odor plumes is however scarce, and potentially impaired by passive movements of the animal induced by, e.g., swinging branches. To analyze how arboreal snakes might compensate for such movements, we recorded video sequences at 200 frames/s of tongue flicking behavior in the amazon tree boa (*Corallus hortulanus*) under stationary conditions and during horizontal motion. Snakes were placed on a motorized turntable and rotated sinusoidally at a frequency of 0.2 Hz (±30°). Oppositely oriented horizontal tongue movements up to ±20° were observed along with counter-rotational head movements, initiated by relative movements of the anterior body. This behavior was reliably elicited in all animals tested (n = 4) and robustly shown during movement even in darkness. The persistence of tongue movements in darkness suggests that this reflex is driven by vestibular signals, possibly to stabilize the probing of the olfactory world by spatially maintaining the directionality of the tongue flicking. Further experiments with specific olfactory targets, variations of the motion stimuli, and the relation between head stabilization and tongue displacement will further clarify the potential role of this behavior. In addition, the presumed neuronal pathway between inner ear endorgans and tongue muscle-innervating hypoglossal motoneurons as well as the computational processing will be investigated in morpho-physiological studies.

PP-NB-06 - Optimising the 3D-reconstruction technique for motion detecting neurons in the locust

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Elucidating the anatomy of neurons and localizing the synaptic connections between them, can give us important insights into how the neuronal circuits work. We are using serial block face scanning electron microscopy (SBEM) to investigate the anatomy of a locust's collision detecting circuit including the LGMD 1 (Lobula Giant Motion Detector). When an object approaches on a collision course, the LGMD 1 responds strongly because, in part, of the way afferent neurons feed these cells with input signals from the insect's compound eye. By tracing the cells that have synapses with the LGMD 1 and the LGMD 1 itself one can obtain information about the wiring and gain insight about how the signals could travel in this circuit. The inbuilt ultramicrotome in the SBEM cuts thousands of sections each 50 nm thick from a tissue embedded block. With these data the reconstruction of whole neurons was previously done manually in each section by drawing outlines of each cell separately. This approach was very time consuming. To make it more efficient new software was developed. It uses the morphologic differences, which result in high contrast between the LGMD and afferent neurons, for the segmentation. The user sets starting regions (seeds) manually and the algorithm automatically selects a volume within the neuron until the edges that correspond to the neuronal outline are reached. Internally the algorithm optimizes a 3D active contour segmentation model formulated as a cost function taking the SEM image edges into account. With this approach the segmentation process can be done semi-automatically, thus reducing the reconstruction time approximately six times. This approach will be useful to save time when reconstructing neuronal processes. Grant Sponsor: Land Steiermark, HTI:SMApp 2012

PP-NB-07

Topographic organisation of the octavolateral line nucleus in zebrafish (*Danio rerio*)

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The medullary lateral line nucleus (medial octavolateral nucleus, MON) processes mechanosensory information and passes it to the ventro-lateral nucleus of the midbrain torus semicircularis (vlTS). The peripheral spatial organization of the neuromasts is crudely preserved in the termination of the lateral line nerve in the MON, such that the rostro-caudal fish axis is reflected in the anterio-posterior and ventro-dorsal axis of the terminals in the MON. Further there is physiological evidence that this mapping can also be found in the vlTS of the goldfish. Thus one can assume a functional map in the vlTS where hydrodynamic information from anterior body regions is processed more rostrally than that of posterior regions. For the MON efferent cells itself however, no topography has been described so far, with the exception of the vocal midshipman. In our study we used zebrafish to overcome this gap by focusing on the connectivity between MON and vlTS. Tracer injections into the vlTS as well as in the MON revealed a slight but still robust topographic organization in the MON efferent cells. Our quantitative analysis of transversal sections showed that more medial located efferent MON cells project more rostrally to the vlTS whereas more lateral located MON neurons project more caudally to the TS. Furthermore, injections more rostral in the TS resulted in more rostrally labelled cells in the MON whereas more caudally labelled cells arises from more caudal injections in the TS. We have conclusively shown the presence of a slight but robust topography in the MON. Injections more rostral in the TS result in more medio-rostral located cells in the MON in contrast to more caudal located injection sites which label more latero-caudal located cells in the MON.

PP-NB-08

Anatomical and functional organization and connectivity of sensory maps in electrolocation

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In many vertebrates parallel processing in topographically ordered maps is essential for efficient sensory processing. In Mormyrids active electrolocation sensory input is processed in two parallel hindbrain maps, the DLZ and MZ, where phase and amplitude information are somatotopically mapped. Behavioral and physiological data indicate that these maps need to be merged to enable optimal processing of the active electrosensory input and indeed interzonal projections between both zones have been found [Fechler 2008, this study]. A likely candidate for the merging is the midbrain torus semicircularis (TS), one of several toral nuclei. Preliminary physiological and anatomical data indicates that the detailed somatotopic representation from the ELL is lost, while a crude rostro-caudal mapping may be maintained [Finger et al. 1981]. In our study we investigated the projections between the ELL and the NL in more detail, using tracer injections into the ELL and the TS. Our qualitative and quantitative analyzes showed that information from the MZ of the ELL terminates in a topographic manner within the TS. Furthermore, we specifically focus on the presence of functional connectivity leading to merged sensory processing of phase and amplitude information in the NL. Injections into the DLZ indicate that information from corresponding regions within both zones of the ELL is processed within the same area in the TS. This suggests that electrosensory information about amplitude and phase information converges and is processed together in the TS. The ELL injections will also be used to investigate which neurons in the ELL convey inter-zonal connectivity and how this may be used to enhance parallel sensory processing.

PP-NB-09

Action for perception: electric flow during parallax motion as a source of object distance information

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Precise estimation and discrimination of one's relative distance to surrounding objects is important to successfully and precisely navigate the environment. For weakly electric Mormyrid fish (***Gnathonemus petersii)*** the information for distance estimation is based on the self-generated electric field. This 3-dimensional dipole field surrounds the animals' body following a brief and stereotyped discharge of the electric organ situated in the tail. This electric field leads to a 2-dimensional transdermal current pattern stimulates the electroreceptors embedded in the skin. This current pattern is distorted in presence of nearby objects, commonly termed "electric image" (EI). EIs are the basis of sensory information from which the animals can sense their environment. For distance estimation, an ability well described in a number of behavioral paradigms, both static and spatio-temporally cues have been proposed (von der Emde et al., Nature 1998; Hofmann et al. J Phys Paris, 2013). Both are based on contrast and blur of the sensory input. A common depth cue in visual systems is the apparent change in an objects position along different lines of sight. Such parallax information depends on the visual focal apparatus of the eye. In active electrolocation however, such a focusing mechanism is lacking. Using recordings of the electric field in combination with biophysical modelling, we here investigate if parallax-like information can arise in electrolocation due to the given non-linear shape of the basal electric field. We here show that due to the specifics of the electric field geometry electric images of objects will move at decreasing apparent velocity across the animal's sensory surface. Such potential distance-related parallax cues will arise during the stereotypical peering movements that weakly electric fish show when inspecting novel environments. Our results suggest that these cues may be analyzed both spatially and/or spatiotemporally, such that single electroreceptors could convey distance information over time. In addition, it could specifically aid in the disambiguation of electrical superposition in figure-ground like or multiple object conditions. Future experiments will address **if** *Gnathonemus petersii* actively uses this self-generated information for distance estimation.

PP-NB-10

Investigating the circadian clock of the carpenter ant *C. floridanus*

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As social insects, ants belonging to the species *Camponotus floridanus* are confronted with a number of challenges that need the right timing. These challenges range from collection of nectar, to brood care, to mating. To time such behavior, living beings employ an endogenous clock. As the rhythmic behaviors and underlying endogenous clock of *C. floridanus* have not been studied very well yet, we are striving to characterize the anatomical and molecular properties that constitute the base of the clock. We also investigate patterns of behavior related to the clock, with a focus on locomotor behavior. Anatomical and molecular properties are tested by immunohistochemical stainings of putative clock proteins and quantitative analysis of their mRNA levels. Locomotor activity of single individuals is recorded under different light and temperature conditions. Here we report first results of these experiments.

PP-NB-11 - Connectivity pattern of a movement sensitive neuron in the lobula of the locust *Locusta migratoria*

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The locust, *Locusta migratoria* posseses a neural system that helps avoid collisions. This system is situated in the optic lobe, a large neuron in the lobula called lobula giant movement detector 1 (LGMD 1) is a key part of this system. In the third optic neuropile, or lobula complex, thousands of afferent cells converge onto the LGMD 1, each signalling changes in light level in a distinct spatial position. Currently little is known about the overall connectivity pattern between afferent cells and LGMD 1 or the connections among the afferent cells themselves in the lobula complex. To elucidate these patterns we use serial block face scanning electron microscopy (SBEM) in combination with a 3D-reconstruction tool called Amira©. With this method we are not only able to describe the course of the afferent cells' branches in the lobula complex, but can also see how they interact with the LGMD 1 and with each other via synapses. This will give us a better understanding of how the locust`s collision avoiding system functions. So far we have reconstructed the processes of 13 afferent cells and the LGMD 1 over a distance of 42 µm. We found a total number of 156 synapses between the afferent cells and the LGMD 1 respectively between the afferent cells themselves. This confirms previous observations, that afferent cells are connected with the LGMD 1 and also with each other in the lobula (Rind, F. C. and Leitinger, G. (2000), J. Comp. Neurol., 423: 389-401). Here we will present data on the connectivity between the afferent cells and the LGMD 1 which could form the basis for a better understanding of the collision avoidance circuit. Grant Sponsor: Land Steiermark; Grant Sponsor: HTI:SMApp 2012.

PP-NB-12 - What makes a clock „social"? Characterisation of the circadian clock of honeybees (*Apis mellifera*) and red mason bees (*Osmia bicornis*)

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The seasonal and daily changes in floral resources are a great challenge for bees. To predict the regular oscillations in the environment bees have evolved a circadian clock. This clock is involved in timing daily activities and in their sun-compass orientation. So far many studies concentrate on the honeybee's (*Apis mellifera*) circadian clock. Honeybees have a complex social organization in the hive, which shows influences on their circadian rhythm. On the contrary much less is known about the circadian clock of another bee species: The red mason bee (*Osmia bicornis*). These are solitary living bees without the social context of an hive community. In the honeybee, the molecular clock is based on transcriptional/translational negative feedback loops in which at least four clock genes - *period* (*per*), c*ryptochrome-m* (*cry-m*), *cycle* (*cyc*) and *clock* (*clk*) - are involved. But other factors like the neuropeptide PDF (Pigment Dispersing Factor), which has been shown to be part of the circadian clock in different insects, seem to be important for bee circadian timekeeping, too. In the red mason bee, we have started to investigate putative clock genes on the transcriptional level. In addition, we are comparing the expression of PDF and *period* in the brains of the red mason bee and the honeybee by immunocytochemistry. To understand better about possibly different outputs of the clock, we have developed a setup to monitor locomotor activity of individual bees. Considering the complex social interactions between honeybees we put these in this set up in social contact to a miniature beehive in order to create a more natural environment. Our aim is to shed new light on "social" and "non social" clocks by comparing the circadian clocks of the two bee species.

PP-NB-13

The optic chiasm in the *Octopus vulgaris* hatchling

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Cephalopod visuals systems are on par with those of vertebrates regarding complexity but differ in several aspects of their organization. In cephalopods, e.g., the photoreceptor axons contact secondary order neurons not until they leave the eye cup and enter the outer plexiform layer (opl) of the optic lobe. Axon bundles from the dorsal retina run into the ventral lobus and vice versa (no latero-medial cross over) resulting in a horizontally oriented optic chiasm with the shortest axons in the equatorial plane. To prepare a study on the opl-connectomics of *Octopus vulgaris* hatchlings, we tried to localize a region with axons as short and straight as possible, to open the way for a complete axon tracking from somata to synaptic terminals on the EM resolution level. Two *O. vulgaris* hatchlings were resin embedded, cut into (1) a continuous 1.5 µm section series (frontal sections) and (2) an alternating semi-ultrathin section series (1x 600 nm; 5x 70 nm), stained/contrasted and digitally imaged with LM and TEM. Series 1 was aligned (Amira®) to find optimal orientation for series 2 (parallel to retinal fundus). Series 2 was processed with the same software: parallel alignment of LM and TEM sections, segmentation and 3D rendering of axon bundles. After stretching the z-axis of the 3D models, evidence for the above mentioned chiasmatic organization was found already in the hatchling and a region with steeply ascending axon bundles was detected centrally. This work will be continued by (1) analysis of the ultrathin section series of selected axons from the eye cup into the optic lobe to prove retinotopic projections of neighboring receptors; and (2) a FIB-based 3D EM study investigating the connectivity of photoreceptors and interneurons within the opl.

PP-NB-14

Anatomical organization of tangential neurons of the central complex in the brain of the desert locust

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Insects show impressive abilities for spatial orientation that in many aspects come close to those of vertebrates. In many navigational tasks, an assembly of midline-spanning neuropils in the insect brain, the central complex (CX), is involved. The CX constitutes a 3D matrix composed of rows of 16 vertical slices within its subdivisions, the protocerebral bridge, the upper and the lower division of the central body, and a pair of noduli composed of stacks. Following the analysis of columnar neurons that innervate and interconnect single slices of CX subunits (Heinze and Homberg 2008, J Comp Neurol 511:454), we studied the organization of tangential neurons as a basis for further functional analyses of the CX. Data are based on reconstructions of single dye-injected neurons and mass injection of dye for mapping cell clusters of tangential neurons. With few exceptions, tangential neurons have fine, putatively dendritic ramifications outside the CX and beaded or varicose ramifications likely to be axonal within the CX. Ramifications of tangential neurons outside the CX were largely subdivision-specific. Tangential neurons of the upper division of the central body showed the largest variety of cell types. Their ramifications outside the CX were concentrated in subfields of the lateral accessory lobes or the superior medial protocerebrum and the lateral protocerebrum. The data suggest input from specific brain areas to the protocerebral bridge, the noduli, and the lower division of the central body and, in contrast, a large variety of brain areas directly connected to the upper division of the central body. No direct connections were found with the mushroom bodies. Supported by DFG grant HO 950/23-1.

PP-NB-15

Are auditory sensilla numbers in hearing organs of Tettigoniidae (Insecta: Orthoptera) determined by allometric relationships?

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Sensory organs are shaped by multiple factors in their structure and function, including adaptations to signals, the ecological conditions of signal transmission, developmental constraints, or phylogenetical ancestral states. The tympanal hearing organ of tettigoniids is a highly ordered, tonotopically organised receiver for airborne sound. The number of sensory sensilla in the hearing organ, the crista acustica, is species-specific and ranges between 15 to >80 sensilla. The sensilla are individually tuned with highest sensitivity to different characteristic frequencies, which are shifted across the array of sensilla from lower to higher frequencies. This system shows highly adaptive features, e. g. tuning to acoustic signals of conspecifics, or to sounds of echolocating bats in ultrasonic frequency ranges. Little is known about the factors which determine or limit the ranges of sensory neurons in the crista acustica. Evolutionary regression can be inferred, resulting in lowered auditory sensitivity and also lower numbers of auditory sensilla. Body size has been found to affect hearing sensitivity and some morphological structures in the auditory system, but the number of sensilla have not yet been studied thoroughly for allometric relations. Allometric correlations can be analysed within or between species. Here, case studies are presented from different tettigoniid species, some of which are closely related, as well as from individuals of the same species. For some cases, there is indeed significant support for allometric relationships. These findings are correlated to auditory functions and selection pressures on auditory structures.

PP-NB-16

Electrophysiological investigation regarding anaesthetization of the decapod crustaceans lobster (*Homarus spec*) and crayfish (*Astacus spec*)

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Crustaceans are used for physiological experiments as well as human consumption. To monitor signal propagation in the CNS during different methods of anesthesia, an electrode was implanted into the CNS of lobster and crayfish and the necessary opening was sealed with tissue glue to deal with freely moving animals during the experiments. Cooling to 0°C (tap water) or -1,8°C (sea water) for 1h is no method for anesthesia as external stimuli still are measurable. $MgCl_2$ is successful for anesthesia in most of marine animals but not in decapod crustaceans during 10% bath application for 1h. As partially successful method of anesthesia can be considered a continuous CO_2 bubbling of aquaria water. The pH decreases down to values of pH 5, which most probably induces stress to the animals. Electro-stunning induces epileptic-form seizures in the crustacean CNS (lobster, crayfish), which overlay external stimuli for a couple of minutes. After several minutes the activity declines before the nerve system starts to recover. Slowly rising water temperature (1°C/min) did not cause excitation of CNS electrical activity until at about 30°C the CNS refuses to show any electrical activity. Prior to this point the animals did not show obvious signs of stress or escape behavior (e.g. tail flips).

PP-NB-17

Cellular and network adaptations for superfast motor control in the rattlesnake *Crotalus atrox*

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Superfast muscles are highly specialized to exceed the contraction rates of muscles involved in classical locomotor behavior. Intrinsically these muscles use rapid calcium binding proteins to perform superfast contraction rates. While superfast muscles are present across vertebrates, the neuronal circuits that drive these muscles have not received much attention. To this date neuronal circuits controlling superfast muscles have only been studied in the hindbrain of vocalizing fishes. Superfast motor control, however, is not only limited to hindbrain levels, but also occurs in the spinal cord. Here we investigated the single cell and network properties of the superfast spinal system that drives the shaker in the rattlesnake *Crotalus atrox.* In order to differentiate the adaptations of the shaker circuit from general rattlesnake spinal cord features, we additionally investigated the properties of spinal cord segments involved in locomotor behavior. To test for differences in the local neuronal circuitry, we evoked field potentials in the ventral roots of an isolated rattlesnake spinal cord preparation by stimulating the dorsal roots in the same cord segment. We show that, only weak differences between the two circuits are present. Using patch clamp recordings of acute spinal cord slices, we characterized the membrane properties of these motoneurons. We found specific biophysical adaptations of the shaker motoneurons for high frequency firing similar to the ones in vocalizing fishes. Our results suggest that independent of hindbrain or spinal control similar adaptations have evolved for superfast motoneuronal control.

PP-NB-18

Microglomerular Synaptic Complexes in the Polarization Vision Pathway of the Honeybee

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Honeybees use the polarization pattern of the sky for spatial orientation and navigation. While this ability has been investigated in behavioral studies, the underlying neuronal system has so far received less attention. Polarization sensitive photoreceptors are concentrated in a dorsal rim area of the compound eye. Signals are relayed through the optic lobe to the anterior optic tubercle (AOTU). The AOTU consists of one large and two small subunits. TuLAL1 Neurons originating in the two small subunits of the AOTU connect to tangential (TL) neurons of the central body via conspicuous microglomerular complexes. To study the morphology of these complexes, we stained TuLAL1 neurons by tracer injection and tangential TL neurons using an antiserum against GABA. In addition we investigated the ultrastructure of the synaptic connections by transmission electron microscopy (TEM). We found microglomerular synaptic complexes, each formed by one large presynaptic terminal of a TuLAL1 neuron that enclosed numerous small postsynaptic processes from TL neurons. The complexes could be separated into two subpopulations: TuLAL1a neurons that originate in the more dorsally located the small AOTU unit form complexes with TL2 neurons in the lateral bulbs of the lateral complex. TuLAL1b neurons, branching in the more ventrally located small unit of the AOTU, are connected to TL3 neurons in the medial bulbs. TEM images showed the ultrastructure of the complexes including two types of synapses: dyads and tetrads. The data suggest that the microglomerular complexes provide divergent synaptic connections, while maintaining topographic relations between subunits of the AOTU and TL cell types of the lower division of the central body.

PP-NB-19

Compartmentalization within the Small Subunits of the Anterior Optic Tubercle in the Honeybee

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Honeybees, *Apis mellifera,* are able to use the sky polarization pattern for spatial orientation and navigation. The neuronal pathway that conveys polarization information to the central brain originates in a specialized polarization-sensitive dorsal rim area of the compound eye and projects through the dorsal rim area of the medulla (DRAME) and the anterior optic tubercle (AOTU) towards the central complex. To get new insight into the functional role of the AOTU within this pathway we investigated its substructure using tracer injection and immunostaining with an antibody against the synaptic vesicle protein synapsin. The AOTU is located between the antennal lobe and vertical lobe of the mushroom body at the anterior surface in the protocerebrum. It is divided into a larger upper unit and two smaller units. Tangential medulla neurons that connect the DRAME to the AOTU were stained by tracer injection into the DRAME. These neurons projected exclusively to the two smaller subunits of the AOTU. The terminals within the AOTU were confined to small glomerular areas within the subunits. The projections also revealed a stratification of the more ventrally located small subunit into four horizontal layers. These layers could also be observed when staining the neuropil for the synaptic vesicle protein synapsin. To further investigate the stratification, we injected tracer into the AOTU. In these experiments we labeled three types of interneuron each of which heterolaterally connected specific layers of the small subunits . The functional significance of the layers is not known yet, but it is conceivable, that a segregation of spatial directions, as found in the slices of the central complex is already present at this early processing stage.

PP-NB-20

Neuronal basis of vocalization in the catfish *Ariopsis seemanni*- an anatomical study

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Vocal communication is not only restricted to terrestrial vertebrates, but also occurs in a vast diversity of teleost fishes. While the organization of the neuronal circuitry that produces sounds in the Batrachoidid family has been well studied, the neuronal organization of vocal systems in other families of fishes with different sound producing mechanisms remains elusive. Here, we investigated the organization of the vocal motor nucleus in the ariid catfish *Ariopsis seemanni*. Ariids produce vocalizations with sonic swim bladder muscles which are not directly linked to the swim bladder, but indirectly connected to it through an “elastic spring” which vibrates the swim bladder. To reveal the morphology and location of motoneurons we backfilled the occipital nerve roots that carry the vocal motoneuron axons in a whole brain in vitro preparation. Unlike the well studied batrachoidiformes, *Ariopsis seemanni* shows two separated sonic motor nuclei positioned lateral to the medial longitudinal fasciculus. They further show no sign of transneuronal coupling as biocytin application to one sonic nerve resulted only in ipsilaterally labeled motor neurons. Immunohistochemical analysis including GABA and glycin revealed several candidates for pre-motoneuronal populations of the vocal CPG. The organization differences compared to batrachoidid fishes raise the question of how the vocal motor nuclei are modulated in order to produce vocal behavior in ariid catfishes.

PP-NB-21

Aminergic modulation of interneurones with synaptic inputs from antennal mechanoreceptors in the cricket brain

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Mechanical stimulation of the antennae in crickets can elicit various behaviors, including aggression, that are themselves subject to modulation by the biogenic octopamine. We have identified local and descending interneurons in the cricket brain that respond to mechanical stimulation of the antennae, and found these responses to be modulated in different ways by octopamine. The contra-laterally descending brain interneurones DBNc2-2 and DBNc1-2 (cf. Schöneich, Schildberger, Stevenson, J Comp Neurol 519:1677-1690, 2011) each receives direct (monosynaptic) connections from campaniform sensillae located in the scapus and usually generate a single spike in response to lightly touching the antennae with an antenna-like bristle. After bath application of octopamine, or its agonist chlordimeform (CDM), DBNc1-2 responds to the same touch stimulus with several spikes, whereas the response in DBNc2-2 is either blocked or remains unaffected. A further, as yet not fully characterised descending brain interneurone seems only to respond to antennal stimulation in the presence of CDM. These effects were reversed by washing, and reversibly blocked by the octopamine antagonist epinastine. Octopamine seems to act directly on the central synaptic connection with the interneurones, since nerve recordings from antennal afferents revealed no effect. Stains of single campaniform sensillae on the scapus revealed that their terminal processes are closely associated with the presumptive spike initiating zone of DBNc2-2 and DBNc1-2. Immunocytochemistry revealed numerous octopaminergic terminals adjacent to this site, some but fewer dopaminergic terminals but no serotonergic terminals. We are currently investigating the effects of dopamine. We speculate that octopaminergic modulation of the studied neurones will influence whether male crickets approach or retreat from conspecifics during agonistic encounters.

PP-NB-22

Neuronal coupling between the motor pattern generating networks for singing and breathing in field crickets

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In field crickets, the network that generates the singing pattern is located in the anterior abdominal neuromers of the CNS (Schöneich & Hedwig 2011, 2012). This strongly supports the idea that the stridulatory motor pattern may have evolved from abdominal ventilatory motor pattern. Singing activity considerably increases the rate of ventilatory abdominal pumping and a neuronal linkage between the stridulatory and respiratory motor pattern generators is indicated by the coupling of abdominal pumping cycles to the chirp rhythm. Here we investigated the neuronal coupling between breathing and chirping rhythm by intracellular recordings of ventilatory and stridulatory interneurons in the abdominal ganglia of fictively singing crickets. The two motor patterns were monitored by extracellular recordings from transverse abdominal muscles and the mesothoracic wing nerve N3A, respectively. Although, ventilatory pumping of the abdomen usually occurred in phase with the chirp cycles of the singing activity, sometimes the two rhythms became uncoupled and resynchronised within a few cycles. Recordings of ventilatory interneurons revealed that during singing they receive additional EPSPs, which strictly reflected the syllable pattern of the song. We never recorded any synaptic input reflecting the ventilatory rhythm in singing interneurons. We conclude that the ventilatory and stridulatory rhythm originate from discrete pattern generating networks that are synchronized by subsequent synaptic coupling. Coupling of the two rhythms is established by sub-threshold excitatory synaptic inputs from the singing to the ventilatory pattern generating network which entrain the somewhat slower ventilatory rhythm.

PP-NB-23

Strategy to quantify neurotransmitter from individual Drosophila cells

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Single cell analysis by mass spectrometry such as MALDI-TOF MS allows for precise determination of neuroactive substances at the cellular level. A MS-based method for the detection of neuropeptides in single Drosophila melanogaster neurons has been already published. Here, we add classical transmitter measurements focusing on single octomaniergic Drosophila cells to the direct MALDI-TOF MS-based peptide profiling using chemical treatment. However, the detection of biogenic amines by direct MALDI-TOF MS from such small sample units has been challenging in analytical task so far. In a first experimental step, we develop and optimize a strategy for a robust, stabile and reproducible measurement of synthetic octopamine by using on-plate chemical treatments to increase the detection limit from 10^{-6} M up to 10^{-9} M which allows us to deal on single cell level. First analyses of biological samples were focused on individual octopaminergic neurons of the ventral midline cluster (Vm neurons) from the subesophageal ganglion using a GAL4-TdC2, UAS-mCD8::GFP strain for cell identification. For that, sample preparation technique of individual V_m somata, transfer on a MALDI sample plate, subsequent on-plate derivatization procedure, and internal standard for quantifications as well as matrix application were tested and optimized. The quantification method was validated by analysing relative peak intensities at different concentration of synthetic OA and calculating the respective linearity, precision and accuracy after standards published by Persike et al. 2010 and U.S. DEPARTMENT OF HEALTH AND HUMAN SERVICE et al. 2001. Finally, fragmentation experiments were used to confirm and reconstruct OA by using MELTIN database.

PP-NB-24

Waveguiding properties of primate and human cone photoreceptors

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The optical waveguiding properties of mammalian photoreceptors constrain how light is captured by the retina and influence several aspects of visual perception. Modeling suggests that cone photoreceptors can behave as multimodal waveguides, depending on the cone diameter and wavelength of the incident light. If these optical principles operate in the living eye, then the waveguide modes will determine the appearance of a cone in a retinal image taken at the microscopic scale. When light is incident on the waveguiding axis of a cone, it will appear as a Gaussian-like distribution of intensity as the fundamental mode is dominant. When the incident light is off axis, the fundamental mode is less efficiently excited and higher order modes can become prominent, with their superposition giving cones a more complex appearance. Optical modeling suggests that such behavior is more likely to be seen at shorter wavelengths than long. Using an adaptive optics scanning laser ophthalmoscope (AOSLO), we imaged the cone mosaic in macaques and humans with subcellular resolution in the living eye. By analyzing the retinal images captured with the AOSLO for 543 nm (green) and 710 nm (red) light separately, we assessed whether waveguiding of cones is wavelength-dependent in retinal images as predicted by theory. Cones with complex profiles were often visible when imaged with green light; the same cones imaged with red light more often exhibited a Gaussian-like profile. We are currently examining if the prevalence of multimode cone profiles is influenced by the angle of incidence of the imaging beam. Our data suggest that higher order waveguide modes can be seen *in vivo*, and may enable a comparison of the optical properties of human and primate cone photoreceptors.

PP-NB-25

The role of thermal stimuli during mate choice in acoustic insects

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Mating preferences based on variation in acoustic signals in insects have been studied extensively in the past. In many acoustic insect species, females show phonotactic approaches towards the long range acoustic signals of males. But the final decision for mating may be based on further assessment of additional close range cues. Sound production by males is a costly trait, since only a fraction of muscle energy used to produce the sound is converted into acoustic power. Recent work revealed that in some katydid species with long-lasting love songs the male thorax housing the singing muscles increases its temperature by up to 10°C after several minutes of singing. Therefore, the energy invested in sound production is not wasted but reflected in an elevated thorax temperature. This increased temperature could be evaluated by females via thermo-sensitive sensilla housed on their antennae. Thus, thermal information could be a crucial cue for final mate choice decision. To investigate the role of thermal stimuli during mate choice in the katydid species, *Mecopoda elongata* we use morphological, physiological and behavioral approaches. As a first step we describe the typology, numbers and location of antennal sensilla in both male and female *M. elongata* to create a firm base for following experiments. In addition we also present preliminary physiological data suggesting that at least coeloconic ("peg in pit") sensilla on the antennae of both sexes respond with high sensitivity to changes in temperature caused by convective as well as radiant heat.

PP-NB-26

Neuropeptidergic and aminergic neurons in the *Daphnia* optic ganglia-brain complex

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We investigated the neuroanatomy of *Daphnia magna* optic ganglia-brain complex (OGBr) with conventional techniques and mapped various neurons expressing neuropeptides and neurotransmitters. The complex contains fused lamina, separate visual tectum neuropiles and associated neurons and the brain consists of 10 cell clusters, four lateral and five midline-spanning neuropiles, including an insect-like central complex. Neurons have been identified using antisera immunoreactive (ir) to FMRFamide (RFa), allatostatin (ASTA), allatotropin (AT), pigment-dispersing hormone (PDH), adipokinetic hormone (AKH), Arg^7-corazonin (CRZ), tachykinins (TK) and neurotransmitters serotonin (5HT) and histamine (HA); the neuropeptides are previously and/or here first biochemically identified daphnid peptides. The largest distribution throughout the OGBr show RFa-, AT-ir and PDH-ir as well as 5HT-it and HA-ir neurons whereas the origin of ASTA-ir, TK-ir, AKH-ir and CRZ-ir neurons is restricted to the central brain. Thus far detected first time and only for AKH-ir neurons, however, are projections to a novel putative neurohaemal organ dorsal to the tritocerebrum-ventral nerve cord transition, which is a hint for the occurrence of true AKH-neurohormones in *Daphnia*. Similar neuropiles and primary structures of neuropeptides as well as their neuronal distributions suggest common evolutionary histories in arthropods.

PP-NB-27

Adaptation-induced modification of motion selectivity tuning in visual tectal neurons of adult zebrafish

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In the developing brain training-induced emergence of direction selectivity and plasticity of orientation tuning appear to be widespread phenomena found in the visual pathway across different classes of vertebrates. Moreover, short-term plasticity of orientation tuning in the adult brain has been demonstrated in several species of mammals. However, it is unclear whether neuronal orientation and direction selectivity in non-mammalian species remains modifiable through short-term plasticity in the fully developed brain. To address this question we analyzed motion tuning of neurons in the optic tectum of adult zebrafish by calcium imaging. In total, orientation and direction selectivity was enhanced by adaptation, responses of previously orientation-selective neurons were sharpened and even adaptation-induced emergence of selectivity in previously non-selective neurons was observed in some cases. The different observed effects are mainly based on the relative distance between the previously preferred and the adaptation direction. In those neurons, in which a shift of the preferred orientation or direction was induced by adaptation, repulsive shifts (i.e., away from the adapter) were more prevalent than attractive shifts. A further novel finding for visually induced adaptation that emerged from our study was that repulsive and attractive shifts can occur within one brain area, even with uniform stimuli. The type of shift being induced also depends on the difference between the adapting and the initially preferred stimulus direction. Our data indicate that, even within the fully developed optic tectum, short-term plasticity might have an important role in adjusting neuronal tuning functions to current stimulus conditions.

PP-NB-28

Dissecting the influence of clock and environment on the eclosion rhythms of *Drosophila* under natural conditions

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The circadian timing of behaviour allows animals to adapt to environmental conditions and is thought to increase their fitness. A classical model for a circadian-timed behaviour is the eclosion (adult emergence) of the fruit fly. *Drosophila* eclosion is gated to the morning hours, which is commonly assumed to be an adaptation to prevent water loss and thus optimising fitness. Laboratory studies have shown that the *Drosophila* eclosion rhythm can be entrained to different Zeitgebers like light or temperature and depends on a functional molecular clock and PDF signalling. Very little, however, is known about eclosion rhythms in nature. A major question here is whether and to what extent the circadian clock and abiotic Zeitgebers contribute to ensure that flies eclose at the right time of the day. We started to monitor the eclosion of wildtype and mutant *Drosophila* under natural conditions using a newly developed camera-based eclosion monitoring system called WEclMon (Würzburg eclosion monitor). A statistical model allows to dissect the role of the circadian clock and abiotic factors on eclosion rhythm and a possible hierarchy of the different Zeitgebers. We present data from the first field seasons which already suggest that the relative importance of the clock and the various Zeitgebers differs between genotypes. Moreover, and unlike in the laboratory, eclosion timing seems to be influenced by multiple interdependent factors. *Funded by the Deutsche Forschungsgemeinschaft within the collaborative research center SFB 1047 "Insect timing", TPB2 to CW and TPC6 to TH.*

PP-NB-29

Signalling patterns and interactions during electrocommunication between real and artificial weakly electric fish

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African weakly electric fish (Mormyridae) use an electric organ in their tail to generate electric fields that are emitted as short, often biphasic pulses. These signals are used for both active electrolocation and electrocommunication, which is supported by the existence of independent types of electroreceptors and central processing pathways for both functions. Variations in inter-discharge intervals have been linked to optimization of sensory acquisition during active electrolocation, as well as to the transmission of behavioural states and intentions during electrocommunication. Mormyrids are known to communicate using distinct temporal signalling patterns as well as by synchronizing their discharge activity with other individuals. In addition, their propensity to follow a mobile fish dummy is strongly increased by playbacks of species-specific pulse sequences. Here, we tested how single individuals of *Mormyrus rume* responded to playback sequences of electric signals that were taken from various behavioural contexts, and which were emitted by a moving electric fish dummy. On average, animals did not adopt the overall interval distribution of the playback, but synchronizations to the different pulse sequences occurred frequently and largely independent of the playback's interval distribution. Fish emitted characteristic double pulse patterns exclusively as a reaction to electrical playbacks, and they occurred more frequently if the playback also featured double pulse patterns. Differences in response were found as a reaction to different playback patterns, as well as between individual fish, suggesting individual dispositions in signalling style, some of which correlated with social rank.

PP-NB-30

Detection of acoustic predator cues under high background noise in tropical crickets

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For nocturnally active crickets on the wing, insectivorous bats represent an important predatory threat. Consequently, their ears evolved sensitivity in the high sonic/ultrasonic range to detect echolocation signals. However, in habitats with high species diversity this task is complicated by high levels of background noise that includes ultrasound events not originating from predators. While correctly reacting to bats provide benefits for survival, false alarms to background noise may present substantial costs. Here we combined behavioral and neurophysiological studies on the bat avoidance in several species of neotropical crickets in Panama, where nocturnal, high-frequency background noise originating from katydid communication may be a major problem for bat detection and avoidance. We tested two hypothesis how crickets can avoid costs of false alarms: (1) crickets may respond only to repetitive HF pulses, indicative of the search phase of echolocating bats, thus avoiding false alarms towards single sound events in the background. (2) Crickets have reduced sensitivity in the ultrasonic range, thus background noise only rarely induce false alarms. This solution also bears costs due to a reduction of the detection range for bats. Results indicate that crickets indeed respond to single sound pulses, but the behavioral threshold of 80 - 90 dB SPL is so high that noise in the background rarely exceeded this threshold. We also found two different modes of responses: Many of the smaller species of Trigoniidae always stop flying in response to any HF stimulation. By contrast, larger crickets (Eneopterinae) show a typical negative phonotactic steering response, when stimulated with ultrasound.

OP-P-IT-01

The regulation of *aqp-8* in the excretory cell of *C. elegans*

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In his natural environment of rotting fruits, the nematode *C. elegans* is exposed to strong changes in the osmolarity of his environment. Studying the effects of environmental stress on *C. elegans* with a focus on hyperosmotic and hypoosmotic stress conditions, we analyse the involvement of aquaporines in the maintenance of the water balance under osmotic stress conditions. In addition, we investigate the effect of aquaglyceroporines onto the hyperosmotic stress response.

In our recent project, we concentrate on *aquaglyceroporine-8* (*aqp-8*). *aqp-8* is expressed in the excretory cell of *C. elegans*, where it has been shown to be involved in the excretory canal growth. In addition, our recent findings suggest a secondary role of *aqp-8* in the stress response upon hyperosmotic conditions in the surrounding environment. We were able to show that *aqp-8* mRNA levels and protein concentration are regulated according to the osmotic pressure set by the environment. Furthermore, we identified genes that are involved in the regulation of *aqp-8* under isotonic and hypertonic stress conditions by using RNAi techniques. With the data thus obtained, we are starting to build a model of the *aqp-8* regulatory pathways and to understand the interaction between *aqp-8* regulation and known stress response pathways of *C. elegans*.

OP-P-IT-02

The challenged consumer - aquatic herbivores' responses to dietary constraints

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Herbivorous animals face multiple challenges with respect to their dietary resources. In particular, not only the acquisition of sufficient food amounts, but also the nutritional suitability or quality of resources is a critical parameter. This is especially the case for herbivores, which ingest primary producer biomass that often deviates strongly from the consumers’ requirements in terms of nutrient content or biochemical composition. Consumer biomass accrual is thus not only dependent on the quantity of available resources, but also on the relative imbalance between the supply (in the diet) and the consumers’ specific requirements of certain dietary compounds. On the other hand, the herbivores’ evolution leads to the development of adaptive responses to such dietary imbalances. Using several case studies from aquatic herbivorous invertebrates and their algal prey, I here highlight a variety of dietary constraints and their ecological and physiological implications for herbivorous consumers. Furthermore, I demonstrate how adaptations and responses on the consumer level, ranging from alterations of the set of digestive enzymes or other changes on the level of the expression of specific diet-dependent genes to complex, infochemical-mediated behavioural adaptations, help these herbivorous animals to cope with spatially and temporally fluctuating resource quantity and quality and allow them to adapt to dietary challenges.

OP-P-01

A transcriptome approach to the hypoxia tolerance of the seal (*Cystophora cristata*) brain

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During the dive, the brains of seals experience a reduced supply with oxygen. The neurons of the brain of the hooded seal (*Cystophora cristata*) are more tolerant to low oxygen conditions (hypoxia) than those of mice. Seal neurons also better survive a reduction in the supply with glucose and high concentrations of lactate. This tolerance may be accompanied a shift of the oxidative energy metabolism to the astrocytes while in terrestrial mammals the aerobic energy production mainly takes place in neurons. We employed RNA-seq to approach the molecular basis of the unusual hypoxia tolerance of the seal brain. Transcriptomes were generated by Illumina sequencing from the cerebral cortex of the hooded seal and the ferret (*Mustela putorius furo*), which is a terrestrial relative. Selected differentially expressed genes were verified by quantitative real-time PCR. We found clusterin, an extracellular chaperone with a variety of cytoprotective functions, is the most highly expressed gene in the seal brain. Compared to the ferret, clusterin has a fourfold higher level in the seal and displays an alternative 5' exon. Gene ontology (GO) and KEGG pathway analyses showed higher levels of mRNA coding for metabolic processes in the brain of the hooded seal, while lower levels were found for genes involved in neuronal signaling and protein synthesis. These differences may be interpreted in terms of an energy saving strategy is the seal's brain. We further used RNA-seq to compare the effect of hypoxia and reoxygenation on brain slices from layer V of the visual cortex of hooded seals. Compared to the normoxia control, hypoxia caused the preferential upregulation of genes related to various signaling pathways, and a downregulation of genes involved in ion transport and other neuronal processes, indicative for a neuronal shutdown.

OP-P-02 - Hormonal switches in semelparous reproduction

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One of the most extreme reproductive principles is semelparity, an all or-nothing strategy leading to the death of the individual. Semelparous reproduction often culminates in mass spawnings as observed in many aquatic species ranging from corals to salmon. Characteristic for this mode of reproduction is not only a massive generation of germ cells, that can amount up to 80% of the individuals` body mass at spawning; but also the synchronisation of germ cell development in the individual as well as in the population to ensure a maximal reproductive success. We study the molecular cues involved in the synchronisation and regulation in the polychaete *Platynereis dumerilii,* in which sexual maturation has been linked to the sinking titer of a brain-borne hormone termed nereidin. Despite its central role in mediating the switch between a feeding and growing live style to a non-feeding, reproducing one, molecular nature of nereidin has remained enigmatic. In order to identify the responsible bioactive molecules, we have established a quantitative molecular assay using primary cell cultures of eleocytes, cells that are responsible for the massive production of the yolk precursor vitellogenin during sexual maturation. Fractioning of *Platynereis* head extracts demonstrated the existence of distinct positive and negative regulators of vitellogenesis, and the involvement of a conserved hormone pathway. To complement these assays, we have also generated systematic head transcriptome profiles that allowed us to identify genes significantly regulated in the process of maturation. Together, our assays draw a first map of the candidate regulators and effectors involved in the major metabolic switch underlying semelparous reproduction.

OP-P-03

Cockroach GABA$_B$ receptor subtypes: molecular characterization, pharmacological properties and tissue distribution

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γ-aminobutyric acid (GABA) is the predominant inhibitory neurotransmitter in the central nervous system (CNS). Its effects are mediated by either ionotropic GABA$_A$ receptors or metabotropic GABA$_B$ receptors. GABA$_B$ receptors regulate, *via* G$_{i/o}$ G-proteins, ion channels, and adenylyl cyclases. In humans, GABA$_B$ receptor subtypes are involved in the etiology of neurologic and psychiatric disorders. In arthropods, however, these members of the G-protein-coupled receptor family are only inadequately characterized. Interestingly, physiological data have revealed important functions of GABA$_B$ receptors in the American cockroach, *Periplaneta americana*. We have cloned cDNAs coding for putative GABA$_B$ receptor subtypes 1 and 2 of *P. americana* (PeaGB1 and PeaGB2). When both receptor proteins are co-expressed in mammalian cells, activation of the receptor heteromer with GABA leads to a dose-dependent decrease in cAMP production. The pharmacological profile differs from that of mammalian and *Drosophila* GABA$_B$ receptors. Western blot analyses with polyclonal antibodies have revealed the expression of PeaGB1 and PeaGB2 in the CNS of the American cockroach. In addition to the widespread distribution in the brain, PeaGB1 is expressed in salivary glands and male accessory glands. Notably, PeaGB1-like immunoreactivity has been detected in the GABAergic salivary neuron 2, suggesting that GABA$_B$ receptors act as autoreceptors in this neuron.

OP-P-04

Regulation of metabolic traits by octopamine and tyramine in Drosophila

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The biogenic amines octopamine and tyramine are the invertebrate counterparts of epinephrine and norepinephrine. They act as transmitters and hormones controlling various aspects of behaviour. Moreover, they have been implicated as being responsible for controlling the famous fight-or-flight response. Here we showed that especially octopamine is of central importance for controlling various metabolic traits in the fly comprising body weight, fat content and metabolic rate. Flies deficient in the synthesis of octopamine develop a severe couch-potato syndrome with reduced physical activity, high body fat and low metabolic rates. Targeted release of octopamine from endogenous stores induced exactly the opposite phenotype of highly active and lean animals. Regulation of these metabolic parameters involves different signalling systems with insulin-signalling being the most important one. Octopamine deficient flies have high insulin hemolymph levels and consequently low hemolymph carbohydrate concentrations. Taken together, octopamine and to a certain extent also tyramine are operative to translate stressful situations into a suitable metabolic response.

OP-P-05

Tracing a proteinaceous labelled diet in a honey bee colony

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A well-balanced nutrition plays a key role for the development of a strong and resistant honey bee colony. Pollen and nectar are the most commonly gathered products which provide honey bees with all the required essential nutrients. But seasonal changes or the increasing cultivation of monocultures can prevent honey bees from satisfying their nutritional demands by their own. Malnutrition of a honey bee colony is particularly reflected in the decrease of brood production to the point of brood cannibalism. But honey bees can be provided with artificial diets by beekeepers to counteract starvation or to overcome pollen dearth or seasonal fluctuations. Previous studies gave attention to the adequate nutrient content and most of all the impact of the diet on the physiology and the development of honey bees. But so far the question still remains unanswered in which way an artificial pollen diet is distributed within a honey bee colony? Therefore we labelled a commercial pollen substitute with ^{14}C polyethylene glycol (^{14}C PEG) and offered this artificial diet to three honey bee colonies overnight. This experimental setup allows us to trace an artificial diet among workers bees and larvae and even in honey or pollen cells. In our study we found that within twelve hours 82-98% of the bees and 71-77% of the larvae received shares of the radioactive labelled pollen substitute. Especially in larvae older than two days we found high activities of the ^{14}C PEG. While we could trace the radioactive marker in 1to 3 % of the honey cells we only detected radioactive quantities lower than 1% in pollen cells. With our experiment we proofed that the main part of an offered diet is spread to the worker bees and to the larvae older than two days and only small amounts can be found in honey and pollen cells.

PP-P-01

More than just one: Multiplicity of Hirudins and Hirudin-like Factors in the Medicinal Leech, *Hirudo medicinalis*

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Blood-sucking leeches like the medicinal leech, *Hirudo medicinalis*, have been used for medical purposes since ancient times. During feeding, medicinal leeches transfer a broad range of bioactive substances into the host`s wound to prevent premature hemostasis and blood coagulation. Hirudin is probably the best known of these substances. Despite its long history of investigation, recombinant production and clinical use, there still exist conflicting data regarding the primary structure of hirudin. Entirely unclear is the potential biological significance of three different subtypes and many isoforms of hirudins that have been characterized so far. Furthermore, there is only incomplete information on their cDNA sequences and no information at all on gene structures and DNA sequences are available in the databases. Our efforts to fill these gaps revealed the presence of multiple hirudin-encoding genes in the genome of *Hirudo medicinalis*. We have strong evidence for the expression of all three subtypes of hirudin within one individual leech and for the expression of additional hirudins or hirudin-like factors that may have different biological functions and may be promising candidates for new drugs.

PP-P-02

Synthesis of salivary proteins and refilling of salivary gland cell reservoirs in the medicinal leech (*Hirudo verbana*) upon feeding

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Sanguivorous leeches, e.g. *Hirudo verbana*, are ectoparasites that have access to potential hosts only infrequently. They have evolved mechanisms that allow them to take up large amounts of host body fluids (up to 10 times their own body weight during one meal) and store the un-degraded nutrients for long periods (up to 1 year) in their crops. Leeches produce various salivary proteins which are synthesized by and stored in unicellular salivary gland cells. They are almost completely transferred to the skin wound of the host during one act of feeding. Our question was, whether leeches that have released their salivary proteins during a blood meal refill their salivary gland reservoirs immediately after the meal or start synthesis and refilling of their salivary gland reservoirs only after the stored material in the crop is used up. Using histological techniques, we observed that the sizes of the salivary gland cells started to increase already within a few days after feeding reaching the control level of unfed leeches within 2 weeks. This indicated that leeches start to synthesize salivary gland proteins immediately after feeding. To confirm this conclusion, we determined the abundance of hirudin-cDNA prepared from total RNA in samples extracted 3 and 5 days after feeding by semi-quantitative PCR and compared these data to those obtained from samples of control leeches. In addition, we performed 2D gel electrophoresis using protein extracts prepared from fed leeches (1, 3, 5, 7, 14 and 21 days after feeding). In summary, the results indicated that salivary protein synthesis occurs within the first week after feeding, and that refilling of the reservoirs in salivary gland cells is essentially complete approximately two weeks after feeding.

PP-P-03

Adjustments of serine proteases of *Daphnia pulex* in response to temperature changes

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Elevated temperatures considerably challenge aquatic invertebrates, as in poikilotherms, the enhanced energy metabolism and protein turnover under these conditions must be met. Thus temperature acclimation or acute thermal stress requires adjustments of proteolytic digestion. In *Daphnia*, the serine proteases chymotrypsin and trypsin represent the major proteolytic enzymes. Effects of changes in ambient temperature on these key enzymes were studied in *Daphnia pulex* acclimated to different temperature conditions (10, 20, and 24°C) or subjected to acute heat stress (transfer from 20°C acclimation to 30°C). Results showed increased expression level of serine proteases with rising temperatures. Transcripts of trypsin isoforms were present in higher amounts than observed for chymotrypsin. Additionally, trypsin isoforms were induced by elevated temperatures to a larger extent. Correspondingly, photometric assays with enzyme-specific substrates revealed higher trypsin activity in cold-acclimated animals. However, the enzymatic activity of chymotrypsin increased at elevated temperatures, whereas trypsin activity slightly decreased, resulting in a shift to dominating chymotrypsin activity in warm-acclimated animals. Activity staining after gel electrophoresis (zymograms) revealed eight bands with proteolytic activity, which were assigned to trypsin or chymotrypsin activity applying specific inhibitors or identifying the cleavage products of the substrate casein by mass spectrometric analysis. The observed phenotypic plasticity adjusts the set of active proteases to the altered needs of protein metabolism, optimizing protein digestion for the temperature conditions experienced in the habitat.

PP-P-04

What pumps fresh hemolymph throughout the legs of insects?

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Leg circulation in insect legs is caused by pressure changes that enter the internal space of the leg segments from the body cavity. Pumping of the dorsal longitudinal heart rhythms is not involved. This was first demonstrated for several more or less transparent aquatic insects (Meyer 1931). He also observed that in insect legs the centrifugal and the centripetal flow of hemolymph pass ventrally and dorsally through narrow apertures where trochanter and femur are connected. More distal in the femur and in the outer leg segments the available space for the hemolymph widens, separated only by a longitudinal septum. Physically that should slow the progress of the hemolymph considerably, both on the way towards and back from the tip of the leg. Why can we observe a rapid flow? This study shows that in locusts specific narrow pathways ensure rapid progress of hemolymph to and from the tip of each leg. The main drive of leg circulation is increasing pressure caused by abdominal expiration movements. Valves that make directional (and not only tidal) flow possible inside the legs were not found. The mechanisms that induce directional flow during general increase of pressure at the base of legs are elastic bulging joint membranes in the ventral (efferent) compartment and predominant collapse of tracheal air sacs in the dorsal (afferent) compartment which cause rapid longitudinal propulsion of hemolymph in insect legs. Assisting muscular pumps for leg circulation were found in hemipteran tibiae and the middle legs of locusts only (review: Pass 2002).

PP-P-05

The resting metabolism of three common hymenopterans: different energetic survival strategies in species of similar size.

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The resting metabolic rate (RMR) is a very important parameter in insect life concerning their energy balance. It represents the energetic costs of simple subsistence, determining an individual's minimum energy requirements under a standardized set of conditions. It is fundamental for comparing the relative energy expenditures of particular activities and enables the assessment of basic energetic costs across species. The RMR is presumed to reflect the energetic costs of adaptation to a particular thermal environment and is therefore an important measure in a warming world. Honeybees (*Apis mellifera*), Vespine and Polistine wasps (*Vespula* sp., *Polistes dominulus*) are social insects with similar size and shape. Are they similar in their basic energetic expenditure despite considerable differences in active metabolism? To determine the insects' RMR, CO_2 emission was measured in a broad temperature range in order to detect dependence on ambient temperature. The RMR showed a strong dependence on temperature in all species. However, the shape and level of dependence differed considerably between species. The RMR of honeybees and Vespine wasps changed in a complex (only partial exponential) form with temperature, whereas in Polistine wasps the metabolism increased exponentially. Vespine wasps and honeybees are "high energy turnover" hymenopterans in contrast to Polistine wasps. *Vespula* exhibited the highest resting metabolic performance. The RMR of *Polistes* was below that of *Vespula* and *Apis*, but above 25 °C it surpassed that of the honeybee. The comparison of these three species revealed that the "aerobic capacity hypothesis", which postulates that a lower active metabolic capacity should be reflected in a lower standard metabolic rate, is not valid in any case. The research was funded by the Austrian Science Fund (FWF): P20802-B16, P25042-B16.

PP-P-06

Effect of protein and different pollen diets on internal glands development of adult honey bees

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Pollen is the only source of proteins for honey bees. Protein content and the quality of pollen protein are thought to have an important effect on the development of honey bees. In this study we examined the consumption rate of protein diets in cages and in colonies. We also tested the effect of six different diets (protein free diet, Feedbee®, *Helianthus* sp. pollen, *Sinapis* sp. pollen, *Asparagus* sp. pollen, *Castanea* sp. pollen, and a mixture of the four latter) on the hypopharyngeal glands and acid gland development in caged newly emerged worker bees. Data show that protein diet of caged bees was mainly consumed between days 1 to 8 with the highest consumption on day 3. In full colonies, *Castanea* sp. pollen and mixed pollen were consumed more than other pollen diets (Fisher LSD, $p<0.05$). In caged honey bee workers we found differences among diets regarding glands development. The hypopharyngeal glands acini were best developed at the age of 5 days and bees fed with mixed pollen or *Castanea* sp. pollen dough had the best developed glands at this age (Fisher LSD, $p<0.05$). In contrast to hypopharyngeal glands, the acid gland sacs continued to grow with age until the age of 12 days and bees fed with mixed pollen, *Castanea* sp. pollen or *Asparagus* sp. pollen dough had the biggest acid gland sacs volume in ages of 12 and 18 days (Fisher LSD, $p<0.05$). We found differences in the effects of different pollen diets, and that in many cases a mixture of pollen was favorable for honey bee nutrition, although some monofloral pollen diets alone also had good nutritional quality. Our results strengthen the hypothesis that monofloral pollen nutrition may hinder full development of honey bees' internal glands, which could impair the fitness of colonies.

PP-P-07

The role of proline in honeybee drone (*Apis mellifera* carnica) flight

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Honeybee flight is among the most energy demanding behaviours in the animal world. Carbohydrate is well established as the primary energy source in honeybee drone flight. Yet a high concentration of proline in tissue and haemolymph allows for a role of this amino acid as a secondary, intermediate pathway of energy transfer to the flight muscle mitochondria. In this work we show that proline is metabolized rapidly during honeybee-drone flight. Drones, in tethered flight in a roundabout, undergo a flight-duration related decrease in radioactive label after preflight injection ^{14}C labeled proline into the haemolymph stream. Yet, the overall concentration of proline shows less fluctuation. We propose a concomitant in-flight proline oxidation and resynthesis of proline from carbohydrate in honeybee-drone flight.

PP-P-08

Effects of different pesticides and pathogen exposure on hemocytes in honeybee larvae (*Apis mellifera*)

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Honeybees (*Apis mellifera*) have developed an effective immune system, which differs significantly from the immune system of vertebrates, e.g. in the lack of antibody mediated defense. The innate immune system of insects is composed of humoral and cellular defense mechanisms. In the cellular defense mechanism, honeybees have 4 types of hemocytes within their hemolyph i.e., prohemocyte, plasmatocyte, granulocyte and oenocytoid. We evaluated whether pesticides and/or *Paenibacillus larvae* (*Pl*), a spore-forming bacterium causing American foulbrood, affect the cellular immune system. For this purpose we studied effects of different pesticides, such as dimethoate, clothianidin and fluvalinate on the total and differential hemocyte number in honeybee larvae. For dimethoate, the LD_{50} of adult bees, for clothianidin the 8-fold LD_{50} of adult bees was employed. Additionally, the influence of *Pl* spore infection, responsible for 50% mortality, on the above mentioned parameters was assessed as well as a combination *Pl*/pesticides. An *in vitro* bee larval rearing method was employed, where doses of pesticides were orally administered to the larvae within 4 days. In this treatment we observed a 50% increase in total hemocyte counts. The results point out that total hemocyte number increases highly significant under treatments with doses of dimethoate [120 ng/larva], clothianidin [32 ng/larva] and *Pl*. Our results further confirm a significant alteration of the number of differential hemocytes in pesticide-treated groups as compared to the control. This study shows that pesticide exposure has a significant effect on the recruitment of a cell-specific immune response in honeybee larvae.

PP-P-09

Significance of ABCB-transporters for a leaf beetle's defense strategy

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North American leaf beetles of the species *Chrysochus auratus* (Coleoptera, Chrysomelidae, Eumolpinae) feed on plants in the family Apocynaceae which contain toxic cardenolides. These secondary plant compounds are able to inhibit the sodium-potassium pump of animal cells, thereby blocking essential physiological and neural processes. In contrast to the Eurasian species of the genus, *C. auratus* is able to sequester (enrich) cardenolides and transport them into defensive glands to deter predators. This ability requires a number of adaptations and mechanisms that are still unknown. We suggest that ABCB-transmembrane (ATP binding cassette, ABC) transporter are an essential component at the cellular and physiological tissue barriers. Members of this protein family are known to transport xenobiotic substances in other organisms and to play an important role as efflux transporters in the blood brain barrier. We identified 3 ABCB-transporter in the transcriptome of *C. auratus* and cloned them into expression vectors. By using baculovirus infection of insect cells we achieved the heterologous expression of these proteins. In order to investigate their function we are establishing transport assays based on inverted membrane vesicles isolated from these cells. In this system, the activity of the ABCB-transporter can be measured by the rate of ATP hydrolysis (ATPase assay) coupled with substrate (cardenolide) transport. The quantity of the transported cardenolides can then be determined by liquid chromatography-mass spectrometry (LC/MS).

PP-P-10

Comparing cardenolide resistance by substitutions in the Na,K-ATPase of *Homo sapiens* and *Drosophila melanogaster*

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The Na,K-ATPase is likely the most important ion carrier in the animal kingdom, enabling e.g. the excitability of nerve and muscle cells. In almost all animal species this carrier can be blocked by cardenolides, plant metabolites that bind with high affinity to a specific binding pocket in the Na,K-ATPase α-subunit. Only some animals are resistant to the blocking effect of cardenolides, as first discovered for the rat Na,K-ATPase 1α and later for several insects feeding on cardenolide containing plants. In this study we compare the effect of the two resistance-conferring pairs of substitutions, Q111R, N122D from the rat and Q111V, N122H from the monarch butterfly, *Danaus plexippus*. Although both substitution pairs are well known, their effect in the genetic background of distantly related species is unknown. In this study each pair of substitutions was introduced by site-directed mutagenesis into both the human and fruit fly Na,K-ATPase α-subunit gene. The recombinant genes were expressed by baculovirus infection of Sf9 insect cells. The harvested recombinant proteins were tested for their cardenolide sensitivity under increasing concentrations of ouabain. This analysis is complemented by ligand docking simulations to rationalize the observed differences in cardenolide sensitivity.

PP-P-11

Characterisation of the interaction between *Plasmodium falciparum* infected erythrocytes and human endothelial receptors

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The human malaria parasite *Plasmodium falciparum* is able to avoid spleen-dependent killing by adhesion of infected erythrocytes (IEs) to human endothelial receptors that line microvascular venules. This sequestration of IEs is the major reason for the most severe pathological phenotypes observed in malaria, including obstruction of blood flow, hypoxia, tissue damage and ultimately, organ failure. Parasite-derived proteins located on the membrane of the IEs cause the specific binding. Currently, only one protein family of the parasite is known to be involved in these receptor-ligand interactions, the *P. falciparum* erythrocyte membrane protein 1 (*Pf*EMP1) family. The *Pf*EMP1 family is encoded by about 60 *var* genes per parasite genome and the *var* gene sequences vary greatly from parasite to parasite, giving rise to an enormous repertoire of different *var* genes in nature. The various *Pf*EMP1 molecules display different binding characteristics, which is thought to be important for the different clinical outcomes. To date, at least 22 endothelial receptors or molecules are described to be involved in the interaction with IEs. Nevertheless, for most of the receptors that were described to cytoadhere to IEs the parasite ligand is not known. In this study we try to identify the specific *P. falciparum* ligands involved in the interaction to various receptors. Furthermore, the interaction of IEs enriched for the binding to a specific receptor will be characterised under dynamic flow conditions. This work is supported by the DFG (BR1744/12-1)

PP-P-12

Pyruvate dehydrogenase activity as a putative mechanism to enhance the hypoxia tolerance in the brain of the hooded seal (*Cystophora cristata*)

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Pyruvate dehydrogenase (PDH) plays a central role in the energy metabolism: PDH activity determines whether carbohydrates or lipids are oxidized for energy production by the cell. If PDH is activated, glucose-borne pyruvate is decarboxylated, and the resulting acetyl-CoA fills the tricarboxylic acid (TCA) cycle. If PDH is inhibited, the acetyl-CoA generated from fatty acids or ketone bodies will be used in the TCA cycle. The regulation of PDH activity is a crucial component of the metabolic adaptation to hibernating mammals. Here, we evaluate the role of PDH in the metabolic adaptations of the brain of diving mammals. We compared levels of PDH mRNA, PDH subunit content and PDH activity among brain samples of the hooded seal (*Cystophora cristata*), the ferret (*Mustela putorius furo*) and the mouse (*Mus musculus*). While the brain of the hooded seal showed the highest Pdha1 mRNA levels, the Pdhe2 content and the PDH activity were lower than those in the non-diving mammals. The activity of PDH in the brain of the hooded seal reaches equilibrium before the PDH activities in the brain of the mouse and the ferret, suggesting a higher susceptibility to product inhibition. Reperfusion increases the reactive oxygen species (ROS) generation due to a compensatory acceleration of the electron flux in the mitochondrial electron transport chain (ETC). During the recovery phase after the dive, when the O_2 levels are reestablished, a lower and more susceptible to inhibition PDH activity could be beneficial to prevent the NADH accumulation and thus the acceleration of the ETC resulting in a decreased ROS generation. MLMH is supported by a PhD Scholarship CAPES/DAAD (# 5125/11-1).

PP-P-13

Hypothalamic gene expression profile during torpor entrance in Djungarian hamsters

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Djungarian hamsters (*Phodopus sungorus*) exhibit multiple physiological adaptions to their seasonally changing environment. The most extreme measure of this animal to maintain energy balance during winter is the expression of spontaneous daily torpor. Daily torpor is a voluntary, normoxic hypometabolism that reduces energy requirements by up to 70%. The hypothalamus has been proposed to play a role in the regulation of daily torpor. However, endocrine and neurological signals, which initiate the metabolic depression during the entrance into torpor, are still unknown. To uncover genes that are involved in the initiation of daily torpor, we investigated the hypothalamic transcriptomes of torpid hamsters during the entrance into torpor (ZT 1, $T_b \leq 31$ °C) using Illumina sequencing. About 28 000 genes were detectable (RPKM ≥ 0.1) in the hypothalamus of Djungarian hamsters. The expression of 284 genes was significantly altered during entrance into the torpid state. 181 genes were up- and 103 down-regulated. Analysis of gene ontology patterns and most strongly regulated transcripts show evidence of remodeling and plasticity during torpor entrance. Five of the twenty most strongly up-regulated genes were collagens which are major extracellular matrix structural constitutes. Additionally Dnha2, Micalcl and Myo15a, components of the cytoskeleton, rank among the most strongly up-regulated genes. Furthermore five zinc finger proteins belong to the most down-regulated genes. Zink finger proteins are proposed to be involved in transcriptional regulation. These results provide the hypothalamic gene expression profile during torpor initiation and build the basis to uncover regulatory pathways of metabolic depression.

PP-P-14

Nutrient deficiency of larvae – effect on adult honey bees (*Apis mellifera carnica*)?

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Malnourishment during the larval stage influences the physiology of larvae as well as the physiology and behavior of adult honey bees. Former experiments focused on the impact of long starvation periods during larval development on larvae and adult honey bees. In contrast to previous experiments, we investigated whether there is an impact of short starving periods on the physiology of the larvae and on the behavior of adult honey bees. For our experiments we put a grid on the brood comb to prevent nurse bees from feeding larvae at the age of 3-3.5d and 4-4.5d for ten hours each. After cells were capped we sampled larvae and measured fresh weight. Fresh and dry weights from newly emerged bees were analyzed. Newly emerged bees were marked and hosted in a colony until the flight experiments started. Flight experiments were conducted in a roundabout with bees older than 20 days. The control group and the experimental group had to complete two flights, one with 1 molar glucose solution and the other one with 2 molar glucose solution. We measured the following parameters: flight distance, maximum speed, average speed and flight duration. Starved larvae were significantly lighter (Mann-Whitney-U test, $p<0.05$) in comparison to the control group. In contrast to this, we did not find any significant differences in fresh weight of newly emerged bees, but we found differences in the dry weight (Mann-Whitney-U test, $p<0.05$). We found differences when we compared the results of the 1 molar and 2 molar flights within the control group and the experimental group, but we did not find any significant differences between the two groups. Short larval starvation periods cause deficits in weight, but these deficits can be compensated in the flight performance of adult honey bees.

OP-ZS-IT-01

Palaeo-Evo-Devo: Fossils and ontogenetic data increase the explanatory power of phylogenetic reconstructions

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Phylogenetic analyses produce in a first step a "naked tree", i.e., it first results in a depiction of relationship. Based on this, the evolutionary changes of characters (character transformation) can be reconstructed, following the principles of evolutionary morphology. In fact, the process of phylogenetic analysis and reconstruction of character transformation represent an interactive process, originally addressed to as reciprocal illumination, but also as hermeneutic spiral. The reconstruction of character transformation and, in a further step, the attempt of an evolutionary reconstruction or 'narrative', is therefore an essential task of phylogenetic systematics. In many cases the reconstruction of character transformation remains rather incomplete, or fragmentary. More precisely, we often lack many 'steps in between' and hence have gaps in our knowledge of character transformation. These gaps can be narrowed by including information from the study of 1) exceptionally preserved fossils, and 2) the ontogenetic changes of morphology. Usually the second point is restricted to extant species, yet in certain cases it is even possible to combine the two points and include data on the ontogeny of extinct species. I will present some examples from lineages of arthropods following the approach outlined above. Especially within different crustacean lineages surprisingly well preserved fossils, including larval and juvenile stages, combined with the study of extant larval series provide the opportunity to reconstruct finely graded step-wise character acquisitions. This significantly improves the explanatory power of these evolutionary phylogenetic reconstructions.

OP-ZS-IT-02

The potential of museomics to revitalize the taxonomy of aplacophoran molluscs

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In the past decades the barcoding endeavor has made considerable progress in documenting diversity of faunal communities and in enabling easier re-identification of the covered species via deposited molecular barcodes. Despite all advances, the accuracy of these barcodes entirely depends on the correct initial species assignment and some clades still remain in their taxonomic hibernation as recollecting of fresh material for molecular purposes is either not feasible or assignment to described species is highly problematic. New opportunities have arisen to work with museums' samples (type material) and degenerated DNA via next generation sequencing (NGS) technologies ('museomics'), which are superior to direct amplification attempts and dramatically augment the amount of data available for phylogenetics and molecular species delineation. The present study explores the potential of museomics to revise the taxonomy of one of the traditional 'classes' of Mollusca. The current taxonomy of Solenogastres requires time-consuming assessment of scleritome and radula characters in combination with histological and ultrastructural anatomical characters, i.e. multiple individuals are needed for identification to family level and beyond. Their inaccessible taxonomy has led to ignorance towards this interesting, evolutionary old clade, which mainly inhabits the deep-sea. Reference genomes of museums material were generated for each of the two main clades on the Illumina HiSEQ2500 Platform. These serve as backbone to annotate results of shot gun sequencing approaches from older type material and help to establish effective filters against typical contaminations. The discussed outline and initial lab experiences shall serve as showcase for the broader application of NGS in taxonomy.

OP-ZS-01

A transcriptomic phylogeny of the Platyhelminthes

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Morphological and molecular phylogenies using one or two genes were not able to unambiguously resolve the interrelationships of the major taxa of the phylum Platyhelminthes (flatworms), often leaving polytomies or showing low support for several branches. We have extracted and sequenced RNA and analysed transcriptomes from representatives of all major taxa of flatworms and have reconstructed phylogenetic trees with Maximum Likelihood and Bayesian Inference with an amino acid matrix of more than 100,000 positions and an averageness completeness of about 72%. Our trees supports a sister group relationship between the Catenulida and the Rhabditophora, the latter encompassing the vast majority of known flatworm species. The Macrostomorpha, including the model organism *Macrostomum lignano*, are sister group to all other Rhabditophora, and the Polycladida+Prorhynchida are sister group to the remaining Rhabditophora. The free-living Bothrioplanida, represented by a single cosmopolitan species, *Bothrioplana semperi*, are the sister group of the medically and economically important Neodermata, the obligatory parasites including tapeworms and flukes. The sister group relationship between Polycladida and Prorhynchida implies that ectolecithality, i.e. the inclusion of non-embryonic yolk cells within the egg capsule along the oocyte, has arisen at least twice within the flatworms, once in the Prorhynchida and once in the Euneoophora. If the non-parasitic larvae of the Polycladida were primary larvae, they would have been lost at least five times: in the Catenulida, the Macrostomorpha, the Prorhynchida and the Euneoophora, and also within some groups of the Polycladida. *Bothrioplana* has been moved into the spotlight as the sister group to the parasitic Neodermata, but shares no obvious morphological similarities with the latter.

OP-ZS-02

Species delineation: Comparing the powers of DNA-barcoding and shell morphometrics in the trochid gastropod genus *Gibbula*

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About 20 species of the genus *Gibbula s.l.* are described from European sea shores. Vague descriptions and considerable intraspecific variability led to problems in identification and delineation of several species. We attempt to resolve some of the complexities of the genus using DNA-barcoding and geometric shell morphometrics on 8 taxa. Some species are well resolved with CO1 and ITS data, even if shell shapes do not differ, e.g. in *G. varia* and *G. rarilineata*. The genetic separation of *G. varia* and *G. divaricata* is ambiguous, although shell shape is highly diagnostic. *Gibbula (Phorcus) mutabilis* shows deep genetic and morphometric differentiation among disjunct populations. Although the gene tree supports the monophyly, shells from Crete resemble *G. (Ph.) richardi* and those from Croatia are similar to *G. divaricata*. Thus, combining both methods is the most effective approach to characterizing these species without using often misleading characters like shell sculpture and colouration. We also address taxonomic issues regarding the status of the subgenus *Phorcus* and the potential para- or polyphyly of *Gibbula*.

OP-ZS-03

Cryptic diversity research: taxonomy and evolution of the *Tetramorium caespitum*/*impurum* complex (Hymenoptera: Formicidae)

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Delimitation and determination of species within the *Tetramorium caespitum*/*impurum* complex provoked controversial discussions over the last decades, and fundamental knowledge gaps about this cryptic species complex remain. Based on a multidisciplinary approach, we revise the taxonomy and aim to understand the evolution of the *Tetramorium caespitum*/*impurum* complex. We collected several thousand nest samples from 35 nations in Europe, Anatolia, the Caucasus, and Central Asia. Our investigation is based on integrative taxonomy, i.e. the combination of independent methods using the same biological samples. About 900 workers were used for traditional morphometric analyses of 32 characters. Qualitative male-genital-structure investigations complement the morphological data. For phylogenetic reconstruction, we sequenced 1,113 bp of the cytochrome c oxidase subunit 1 gene of 1,247 workers and scored amplified-fragment-length polymorphisms for 406 workers. Based on our multidisciplinary dataset, we demonstrate the presence of at least 10 well-separated European species and use this insight for our taxonomic revision. Furthermore, we show ecological data and distribution maps of selected species. Contradictory results of different methods require evolutionary explanations, e.g. intraspecific variability due to geographical distance, interspecific similarity due to morphological stasis and/or incomplete lineage sorting, and hybridization. We defend the evolutionary stability of the species boundaries we draw because of a considerable congruence of different methodological results of samples across the western Palearctic.

OP-ZS-04

Dating the Phasmatodea tree of life: Uncertainties surrounding stick insect origins

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TBA

OP-ZS-05

The biological limits of phylogenetic resolution - a case study on the explosive radiation of neoavian birds

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The diversification of neoavian birds is one of the most rapid adaptive radiations of extant organisms. Recent whole-genome sequence analyses have much improved the resolution of the neoavian radiation and suggest concurrence with the Cretaceous-Paleogene (K-Pg) boundary, yet the causes of the remaining genome-level irresolvabilities appear unclear. Here we report genome-level analyses of 2,118 retrotransposon presence/absence markers, rare genomic changes that exhibit negligible amounts of homoplasy. Our analyses converge at a largely consistent Neoaves phylogeny and detect a highly differential temporal prevalence of incomplete lineage sorting (ILS), i.e., the persistence of ancestral genetic variation as polymorphisms during speciation events. We find that ILS-derived incongruences are spread over the genome, and involve 35% and 34% of the analyzed loci on the autosomes and the Z chromosome, respectively. Surprisingly, Neoaves diversification comprises three adaptive radiations, an initial near-K-Pg superradiation with highly discordant phylogenetic signals from near-simultaneous speciation events, followed by two post-K-Pg radiations of core landbirds and core waterbirds with much less pronounced ILS. We provide evidence that, given the extreme level of up to 100% ILS per branch in superradiations, particularly rapid speciation events may neither resemble a fully bifurcating tree nor are they resolvable as such. As a consequence, their complex demographic history is more accurately represented as local networks within a species tree.

OP-ZS-06 - Studying deep metazoan phylogeny by very conserved positions of 9 mitochondrial encoded proteins

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Using the data of Max Telford which were analysed by Philippe & al. (1911) it is possible to align sequences of the proteins MTATP6, MTCO1, MTCO2, MTCYB, MTND1, MTND2, MTND3, MTND4 and MTND5 of *Monosiga* (Choanoflagellata), *Trichoplax* (Placozoa) and *Mnemiopsis* (Ctenophora) and to complete alignments of MTND2 of *Symsagittifera* (Acoela). Aligning was very difficult in the case of *Mnemiopsis* since the mtDNA is extremely reduced and changed in *Mnemiopsis* (Pett et al. 2011) and *Pleurobrachia* (Kohn et al. 2012). Methods were developed to isolate very conserved positions. In such a way 132 very conservative positions were found. In *Monosiga* there are 10 differences from the sequences of the Porifera and Cnidaria which show no differences in these very conserved positions. The Ctenphora share K at position MTND4 218, A at position MTND5 219, A at position MTND5 292 with most of the Bilateria and L at position MTND5 247 with Deuterostomia (position numbers are those of the proteins coded by the human reference sequence). Hence it is probable that the Ctenophora form a monophyletic clade with Bilateria. A basal state of Placozoa within the Non-Bilateria is not supported. They share a U (Ser with codons TCT, TCC, TCG, TCA) at MTCO2 17 with the Ctenophora and a F at MTCO1 450 and a K at MtND4 218 with Bilateria. Monophyly of Protostomia inclusive Chaetognatha is strongly supported by D at MTND5 145, Y at MTND5 157, Y at MTND5 158, T at MTND5 171, E at MTND5 238, G at MTND5 239, V at MTND5 247, L at MTND5 252 and E at MTND5 295. Deuterostomia are characterized by W at MTND5 157. But this similarity does not sufficiently support the monophyly and exclude paraphyly of Acoela, *Xenoturbella*, Hemichordata, Echinodermata and Chordata since a second change from W to Y in the Protostomia is possible. Within the Deuterostomia G is shared at position MTND5 333 in Acoela, *Xenoturbella* and Hemichordata and L is shared at MTCO2 199 in Acoela and *Xenoturbella*. These very conservative characters support a clade Xenacoelomorpha originating from Hemichordata as pointed out by Philippe et al. (2011). But differing from this *Mnemiopsis* and *Symsagittifera* seem to form a monophyletic clade branching off before all other Deuterostomia.

OP-ZS-07

ABOL - The Austrian Barcode of Life-Initiative

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Starting with a pilot phase in July 2014, the long-term aim of ABOL is to provide DNA barcodes for all species of fungi, plants and animals recorded from Austria. Constituting a platform for all Austrian experts dealing with all aspects of biodiversity research in Austria, ABOL is cross-linked with other initiatives, like e.g. GBOL in Germany, and SwissBOL in Switzerland at the national scale, and iBOL and EcBOL at the international scale. DNAbarcodes, representing species-specific parts of the genome, primarily approach the genetic aspects of biodiversity. Being collection-based, however, DNA barcoding holds all aspects of an integrative approach, which connects all aspects of biodiversity research. As an open-access initiative the latter is widened to many applied fields, including e.g. conservation, food control or forensics. Harbouring the eastern part of the alpine arc, Austria is likewise of interest for the biodiversity landscape at the European level. The alpine arc constitutes a geographic barrier, which canalized the dynamics of expansion and shrinkage of distribution areas and, moreover, contained numerous smaller refugees during glaciation periods. During the pilot phase of ABOL data is collected in four groups of organisms; (i) vertebrates, (ii) butterflies and moths, (iii) molluscs, and (iv) parasitic worms. The overall project is planned to be organized in organism-specific clusters. Associated projects additionally generate DNA barcodes, which are not covered by the funding of the pilot phase of ABOL. ABOL will not only raise biodiversity survey and documentation onto a new methodological level, but also boost evolutionary research and its public outreach essentially.

PP-ZS-01

Curious phylogeographical patterns in the grasshopper genus *Sphingonotus*

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Sphingonotus is a diverse grasshopper genus with more than 150 species and an almost cosmopolitan distribution. Its centers of diversity are in the Mediterranean, Eastern and Central Asia. The genus has undergone a small radiation with 7 endemic species on the Canary Islands. Further, it has several outposts with single or few species found in Australia, Southern Africa, the Caribbean and Galapagos. We studied the phylogeography of the Canary, Galapagos and Caribbean endemics using a multi-gene approach to place these taxa within the phylogeny of the genus and reconstruct their evolutionary history. We found that the Galapagos and Caribbean species are related to the Eurasian taxa of the genus, which suggests a wider former distribution of the genus followed by mainland extinction in America. The Galapagos taxon splits into several subunits in concert with the island of origin, suggesting the existence of several island endemics. The Canary taxa belong to multiple genetic lineages within the genus and have colonized the archipelago multiple times independently. Overall we show that the phylogeography of the genus is even more complex than previously expected and includes several colonization and extinction events, even across large geographic scales.

PP-ZS-02

Insights into the phylogeny of European green lizards (*Lacerta viridis* complex)

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Green lizards are common in Europe, and have been divided into an eastern and western green species (*Lacerta viridis* and *Lacerta bilineata*, respectively). However, the species status of the two taxa has been repeatedly challenged. In order to obtain more information, we analyzed the mitochondrial (cytochrome *b*) and nuclear DNA sequences (*ß*-fibrinogen-intron7) from 476 samples from different European countries. The results of mtDNA (cytochrome *b*) showed a clear differentiation into four well-supported basal lineages, corresponding to *Lacerta viridis* (western part of the range), *Lacerta bilineata*, the previously identified Adriatic lineage and another lineage corresponding to *Lacerta viridis meridionalis* from Turkey. The nuclear marker suggests gene flow between *Lacerta bilineata* and *Lacerta viridis*

PP-ZS-03

An integrative approach to the diversity of the limnic slug *Acochlidium* (Gastropoda, Panpulmonata, Acochlidia)

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A unique radiation of riverine slugs distributed on the islands of the Indo-Australian Archipelago (IAA) has long challenged taxonomists. The four valid species of *Acochlidium* (*A. bayerfehlmanni, A. sutteri, A. amboinense* and *A. fijiense*) are currently delineated based on radula features and details of the male genital system, but are externally cryptic and new collected material cannot be unambiguously assigned. We collected several individuals of *Acochlidium* from 17 populations from 7 islands along the IAA including type localities and applied an integrative taxonomic approach. Four (tree-based and non-tree-based) methods of molecular species delineation based on two mitochondrial markers (COI, 16S rRNA) were largely congruent in recovering three independent lineages, incongruent, however, with the valid species. We comparatively re-investigated the radula and the complex 'rapto-penis' of specimens from different populations via scanning electron microscopy (SEM) and created a computer based 3D reconstruction of the male copulatory organs of *A. bayerfehlmanni*. Our SEM-examination reveals an asymmetric radula with large pointed rhachidian tooth in all examined specimens, offering little variation for species delineation. We found slight variabilities in the penial armature between individuals but the intraspecific variability of these characters still requires further investigation. The 3D model of *A. bayerfehlmanni* recovered a novel feature, a cuticular groove potentally acting as a 'guide' for the tip of the ejaculatory duct. Based on our data *A. sutteri* and *A. bayerfehlmanni* might present a junior synonym of *A. amboinense*, while the populations from the Solomons and Papua New Guinea form an unnamed lineage.

PP-ZS-04

How universal can it be? The quest for universal primers for barcoding old museum samples of Austrian birds and mammals

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DNA-barcoding, the standardized genetic analysis of a given, species-specific part of the genome, facilitates the rapid and cost-effective genetic characterization of biodiversity, with a wide spectrum of potential applications in biodiversity research, conservation and applied sciences. Currently, many national and/or taxon-specific barcoding initiatives aim at characterizing the diversity present in a particular country and/or taxon. The ABOL (Austrian Barcode of Life) initiative intends to generate and provide DNA-barcodes of all Austrian species of animals, plants and fungi. Vertebrates are undoubtedly the native animals best known to lay people and thus well suited as flagship taxa not only for conservation initiatives, but also for large barcoding projects like ABOL. At present, DNA-barcodes of only a few Austrian vertebrates are publicly available, and data for birds and mammals are particularly lacking. As collecting new samples is often very difficult to (nearly) impossible due to the special federal animal welfare regulations that apply to vertebrates, museum collections represent a particularly valuable source of tissue for DNA-barcoding. Usually highly degraded DNA in old museum samples (bones, feathers, skins, …) implies that only small DNA fragments can be amplified and that the ~650 bp barcode fragment has to be amplified and sequenced in a number of short overlapping segments. Here, we report on the successful development and testing of (nearly) universal primers for birds and mammals that amplify and sequence the COI barcoding region in six short overlapping segments. These novel primer sets will greatly alleviate the effort associated with the generation of DNA-barcodes from old museum samples.

PP-ZS-05

A new gudgeon species (genus *Romanogobio*) from the Upper Mur River - evidence from morphology and molecular data

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In 2014, several gudgeon-like fish that differed by their large fins, elongated body shape, distinct body colouration and habitat use from sympatric Danube gudgeon (*Gobio obtusirostris*) were caught in the Upper Mur River. Further morphological analysis suggested that these specimens do not belong to any of the three *Romanogobio* species known for Austria. Molecular data support this view and large genetic distances to other Eurasian *Romanogobio* species indicate that this new species diverged from its congeners several million years ago. First investigations on the distribution range of this new species suggest that it might be restricted to the Upper Mur River, rendering it the first ancient (pre-glacial origin) endemic fish species of Austria.

PP-ZS-06

Take a closer look!
Caleremaeus (Acari, Oribatida): An underestimated taxon

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Caleremaeus monilipes Michael, 1882 is the only known species of this oribatid mite genus in the Palearctic region. It represents a euryoecious species and can be found in different habitats (alpine meadows, alluvial forests, dry grasslands...) as well as in various substrates (mosses, lichens, soil, deadwood, algae…). Furthermore, this species shows a great vertical distribution from colline to alpine regions. Despite its relative minuteness (~400 µm) *C. monilipes* can easily be determined due to its characteristic habitus. We used a multidisciplinary approach including genetics as well as morphological and ecological data to assess if this easily recognizable, widely distributed and euryoecious mite taxon represents one and the same species. According to both, phylogenetic and species delimitation analyses five distinct clades/species were detected, and were supported by high genetic distances. These genetic lineages correlate well with ecological data. Subsequently, slight morphological differences were found and provide additional evidence that five different species occur in continental Europe. The minuteness and the characteristic habitus of *C. monilipes* tempted to neglect potential higher species diversity. This problem might concern several other “well known” so-called euryoecious microarthropods.

PP-ZS-07

Transcriptomic and phenotypic data related to the geographic distribution of two spurge hawk moth lineages of the *Hyles euphorbiae* complex (Lepidoptera: Sphingidae)

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Spurge hawk moths of the *Hyles euphorbiae* complex (HEC) comprise two major genetic lineages across a large distribution range: The central European *H. euphorbiae* and the northern African *H. tithymali*. Both have their specific distribution ranges, but readily interbreed forming a hybrid zone in southern Europe where the lineages meet. Thus, the HEC is a well suited model to test for functional differences in ecology and physiology that lead to lineage separation in spite of obvious inter-lineage fertility. Differences in cold adaptation and content of tetradecanoylphorbol-acetat (TPA) in spurge food plants (Euphorbiaceae) have been suggested as such separating factors. Recently, we sequenced *H. euphorbiae* transcriptomic data (Illumina) of cold treated overwintering (diapause) pupae and L5 instar larvae having fed on TPA, to identify genomic biomarkers relating to each treatment. Moreover, we determined *H. euphorbiae* and *H. tithymali* phenotypes differing in cold-hardiness and TPA detoxification potential under laboratory conditions, to define ecological niches. These data will be further used to study differential gene expression with respect to functional lineage sorting in the HEC.

PP-ZS-08

How many species of grass snakes are out there? Phylogeography, gene flow across contact zones and taxonomy of *Natrix natrix*

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Grass snakes (*Natrix natrix*) represent one of the most widely distributed snake species of the Palaearctic region. Within *N. natrix*, up to 14 distinct subspecies are regarded as valid. In addition, some authors recognize big-headed grass snakes from western Transcaucasia as a distinct species, *N. megalocephala*. Based on phylogenetic analyses of a 1984-bp-long alignment of mtDNA sequences (cyt *b*, ND4+tRNAs) of 410 grass snakes, a nearly range-wide phylogeography is presented for both species. Within *N. natrix*, 16 terminal mitochondrial clades were identified, most of which conflict with morphologically defined subspecies. These 16 clades correspond to three more inclusive clades from (i) the Iberian Peninsula plus North Africa, (ii) East Europe and Asia and (iii) West Europe including Corso-Sardinia, the Apennine Peninsula and Sicily. Hypotheses regarding glacial refugia and postglacial range expansions are presented. Holocene range expansions led to the colonization of more northerly regions and the formation of secondary contact zones. In Central Europe, there are two contact zones of three distinct mitochondrial clades, one of these contact zones was theretofore completely unknown. In agreement with previous studies using morphological characters and allozymes, there is no evidence for the distinctiveness of *N. megalocephala*. Therefore, *N. megalocephala* is synonymized with *N. natrix*. In addition, first preliminary results of 14 tested microsatellite loci are presented as an outlook on future work.

LAST-MINUTE-SUBMISSIONS

PP-BB-16

Fine-tuned, context-specific manipulation of an intermediate crustacean host by its acanthocephalan parasite

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Parasites with a complex life cycle are supposed to influence the behaviour of their intermediate host in such a way that the transmission to the final host is enhanced, but reduced to non-hosts. Here, we examined whether the trophically transmitted acanthocephalan bird parasite *Polymorphus minutus* adaptively alters the anti-predator behaviour of its intermediate host, the freshwater amphipod *Gammarus pulex*. Uninfected gammarids showed negative phototaxis, whereas infected ones were photophilic indicating that the parasite manipulates the phototactic responses of its intermediate host thereby increasing the probability of ingestion by final bird hosts. In response to specific non-host predatory cues (fish cues in our study) infected gammarids showed stronger anti-predator behaviour than uninfected ones suggesting that the bird parasite manipulates anti-predator behaviour of its intermediate host to reduce the probability of transmission to dead-end hosts. When phototaxis and fish avoidance were jointly examined, uninfected gammarids showed increased photophobia suggesting that both factors act additively. Interestingly, *P. minutus* infected gammarids showed photophobia in this context as well suggesting fine-tuned, context-dependent parasitic manipulation.

SATELLITE SYMPOSIUM I: CICHLID SCIENCE 2015

SS-I-IT-01

Genomic differentiation during repeated sympatric ecological speciation in the adaptive radiations of the Midas cichlid fishes in Nicaragua

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

SS-I-IT-02

Evolvability of the cichlid jaw: Using cichlids to better understand the development and evolution of complex phenotypes.

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A major pursuit in evolutionary biology is to characterize the proximate molecular mechanisms that underlie adaptive phenotypic variation in the wild. While significant progress has been made toward understanding the genetic and developmental origins for many "simple" shifts in morphology (e.g., pigmentation switching), less is known about the basis for variation in more "complex" adaptive phenotypes, including the craniofacial skeleton. Cichlids have undergone extensive evolutionary modifications of their skull and jaws, providing a rich array of phenotypic variation for analyses. Moreover, their evolutionary history is characterized by recent origins and ongoing gene flow, making them especially amenable to genotype-phenotype mapping. Finally, cichlids are easily maintained and bred in the lab, making experimental embryology possible. This combination of evolutionary richness and experimental tractability provides excellent opportunities to address longstanding questions in evolutionary biology. In particular, we have used this system to address the nature of phenotypic evolvability - i.e., the potential for complex traits to evolve. Here, I will highlight recent work in the lab that sheds light into three specific questions: (1) what is the molecular nature of evolutionary change? (2) can we extend the current evo-devo paradigm from genotype à phenotype to genotype à resource use? (3) what is the genetic basis of phenotypic plasticity? In all I hope to underscore the power and utility of the cichlid system in modern evolutionary biology.

SS-I-OP-01

Genetic parentage testing and ‘maladaptive’ parental care in cichlids

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Genetic analysis has made a huge impact on our understanding of how parentage and brood care are organized across animals. In cichlids, genetic data revealed the occurrence of alloparental care (care for unrelated young) not only in cooperative breeders, but also in uni- and biparental breeders due to adoption and extra-pair fertilization. Providing care for offspring is generally costly and thus the provision of alloparental care appears maladaptive. In this talk I present a new research project exploring how breeding males cope with high rates of cuckoldry. I also review the advances of genetic parentage analyses across the various cichlid breeding systems (substrate- and mouth-brooding; uniparental, biparental and cooperative brood care; monogamous and multiple mating).

SS-I-OP-02

Repeatability and heritability of alloparental brood-care in the cooperatively breeding cichlid *Neolamprologus pulcher*

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For natural selection being able to act on a trait it has to be variable within the population, heritable, and affect individual fitness. Most studies on cooperative behaviour aim to understand its adaptive function, but its genetic basis and thus its potential to evolve as a result of natural selection has received less attention. Here we present estimates of repeatability and heritability of cooperative behaviours in *Neolamprologus pulcher*, a cooperatively breeding cichlid species in which subordinates carry out alloparental brood-care tasks, for instance cleaning a clutch and defending it against egg predators. First, we determined repeatability of helping behaviours as this parameter sets an upper limit to heritability. Second, we estimated heritability to assess the potential of natural selection acting on these behaviours. We show that the estimates of repeatability of cooperative behaviours are generally substantial but differ between behaviours: While egg care is highly repeatable, egg defence behaviours show intermediate repeatability. However, the heritability estimates for these behaviours are very low. To our knowledge, this is the first study to address the genetic basis of complex animal cooperative behaviour. Our analysis of variance components suggest that the high within-individual consistencies of helping behaviour over time are predominantly due to environmental effects while additive genetic variance has rather small effects. Since the number of helpers in *N. pulcher* groups varies greatly in the wild, we hypothesize that low heritability but strong environmental influence on the cooperative tendencies of offspring might facilitate the flexible adjustment of the amount of help needed in the territory.

SS-I-OP-03

Dopamine is a modulator of social behaviour in a cooperatively breeding fish

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Cooperation is an evolutionary enigma that has intrigued biologists ever since Darwin. However, little is still known about the physiological regulation of cooperative behaviour. Here we report on an experiment studying the role of dopamine in social behaviour of a cooperatively breeding fish species. Dopamine is involved in the modulation of animals' reward system and also in the social decision network. This suggests that it might be involved in sociability, and that it may modulate interactions between individuals. We studied *Neolamprologus pulcher*, a cooperative cichlid fish from Lake Tanganyika, East Africa. These fish live in families with a dominant pair and a variable number of subordinates. The latter help the dominant breeders in territory maintenance and defense, and they show alloparental care which is considered to be altruistic. We tested the role of the dopaminergic receptors D1 and D2 by blocking or enhancing their activity with injections of agonists or antagonists (SKF-3893, SCH-23390, Quinpirole and Metoclopramide). Our data suggest that the two dopaminergic receptors have different regulatory roles for the social behavior of these fish. The D1 receptor is apparently important for the modulation of aggressive behavior, increasing it when the receptor is enhanced and diminishing it when the receptor is blocked. In contrast, the D2 receptor seems to modulate the affiliative behavior of the fish, showing bigger effects when the receptor is blocked. These data provide the first insight into the role of dopamine for the social behaviour of a cooperative fish species.

SS-I-OP-04

Nonapeptide regulation of helping behaviour in a cooperatively breeding cichlid fish

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Individuals integrate sensory information with internal physiology into context-appropriate behaviours that ultimately promotes fitness. Neuropeptides, from the AVP/OT family, respond acutely to social stimuli and modulate subsequent behaviour. Arginine vasotocin (AVT) and isotocin (IT) expressed in fish brains, are homologs of arginine vasopressin (AVP) and oxytocin (OT) in mammals. Previous studies on the homologs revealed their importance in the regulation of a variety of social behaviours, such as, parental behaviour. *Neolamprologus pulcher* exhibits a remarkably complex social system and demonstrate an impressive diversity of social behaviours and communicative signals. Social groups consist of breeding pair and 1 to 20 helpers. Subordinate group members may actively assist the breeding pair in their reproductive efforts. The present study tries to understand if AVT, IT and Manning compound (AVT V1a receptor antagonist) have an important modulator effect on the expression of territory defence behaviour by the helpers depending on different ecological challenge's, adult and egg predator, and social rank. Our results show that isotocin directly protects homeostasis of the individual by decreasing predator fear response, while vasotocin action directly influences the maintenance of the social group, by reducing aggression levels and increasing group cohesion, this cohesion is lost with the application of AVT V1a receptor antagonist, independent of the ecological challenge.

SS-I-OP-05

Dispersal decisions in a cooperatively breeding cichlid

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Dispersal is a universal feature of life that impacts all aspects of evolution, from individual fitness to gene-flow between populations, extinction risk, and speciation. Dispersal itself is an evolving trait, because dispersal decisions may crucially affect reproductive success and consequently a phenotype´s fitness. As such it lies at the interface between such different ecological factors as breeding systems, social organisation, or range distribution. Thus, understanding how individuals decide when and where to disperse and how this decision influences their fitness may give insights about the feedback mechanisms between different selective forces. Here we report on a combination of long-term field observations and experimental studies in the natural habitat of the cooperatively breeding Lake Tanganyika cichlid *Neolamprologus pulcher*. We show that dispersal decisions are opportunistic, but that dispersal is nevertheless a lengthy process. Further, we show that dispersal is sex-biased, that fish are more likely to disperse before they acquire dominant status, and that dispersal influences growth. Finally, we provide evidence that dispersing individuals generally face lower fitness prospects than non-dispersers. Our data reveal that individual dispersal is tightly linked to the species´ mating system, its social organisation, and individual life-history decisions. This highlights the importance of considering dispersal when investigating any evolutionary processes.

SS-I-OP-06

Predation risk relates to population divergence in a cooperatively breeding fish

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Environmental conditions are generally assumed to be of crucial importance for the evolution of cooperative breeding. Subordinate individuals staying in the territory of dominants decide about dispersal and cooperative effort in dependence of the quality of the home territory and of alternative locations. However, there is currently little evidence from cooperatively breeding vertebrates that large-scale ecological patterns determine group structure and cooperative behavior of group members. Here we measured biotic and abiotic factors of potential importance for behavioral decisions of group members in eight populations of the cooperatively breeding cichlid *Neolamprologus pulcher*, which is distributed across a wide range of habitats in Lake Tanganyika. Our data show that habitat quality, substrate complexity and predation risk all differ substantially between the surveyed populations. This correlates with highly significant differences between populations in group size and composition, and with marked divergence in the type and quantity of cooperative behaviors exhibited by group members. Group size related to habitat type, with habitats demanding more help yielding larger groups. The demand for protection and help seem to largely determine group composition and cooperative behavior, which is in accordance with the “pay to stay” hypothesis postulating that subordinate individuals pay as much as needed to evade being evicted from the territory, if alternative options are scarce or unfavorable. This is confirmed by laboratory experiments showing that breeders more readily accept subordinates if the demand for help is high.

SS-I-OP-07

The role of behaviour in the adaptive radiation of cichlid fishes

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Cichlid fishes are extremely species-rich and phenotypically diverse and have undergone several spectacular adaptive radiations in lakes. Across the world, there are thousands of species endemic to single lakes, and lineages differ in species richness, allowing for comparative studies of correlates of diversity. My PhD research will focus on the role that behavioural change plays in adaptive radiation in cichlids and this can be explored from a variety of angles. The study system will be Lake Massoko, a crater lake situated in the northern section of the Lake Malawi catchment, which contains haplochromine of the genus *Astatotilapia*, related to *Astatotilapia calliptera*. Blue and yellow colour morphs are found in the same lake, with blue dominating in the deeper water and yellow in the shallows. A larger project is currently analysing ecology, trophic morphology and genetics of the morphs, which appear to be in the early stages of sympatric speciation. I plan to investigate the role of behavioural differences in adaptive divergence of these morphs. We predict that fish living in deeper waters will have adapted to the conditions of depth. I plan to analyse foraging efficiencies in laboratory simulations of divergent microhabitats (e.g. light regimes). Experiments focusing on boldness and exploration will investigate the process of colonisation of new microhabitats by different genotypes. Finally, mate choice experiments will address issues of assortative mating and reproductive isolation.

SS-I-OP-08

Detection of species-specific behavioral patterns in how Malawi cichlids use their environments

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The astounding morphological diversity seen within the Lake Malawi adaptive radiation of Haplochromine cichlid fishes in East Africa has been widely studied, particularly with regard to fitness advantages and niche specialization. However, investigations of behavioral phenotypes within and between taxa have been largely limited to those behaviors related to male-male competition and mating displays, e.g. bower building and aggressive displays, in part because identification and quantification of environment-usage behaviors can be difficult. Fortunately, advances in computer vision algorithms have given us the ability to track the movement of individual cichlids in a variety of arenas, providing a way to quantify behavioral patterns in a home tank, as well as differential responses to novel environments, objects, and individuals. For five species from two genera (*Metriaclima* and *Aulonocara*), I have identified specific behavioral patterns at both the species and genus level. While novel object and novel environment responses show patterning by species, they do not differ by sex. We suggest that sex-neutral behavioral differentiation may be occurring during micro-habitat specialization, as changing landscapes provide distinct selection pressures for environment-usage behaviors.

SS-I-OP-09

Speciation hampered by asymmetric dominance between color variants

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Assortative mating promotes reproductive isolation and allows allopatric speciation to continue in secondary contact. Mating patterns within populations are known to be determined by interactions between mate preferences and intrasexual competition, and similar processes may influence assortative mating among distinct taxa. The Lake Tanganyika cichlid *Tropheus moorii* sports numerous geographic color variants. Within populations, female choice is strongly influenced by male territories. Among color variants, female mating preferences vary between random, positive and negative assortative. If color variants differ in their competitive abilities, outcomes of male-male competition can reinforce or interfere with female preferences dependent on dominance/subdominance of the preferred male. Here, we provide evidence for asymmetric dominance relationships among color variants in favor of red-colored males, and investigate the effects of male competition on mating patterns. Dominance of red males further reinforces the strong positive assortative preferences of red females. Moreover, in a two-way mate choice experiment, assortative preferences of red females were not overturned when heteromorphic males were presented in a superior territory. In contrast, genetic analyses of mating patterns in experimental ponds showed that red male dominance promoted heteromorphic mating by females of subordinate color variants, which had lacked strong assortative preferences already in previous experiments precluding male competition. Hence, in a scenario of secondary contact, the interactions of female preferences and male competition promote asymmetric hybridization and may be in the way of further differentiation.

SS-I-OP-10

Mate choice on a phenotypic/genotypic continuum: Divergence-with-gene-flow in African crater lake cichlids

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Mate choice tests have frequently been used to identify the differences which contribute to reproductive isolation among recently diverged and diverging taxa which are capable of producing viable hybrid offspring. There is great potential for sexual selection in haplochromine cichlids, and lab based studies of taxa which differ predominantly in traits such as male courtship colour often reveal complete assorative mating among sympatric species and partial assortative mating among geographic variants. It has been proposed that this pattern is consistent with primary divergence in sympatry, driven, at least in part, by divergent sexual selection. Yet, due to the difficulties of reconstructing past geographic histories of populations, and the sister taxon relationships among the many closely related cichlids from the large East African Rift Lakes, it has proved hard to identify clear examples of the occurrence of either of these historically contentious mechanisms of divergence and speciation - the possibility of a period of allopatric divergence is difficult to disprove. To date, the results from a study of a pair of ecologically/morphologically/genetically divergent sympatric morphs of a haplochromine cichlid population isolated in a small crater lake, suggest that divergence in primary sympatry is likely. There is, however, little evidence for assortative mating among forms under laboratory conditions. It appears that “divergence-with-gene-flow” is possible by divergence at “genomic islands” associated with microhabitat preference, but that sexual selection is unlikely to be the main driver of divergence despite the occurrence of two clearly distinct male colour forms.

SS-I-OP-11

Innate spawning preference of F2 hybrids and its role in the evolution of reproductive isolation in Lake Victoria Cichlids

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We show in a common garden experiment that partial reproductive isolation between two incipient species (*Pundamilia nyererei* with red males and *Pundamilia pundamilia* with bluish males) can be rapidly restored, with 75% of the F2 generation females showing a significant spawning preference for one of the two parental species. Spawning preferences did not change over time (~1 year) nor did they change after a successful spawning event with the non-preferred species in a no-choice single male set-up. We found that LWS genotype significantly influenced female choice: hybrid females homozygous for the allele conferring red-shifted visual sensitivity preferred red males, while females homozygous for the presumably ancestral allele preferred blue males. However, this locus did only explain part of the spawning patterns. We found no evidence for imprinting in the F2 generation, but the F1 hybrid females appeared to be imprinted on their mothers. We suggest that both imprinting in the F1 as well as the strong innate mate choice preference in the F2 can help to curtail genetic introgression in sympatric species with incomplete reproductive isolation. We conclude that the LWS locus controls a multifunctional trait (vision) subject to divergent viability selection and at the same time mediates assortative mating.

SS-I-OP-12 - Evolutionary conservation of brain stress signatures in response to early social environment in vertebrates

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In mammals, low quality maternal care results in persistent reprogramming of the stress axis, high later-life stress responsiveness and a reduced quality of brood care behaviour in offspring. This is achieved by epigenetic modifications lowering the expression of glucocorticoid receptors (GR) in the hippocampus. While similar phenotypic effects are known from other vertebrate groups, we know very little about how this effect of early social experience is mechanistically derived outside mammals. We reared young of the cooperatively breeding cichlid fish *Neolamprologus pulcher* either with or without parents to test for homologies between fishes and mammals in the molecular pathway translating early social influences into later-life alterations of the stress axis and social behaviour. First, we analysed the expression of the glucocorticoid receptor *GR1* and of the transcription factor *egr-1*, which drives the expression of *GR* in the mammalian hippocampus. Like in mammals, we found a link between early social experience and the expression of *egr-1* and *GR1*. Both *egr-1* and *GR1* were higher expressed when fish were reared with parents. These effects appeared in the telencephalon, where the homologous region to the mammalian hippocampus is located in fish, but not in the hypothalamus. Second, a pharmacological manipulation of *GR1* expression by the application of a GR-blocker revealed significant effects on the expressed social behaviour. Our results indicate that the effects of early social environment on stress axis programming are mediated by a molecular mechanism that has been evolutionary conserved among vertebrates.

SS-I-OP-13

Lake Malawi cichlids as a model of dietary response and host-microbiota interactions

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Human disease outcomes stemming from maladaptive diets represent an evolutionary discordance: the human genome has been unable to evolve to match rapid dietary changes brought on by overpopulation and the agricultural and industrial revolutions. If we reveal pathways of genetic evolution taken by other vertebrates as they adapted to diverse diets, we should identify pathways for therapeutic intervention for pathological conflicts in humans brought on by maladaptive diets. East African cichlid fish species have recently evolved diverse dietary adaptations, allowing powerful comparative experimental strategies to understand the genetic basis of dietary response. We are using genomic and developmental techniques to identify species-specific aspects of gastrointestinal biology among species representing multiple trophic levels and specializations. Gut length correlates with trophic level, but functional compartmentalization within the gut does not scale directly with length. Transcriptional patterns are similar in cichlid and mammalian gut, demonstrating a shared genetic toolkit for gut development. Gut microbiota is relatively labile and varies with species, diet, age, and gut region; however, host species-specific differences are identifiable and suggest host genetics plays a strong role in bacterial colonization of the gut. Functional profiles of bacterial assemblages also diverge by host species, with bacteria providing biochemical processes that correlate to the adaptive diet of each species. Our findings to date provide comparative insight into dietary adaptation, and lay a foundation for genetic mapping experiments in hybrid crosses and natural populations.

SS-I-OP-14

Molecular characterization of cryptic gut regionalization in trophically divergent cichlids from Lake Malawi

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One of the best-characterized features of the East African cichlid radiations is their dramatic trophic diversity. While the craniofacial modifications associated with dietary specialization have received significant attention, associated differences in gut morphology are not well understood. Understanding the morphological, developmental, and genetic changes correlated with dietary shifts will not only allow us to better understand how trophic diversity evolved in cichlids, but also broader patterns of vertebrate niche specialization, and the interaction between diverse human gut phenotypes, dietary adaptation, and diet-related disease. Unlike tetrapods, gut regionalization in teleosts is often not easily visualized. The cichlid gut is a simple tapered tube, with no obvious distinction between small and large intestine. Using phylogenetically robust molecular markers of these regions, we have determined that both overall gut length, and the relative percentages of the adult gut expressing large and small intestinal markers follow broad vertebrate trends correlating gut morphology and dietary specialization. Additionally, we have characterized the emergence of these species-specific phenotypes through ontogeny from a generalized larval state. A separate large and small intestine have not previously been identified in cichlids, and our data are the first description of cichlid gut morphology from fishes raised in a common garden, demonstrating that identified differences are not the result of a plastic response to diet, but instead are heritable and species-specific.

SS-I-OP-16

Evaluation of the homoplasy excess test, a popular method to screen multi-locus cichlid datasets for hybrid taxa

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The homoplasy excess test (HET) is a tree-based screen for hybrid taxa in multi-locus nuclear phylogenies. The method relies on the fact that genomes of hybrids are mosaics of their parents' genomes, such that homoplasy between a hybrid taxon and the clades containing the parental taxa reduces bootstrap support at certain nodes in the tree. The HET employs taxon-jackknifing, the exclusion of one taxon at a time, to identify potential hybrid taxa based on taxon-specific effects on node support. HETs have been carried out with AFLP datasets of various groups of cichlids, where the results pointed to numerous putative hybrid taxa and suggested an important role of hybridization in cichlid diversification. Despite a few cases of independent data confirming the hybrid status suggested by the HET, the method's reliability has remained untested. We developed software that automatically generates and parses the numerous files involved in a HET, and used it to assess the hit rate of the test in simulated SNP and AFLP datasets as well as with empirical data. Our analyses indicate a high frequency of false positives (non-hybrid taxa giving rise to HET hybrid signals) as well as a considerable rate of false negatives (hybrid taxa failing to produce hybrid signals). In contrast, we found that careful scrutiny of the taxon-jackknife trees produced in the course of a HET can help to identify true hybrid taxa. This, however, can hardly be automatized.

SS-I-OP-17

Genomic sequencing of two members of the eco-morphologically highly diverse Lake Tanganyika cichlid tribe Tropheini

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The cichlid fishes of Lake Tanganyika represent the oldest and eco-morphologically most advanced adaptive radiation, in which several lineages radiated in parallel. This is why we chose the tribe Tropheini to study adaptive evolution, as they are much more diverse in terms of ecology, morphology and behavior than any Lake Malawi and Victoria cichlid, despite being part of a monophyletic and closely related assemblage. As a basis for further studies in evo-devo context, we sequenced the genomes of two morphologically highly divergent members of the Tropheini, the epilithic algae browser *Tropheus moorii*, and the unicellular algae grazer *Petrochromis trewavasae*. We used a combination of Illumina, 454 and PacBio sequencing technologies to successfully assemble the two genomes. The genomes amount to ~860 Mbps each and there are ~16,000 genes predicted per genome. The Core Eukaryotic Genes Mapping Approach (CEGMA) shows a very high coverage of the core genes (over 94% complete and over 99% partial). Currently, we study the differences of the two species at the genomic level and compare the new sequences with the recently published genomes of six other cichlid species.

SS-I-OP-18

Alternating disruptive selection at different stages in ecological speciation

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Disruptive selection plays a major role in ecological speciation. The haplochromine cichlid fish of Lake Victoria are known for their outstanding species-richness which is thought to be the result of ecological speciation by natural and sexual selection. Several of these haplochromine lineages, including the sister species pair *Pundamilia pundamilia* and *P. nyererei,* occur at different stages of speciation at different sites in the southern part of the lake. We studied four of these *Pundamilia* communities, each at a different island, ranging from clear water, with virtually no habitat overlap and reproductively isolated species, to a site with murky water, complete habitat overlap and a single panmictic population. Estimating fitness landscapes from growth rate data as a fitness proxy, we investigated which, if any, phenotypic traits were under disruptive selection in these four communities. We found strongest evidence for disruptive selection on multiple phenotype traits in communities where the two sister taxa are partly reproductively isolated, whereas less evidence for disruptive selection was found in communities with completely isolated and ecologically differentiated species and also in the fully panmictic community in which phenotypes occupied the same narrow depth range. We conclude, that 1) disruptive selection is not evidenced when a variable population occupies a narrow habitat band with no apparent habitat association of the polymorphic traits, 2) trait differentiation between fully reproductively isolated species is not necessarily associated with current disruptive selection, possibly because speciation has dissipated disruptive selection on phenotypic traits.

SS-I-OP-19

Is selection on habitat gradients correlated with phenotypic and genomic differentiation in cichlid fish populations?

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Textbook examples of adaptive radiation in lakes provide insight into how the origin of species is facilitated. Disruptive selection between habitats and differential resource utilization are thought to play important roles in speciation. However in the majority of cases, speciation does not occur despite the existence of suitable selective environments. The absence of speciation might be due to populations 1) not encountering rugged adaptive landscapes 2) failing to respond to disruptive selection or 3) adapting through mechanisms that do not require speciation. To test these alternatives, we compared individual fitness proxies and genome-wide signatures of selection between sympatric cichlid populations coexisting along environmental gradients. We chose paired populations, in each case contrasting species which show clear morphological divergence or incipient speciation along environmental gradients to species lacking morphological divergence. Using growth rate as a fitness proxy, we inferred fitness landscapes for phenotypic traits and multivariate phenotypes in these populations. We then used genome-wide SNP data to examine patterns of genomic divergence along environmental gradients. By using morphological, genomic and fitness proxy data, we seek to link selection to morphology and to genomic patterns of divergence, and thus provide a unique window onto the basis of genomic divergence during cichlid speciation.

SS-I-OP-20

The role of parasites and the immune system in the adaptive radiation of Lake Tanganyika cichlids

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Habitat adaptation and trophic adaptation have been proposed to be important drivers of cichlid radiations, because differences in habitat and diet between species are often associated with morphological differences. However, habitat and diet shifts likely also imply exposure to different parasites, as well as shifts in infection risk. As strong selective agents influencing survival and mate choice, parasites might therefore play an important role in cichlid diversifications. We explore this possibility for the radiation of Lake Tanganyika cichlids. We first compare infection levels with metazoan macroparasites between the major cichlid tribes. We then describe the genetic diversity at the level of the major histocompatibility complex (MHC), an important set of vertebrate immune genes. Finally, we evaluate to what extent variation in infection levels and the MHC is explained by trophic ecology and morphology. We show that different cichlid tribes harboured partially non-overlapping parasite communities as well as partially non-overlapping MHC diversity. The trophic-morphological axis of diversification among the tribes as well as MHC diversity strongly correlated with infection levels. We conclude that the potential contribution of parasitism and immunogenetic adaptation to the Lake Tanganyika cichlid radiation should not be overlooked.

SS-I-OP-21

Ecological speciation in evolution of cichlids from the Barombi Mbo crater lake

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Cichlid species flocks from small crater lakes represent a text book example of sympatric speciation where evolution happens independently in isolation from the surrounding riverine populations. Barombi Mbo crater lake in Cameroon hosts 11 cichlid species, which putatively underwent a process of adaptive radiation. We integrated genomic approach (RAD-seq) with geometrical morphometrics and stable isotope analysis and our results show that ecological specialization represents the most important driving force of evolution in the crater lake. Morphologically derived species have lower intraspecific genetic variability and have higher position in the trophic chain with the predatory specialists from genus Stomatepia on the top. We have further found that difference in life-history between sister species was high in all four present species pairs. Finally, the phylogenetic analysis based on the RAD-seq (Sbf I) data suggests complete genetic isolation of all 11 species with one exception of Sarotherodon linnellii and S. caroli confirming that Barombi Mbo is the oldest monophyletic lineage of all crater lake systems.

SS-I-OP-22

Speciation in Lake Malawi and in Tanzanian crater lakes

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Understanding the causes and consequences of speciation, including at the genetic level, requires investigation of multiple taxon pairs at different stages on the speciation continuum. The Lake Malawi cichlid radiation is one of the largest adaptive radiations on earth. It has generated over 500 species in less than five million years, involving divergence in habitat, feeding apparatus, nuptial colour and many other traits, thus presenting an opportunity to observe hundreds of varied, recent, and in some cases ongoing, speciation events. However, investigation of the early stages of speciation in the large cichlid radiations is hampered by the difficulty in estimating sister species relationships, in reconstructing past geographical situations, and in accommodating introgression among non-sister taxa. We have obtained high quality whole genome sequences for: a) 117 individuals from over 50 representative Lake Malawi cichlid species, in order to understand the genetic structure, assess the extent of introgression and reconstruct a phylogenetic tree/network, thus clarifying the relationships between the species and providing a solid basis for research on speciation and adaptation in the system. b) 150 individuals of the *Astatotilapia calliptera* lineage that are the subject of more recent radiation in six crater lakes in the Mbeya region of Tanzania, just north of Lake Malawi. These include cases of within-lake adaptive divergence, providing convincing examples of lineage diversification driven by selection, without significant geographic isolation. Together with ecological and morphological data, the genomes paint a picture of selection on specific phenotypes such as sensory systems, hormonal signalling and, pharyngeal morphology driving the emergence of divergent genomic islands in the process of speciation.

SS-I-OP-23

Genome divergence between lake and stream populations in an East African cichlid fish

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Populations occupying distinct ecological environments often undergo divergent adaptive evolutionary change via divergent natural selection. The genetic basis of this divergence is still largely unknown and is here explored via genome scans in four replicate lake-stream systems of the haplochromine cichlid *Astatotilapia burtoni*. Population genomic analyses based on RADseq data revealed different levels of genome-wide differentiation within and among the four lake-stream systems, and heterogeneous patterns of genomic divergence, which are rather inconsistent across systems. Accordingly, F_{ST} outlier analysis detected only few consistent outliers that could potentially be relevant for lake-stream adaptation. Interestingly, these F_{ST} outliers were located in regions corresponding to genes involved in neuronal and immune functions; and analysis of expression patterns of two candidate genes through qPCR identified overall differences along the lake-stream gradient. In addition, phylogeographic reconstruction indicated a very complex evolutionary history of lake and stream populations, most likely triggered by past lake level fluctuations. Further demographic inference based on the site frequency spectrum provides information about effective population sizes, levels of migration, and estimates of divergence times between lake and stream populations.

SS-I-OP-24

Speciation genomics of *Ophthalmotilapia* species from Lake Tanganyika

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Despite significant progress over the last years, many fundamental questions concerning the genetic basis of the speciation process remain unanswered. Many of these questions should be addressed at the genomic level: which genetic elements are of particular relevance to speciation, how many loci are typically involved, what are the locations of the differences that result in speciation? In this study, we investigate the impact of geographic isolation on genetic differentiation within species and we explore genomic differentiation between species. We carried out a mtDNA phylogeographic and a phylogenomic study on the endemic Lake Tanganyika cichlid genus *Ophthalmotilapia*. This genus contains four closely related and ecologically similar species that can occur both in allopatry and in sympatry. We selected 411 specimens representing the complete distribution range of each species. The D-loop sequences yielded 117 haplotypes, 18 of which were shared between two or three species. These haplotypes differed by only a few mutations, which attest to the recent origin of these species. Moreover, we used two samples from each species in a Genotype-By-Sequencing approach to explore the genome-wide distribution of SNP's among the four specific gene pools. This yielded an average of 43 818 and 158 528 locations per individual for PstI and ApeKI, respectively, while the number of polymorphic locations shared between species was very similar (2416 and 2492 for PstI and ApeKI, respectively). Our preliminary results will be discussed in light of the nature of the genomic regions that are differentiated between the species.

SS-I-OP-25

Genome scans identify the genomic architecture of sympatric speciation in Lake Malawi cichlids

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Understanding of the mechanisms by which populations diverge and become species are in their infancy, especially when those populations are in sympatry. We present a genome-wide SNP data set obtained using a RAD-sequencing approach to identify the regions of the genome which may be involved in the divergence and isolation of four Lake Malawi Diplotaxodon species. These deep water species have been previously proposed as examples of sympatric speciation, differing to some extent in morphology, and more obviously in male monochromatic nuptial colour. Principal component analysis and Discriminant analysis of principal components on >20,000 SNPs support significant genetic differentiation between the four species. We apply and compare Fst outlier scan approaches to detect signals of divergent selection. Based on the intersection of three independent approaches we infer a conservative 59 outlier candidate regions, i.e. putative 'genomic islands of speciation'. Gene ontology enrichment analyses of the functional classes of genes in these regions strongly support the hypothesis that the machinery of transcriptional regulation plays a central role in the differentiation of these species. We furthermore infer previously identified differences in head morphological traits between species to be significantly correlated with allele frequencies in one candidate region and find this region to contain a transcription factor associated with the regulation of craniofacial development. Our results indicate a role for ecological selection in driving the genomic divergence between these species.

SS-I-OP-26

Heterogeneous genomic differentiation in East African soda lake cichlid fish

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The unique *Alcolapia* species flock of East African soda lakes Natron and Magadi has long drawn interested from an evolutionary and physiological perspective. The endemic species flock includes three sympatric species in Lake Natron (*A. alcalica, A. latilabris, A. ndalalani*) and a further species (*A. grahami*) in Lake Magadi. The four species exhibit considerable differentiation of trophic morphology and male colour. Here, we investigate phylogenomic differentiation and population structuring of the radiation using an extensive NGS dataset. Current work highlights ecomorphological differentiation of the radiation, with stable isotope analysis indicating trophic niche segregation between *A. alcalica* and the two other sympatric species in Lake Natron (*A. latilabris, A. ndalalani*), and geometric morphometric analysis demonstrating significant morphological differences between all described species. However, analysis of genome-wide variation using RAD data reveals shallow divergences between species, with on-going gene flow. Phylogenomic analysis includes maximum likelihood and Bayesian methods, while population genetic approaches are used to test for introgression and admixture including clustering algorithms, F_{ST}, and the f_4 (four-population) test. Finally, sliding-window F_{ST} analysis exhibits peaks of differentiation between species, suggesting that narrow regions of the genome may harbour genes influencing pigmentation and jaw morphology. Taken together, these results suggest a recent radiation with extensive ecological and morphological diversification, and with genetic differentiation distributed heterogeneously across the genome.

SS-I-OP-27

Parallel speciation in *Crenicichla*

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Cichlid fishes are the prime model group for evolutionary studies of adaptive radiations, sympatric speciation and also of parallel evolution. Here we present a unique evolutionary system that includes sympatric speciation and parallel speciation in the *Crenicichla missioneira* species flock in the riverine environment of the Uruguay River in South America. Parallel speciation is a much rarer special case of parallel evolution within one evolutionary lineage. The studied system also includes parallel allopatric speciation, hybrid speciation and the neighbouring Iguazu River presents a case of parallel evolution of a similarly diverse but unrelated *Crenicichla* species flock. The Uruguay and Iguazu Rivers are located in the geologically complex southern Brazilian Shield where major waterfalls and rapids prevent upstream dispersal and thus provide conditions promoting parallel evolution of strikingly similar phenotypes between two related species flocks, but also parallel speciation within one of them (in the Uruguay River). Previous phylogenetic studies using predominantly mitochondrial DNA markers have found the morphologically and ecologically distinct species in the *Crenicichla missioneira* flock very closely related to the point of being indistinguishable. By phylogenetic and population genetic analyses of genomic SNP markers generated by reduced representation sequencing using ddRAD sequencing on the Illumina platform we demonstrate that most of the described species of the *Crenicichla missioneira* complex are polyphyletic having evolved multiple times in parallel and in several cases probably sympatrically from other ecomorphs in several tributaries of the Uruguay river.

SS-I-OP-28

New *Crenicichla* species flock

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Four sympatric species of *Crenicichla* endemic to the lower Iguazú River form a species flock that represents a case of parallel evolution to the *Crenicichla missioneira* sp. complex from the neighbouring Uruguay River. Species diversity and evolutionary relationships within the *C. mandelburgeri* sp. complex from the Paraná/Iguazú Rivers were studied by a combined morphological and phylogenomic approach. More than 54,000 SNPs were obtained by ddRAD sequencing and bioinformatic processing of sequenced tags. The phylogenetic analysis of the SNPs yielded a robust phylogenetic hypothesis demonstrating that all four sympatric lower Iguazú species of *Crenicichla* form a monophyletic lineage which is in contrast with the previous predominantly mitochondrial multilocus analysis. The four species differ substantially in their head/teeth morphology and related utilization of the ecological niches, and represent all known ecomorphs within *Crenicichla*. Two new species, a gregarious small-mouthed picker/grazer and a large-mouthed thick-lipped cavity explorer/excavator were discovered. The piscivorous large-mouthed *C. iguassuensis* is the ancestral form of the species flock. The fourth species is the small-mouthed picker/molluscivore *C. tesay* with robust lower pharyngeal jaw with molariform teeth. The two new taxa are recovered as sister-species, while *C. tesay* is likely the direct ancestor (in our sampling a sister-species) of *C. taikyra* (both are molluscivorous species), an allopatric middle Paraná species separated from *C. tesay* by the Iguazú Falls. The taxonomic status of the populations referred here to *C. iguassuensis* remains tentative and the Iguazú River probably hosts several other yet undescribed species of *Crenicichla*.

SS-I-OP-29

Phylogeny and systematics of *Hemichromis* (Peciformes: Cichlidae)

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The African cichlid genus *Hemichromis* represents a conundrum of a taxonomic problem since decades, as it exhibits considerable morphological conservatism in external traits. Species delineation among several species was particularly misconceived among various workers. Recently and following Loiselle‘s 1979 revision of the genus, two groups are to recognize: the Five-spotted cichlids with three species (group 1) and the group of the so-called Jewel cichlids with eight described species (group2). The recent study, ongoing since more than ten years, employs anatomical and morphological work, studies of live colourations of a number of populations, including all species, as well as molecular markers for a phylogenetic study, to examine a number of populations and species across the geographical range of the genus in order to clarify the taxonomic status. Four loci, including three mitochondrial and one nuclear loci, had been directly sequenced and were included in the the study. The results support recognition of a number of additional species within group 2 as well as a clear split between members of group 1 and group 2, indicating a genus of its own for group 2. Additionally, three lineages are to be recognized within group 2, a „West-African“, a „Congo-Gabon“, and a „Guinea“ lineage consisting of two recently undescribed species.

SS-I-OP-30

The *Oreochromis* species of Tanzania: impending loss of unique genetic resources?

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In 2012, the global tilapia aquaculture industry, mainly based on *Oreochromis*, was estimated to produce 4.5 million tonnes worth $7.6bn. Its annual growth rate far outstrips that of other major aquaculture subjects, such as salmon and carps. East Africa is the global centre of natural diversity of *Oreochromis* species, with Tanzania alone hosting at least 31 of the ~50 recognised species/subspecies of *Oreochromis*. Unique genes from natural population may be of vital importance in future development of domesticated strains, as is well-recognised with crop plants. I will present an overview of our knowledge of the distribution of the Tanzanian *Oreochromis*, including recent discoveries of several narrowly endemic forms, and at least one suprising range extension (which supports a major fishery of national importance). I will also present information on the spread of exotic strains through aquaculture escapes and recent large-scale deliberate stocking, which has led to introgressive hybridisation which threatens to exterminate (or, at least, irrevocably alter) native populations by genetic swamping. Notably, exotic species are now being cultured in the Lake Malawi catchment. I will discuss research in progress aimed at gaining further insight into this process, including the genomic effects of introgression, and present ideas for possible conservation of Tanzania's unique genetic resources.

SS-I-OP-31

Naming colours: a revision of the Lake Tanganyika genus *Tropheus*.

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Chromatic differentiation is a well-known phenomenon in littoral cichlids. In Lake Tanganyika, the most spectacular example hereof is provided by *Tropheus*. This genus of stenotypic rock dwellers contains over a hundred, mostly allopatric, colour morphs. This renders *Tropheus* an important model for evolutionary research. Yet, the genus' taxonomy is confusing and many populations cannot be assigned to a valid species. Here, the genus is revised using a combined morphological and molecular approach. It had been suggested that *Tropheus* was in morphological stasis. Yet, several case studies showed substantial morphological differentiation although different traits often uncovered different patterns. Hence, we verified which criteria should be used to distinguish species. A comparative study showed that meristics were more suitable for this than body proportions. As intra-specific variation often surpassed inter-specific variation, most populations could only be assigned to a species by analysing average values of morphometric data. Based on morphological grounds, eleven species were distinguished in *Tropheus*, seven of which were new to science. An AFLP-based phylogeny confirmed this classification. Some of the species were chromatically and morphologically very uniform, whereas others were highly diverse. In some cases, convergent evolution was observed, both in colouration and in body form. This explained some of the confusion that previously blurred the genus' classification.

SS-I-OP-32

Central African cichlid parasites: exploring their biodiversity, phylogeny, ecology and introductions

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Studying cichlids enhanced our understanding of speciation and radiation. In contrast, little is known about the evolution of their parasites. Lake Tanganyika's (cichlid) biodiversity and its importance as cradle and reservoir of ancient lineages seeding other radiations has resulted in a significant body of literature. Remarkably, until recently virtually no research was carried out into the Tanganyika parasite fauna. We focus on the monogenean flatworm species flock infecting Tanganyika cichlids. Representatives of *Cichlidogyrus* saw different speciation pathways in different cichlid tribes, e.g. with variable levels of host-specificity, underscoring the uniqueness of Lake Tanganyika's cichlid flock from a parasitological point-of-view as well. We applied *Cichlidogyrus* species distributions when revising a tropheine cichlid genus, and link parasite species richness and community composition to Tanganyika cichlid biology. Apart from the Tanganyika biodiversity hotspot, several primarily riverine cichlids of the Congo Basin are important to fisheries, aquaculture and aquaristics. We explore their monogenean fauna and its potential as threat and tool in introduced species research: the risk of introduction of non-native monogeneans together with Nile tilapia, and the potential of monogeneans in stock identification.Research supported by the Belgian Federal Sciency Policy (BR/132/PI/TILAPIA), the Czech Science Foundation (P505/12/G112 - ECIP), the Austrian Science Fund, the Research Foundation-Flanders, KU Leuven VES and the King Leopold III Fund for Nature Conservation and Exploration.

SS-I-OP-33

Phenotypic plasticity precedes adaptive trait divergence during radiation of cichlid fishes: Evidence from the generalist Lake Malawi cichlid *Astatotilapia calliptera.*

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Vertebrate adaptive radiations are characterised by substantial diversity in ecologically-important morphological traits such as body shape and jaw morphology. However, such traits are also known to exhibit considerable plasticity. The flexible stem model proposes that developmental plasticity in such traits in ancestral lineages directs later adaptive evolution. Here we investigated this concept in *Astatotilapia calliptera*, a "generalist" cichlid fish species from the Lake Malawi radiation with striking variability in morphology, diet and habitat use. We first show that morphological variation across 15 populations within the Lake Malawi catchment is strongly associated with dietary differences, consistent with observed morphological variation having a functional basis. We next tested if variation observed among populations in the wild was present in laboratory-reared populations. Our results clearly demonstrated that variation among populations of wild fish was exaggerated relative to that observed among individuals from the same sites reared in controlled laboratory conditions. These results are consistent with ecologically-relevant plasticity being the necessary precursor of adaptive morphological variability within this Lake Malawi species, and support a flexible stem model of adaptive evolution. We propose that functional phenotypic plasticity within riverine founders of species flocks may have been an important prerequisite for rapid speciation and adaptive radiation.

SS-I-OP-34

Developmental plasticity of a key evolutionary trait in East African cichlids - insights in evolutionary mechanisms that shaped these cichlids' adaptive radiations

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The 'modern haplochromine' cichlid fishes are a famous example of repeated rapid adaptive radiations - one in each of the three East African Great Lakes. *Astatoreochromis alluaudi* is a riverine species that is basal to these adaptive radiations, putatively resembling the common ancestor of this group. A mechanically-stimulating diet induces pronounced plasticity in *A. alluaudi*'s pharyngeal jaw apparatus, a structure considered to be a key evolutionary trait in cichlids. We compared the morphological and transcriptional effects of experimentally induced plasticity in this trait in *A. alluaudi*, to three representatives of the adaptive radiations and one out-group. Our results indicate that the adaptive plasticity is most pronounced in non-radiating species, followed by the recently radiating species and is lowest in the oldest adaptive radiation. Next, we investigated the expression of plasticity-related genes for species that showed a plastic response. Through comparing co-expression between species, we observed that similar sets of functionally related genes were co-expressed in both basal and more derived species, suggesting conserved transcriptional 'modules'. We conclude that the ancestral cichlid lineage was probably phenotypically plastic and that module-like transcriptional alterations in developmental trajectories putatively contributed to the parallel evolution of highly diverse trophic phenotypes among these adaptively radiating cichlid lineages.

SS-I-OP-35

Genetic dissection of hypertrophied lips and foraging performance in cichlid fishes

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The fit between organisms and their environments is one of the most striking outcomes of adaptive evolution. The number of loci that underlie adaptations, their effect sizes, the extent of pleiotropy or linkage and epistatic interactions between them are factors that influence the speed, direction and magnitude of the response to natural selection. Distinctive morphological traits consisting of hypertrophied lips and narrow heads evolved repeatedly in several cichlid species specialized in preying on invertebrates that inhabit rocky crevices. Here, we hybridized two cichlid species from Lake Victoria (*Haplochromis chilotes* and *H. nyererei*) that differ in foraging behavior, lip and head morphology. We developed a measure of foraging performance that mimics the ecological setting and is suitable for genetic mapping. Both species differed in their ability to forage in our assay, allowing the direct test of an association between the putative adaptive function, morphological traits and genomic locations. The genetic architecture of this trophic specialization bears signatures of natural selection and is determined by at least 20 loci of small-to-moderate effects. QTLs were not distributed randomly across the genome, but were enriched in certain linkage groups. In addition, QTLs underlying different traits co-localized extensively. In light of our results, the genetic architecture characterized by extensive genetic correlations and non-additive interactions might direct the response to natural selection and facilitate convergent evolution.

SS-I-OP-36

Genomics and transcriptomics of facial stripes in *Neolamprologus*

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We use *de novo* genome assemblies and skin transcriptomes of *Neolamprologus* species with divergent facial stripe phenotypes to gain insight into mechanisms acting to generate morphological diversity. We find substantial incongruence in the phylogenetic signal at the genome level, which can be attributed to ongoing hybridization after speciation events. Introgression-free species phylogeny suggests that facial stripe phenotypes evolved from non-striped phenotypes within *Neolamprologus*. Using differential expression analyses of skin transcriptome, we identify candidate pigmentation genes involved in facial stripe evolution.

SS-I-OP-37

Visual divergence in the young Midas cichlids radiation is driven by changes in gene expression

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The visual system of cichlid fish is a great model to study molecular evolution and diversification, as both, amino acid substitutions and differential expression of opsin genes are known to contribute to interspecific divergence. However, very little is known about the prevalence of structural or regulatory changes at early stages of divergence, which can occur when populations colonize a different habitat or the habitat characteristics change. Here we take advantage of the Midas cichlids system from Nicaraguan lakes to address this question. Midas cichlids have recently colonized crater lakes from much older and larger lakes, and since have diverged from the ancestral populations. Interestingly, the photic conditions of these lakes are different, with crater lakes transmitting better short-wavelength light than the ancestral great lakes. Hence, we predict divergence in the visual system between ancestral (i.e. great lakes) and derived (i.e. crater lakes) Midas cichlid populations in response to this change in selection pressure. We found very low standing genetic variation in the ancestral populations, and low to no divergence between populations in the coding sequences of opsins. However, we found significant differences in the pattern of opsin gene expression that match our prediction based on the photic differences between the great and crater lakes. These differences appear to have a genetic basis, as specimens from the great and the crater lakes reared under a common environment in the laboratory show a similar pattern of expression to those seen in wild-caught fish. Our results suggest that just in few thousands generations, adaptive divergence in the visual system of Midas cichlids occurred by changes in gene expression.

SS-I-OP-38

Phenotypic plasticity in Midas cichlid opsin expression

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The ability to adapt to challenging environments is crucial for survival of organisms, especially after colonization of novel habitats. Adaptive phenotypic variation across populations could arise as the result of genetic differences or could be environmentally induced (i.e. adaptive plasticity). Cichlid fishes are an excellent model to investigate the roles of plasticity and heritable molecular mechanisms in the adaptive divergence of the visual system. In cichlids, color vision is mediated by differential expression of opsins absorbing light at particular wavelengths in retinal cone photoreceptors. Vision can be highly plastic in response to changes in the photic environment. We found differential opsin expression between Midas cichlids *Amphilophus citrinellus* and *A. astorquii* from Lake Nicaragua and Lake Apoyo, respectively. L. Nicaragua is a relatively old lake with shallow, turbid water whereas L. Apoyo, a young crater lake, has deep and clear water. *A. citrinellus* expresses three opsins absorbing light mainly at longer wavelengths. In contrast, *A. astorquii* expresses five opsins enabling absorption across much broader regions of the spectrum. We exposed the two species to four light conditions to determine whether the distinct expression patterns observed in the field have a genetic basis or are environmentally induced. We found that the differences in opsin expression are maintained under common conditions, suggesting that there is an underlying genetic basis. Moreover, we detected plasticity in opsin expression in *A. astorquii* but not *A. citrinellus*. These results open up the exciting possibility that plasticity recently evolved in *A. astorquii*, probably as an adaptation to heterogeneous light conditions in L. Apoyo.

SS-I-PP-01

Depth segregation and diet disparity among sympatric herbivorous cichlids in Lake Tanganyika: long-term field observation, pyrosequencing and stable isotope analyses on algal farms and stomach contents

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In Lake Tanganyika, five tribes of the Cichlidae have acquired herbivory through its adaptive radiation, with four ecomorphs: grazers, browsers, scrapers, and scoopers. 16 species of the herbivorous cichlids coexist on a rocky littoral slope in the lake. Seven of them individually defend feeding territories to establish algal farms. We observed depth and substratum preference of these cichlids for 14 years. Then, we collected epiphyton from these territories at various depths and also gathered fish specimens. Algal and cyanobacteria community structures were analyzed using the amplicon-metagenomic method, and food web analysis was conducted using C and N stable isotope ratios. As a result, apparently equivalent species in the same ecomorph coexisted by depth segregation in a-few-meter scale, with specific substratum preference on the rocky shore. Based on pyrosequencing of SSU rRNA gene, algal farms differed significantly in their composition among cichlid species, even in the same ecomorph. Cichlids selectively harvested their farms, and the stomach contents were highly diverse, even between species in the same tribe, in the same ecomorph. Irrespective of cichlid ecomorph, δ^{13}C of periphyton correlated with habitat depth, and decreased as habitat depth became deeper. δ^{13}C in territorial fish muscles was related to that of periphyton within their territories, regardless of cichlid ecomorph, which suggests that these herbivorous cichlids depend on primary production of periphyton within their territories. In conclusion, these studies revealed food niche separation based on habitat-depth segregation among coexisting herbivorous cichlids in the same ecomorphs in Lake Tanganyika.

SS-I-PP-02

Morphometric changes in fossil cichlid teeth throughout a 25,000-year African lake-sediment archive

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The evolutionary success of cichlids is often associated with their complex trophic apparatus, which is adapted in peculiar ways to the uptake of specific food sources. This has enabled fine-scaled resource partitioning between species and as a result is an important driver of speciation. Here, we analyse morphometric changes in fossil cichlid teeth preserved in lake sediments as a proxy to trace adaptive modification of the trophic apparatus through time, in response to climate-driven long-term changes in available habitat and food sources. Our study subject is *Oreochromis hunteri*, the only cichlid endemic to meromictic Lake Challa, an isolated crater lake in Kenya. Mainly lake-level fluctuations (i.e., alternating high- and lowstands) are expected to have had a profound impact on the long-term history of available habitat. During highstands, oxygenated habitats are limited to the lake's steep and rocky underwater slopes, where pelagic and epilithic algae are the main food sources, whereas lowstands in dry periods may have brought a soft-bottom, benthic detritivore niche within reach. We collected fossil oral teeth from sediments deposited during six alternating high- and lowstands over the past 25,000 years. As in extant *O. hunteri,* the fossil assemblages included uni-, bi- and tricuspid teeth, which can be assigned to specific positions in the oral jaw. Our results indicate clear shifts over time in the morphology of bicuspid teeth, which are typically front-row teeth that vary in shape according to feeding behaviour and specific diet. However, more work is required to understand how these shifts are linked to environmental changes inferred from climate proxies.

SS-I-PP-03 *Cichlidogyrus* (Dactylogyridae) from Lake Tanganyika: a phylogenetic approach of the monogenean parasite fauna of Tanganyika cichlid tribes

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Lake Tanganyika, the oldest lake in Africa, harbors the most genetically, morphologically and ecologically diverse cichlid assemblages of the African Great Lakes. Its mostly endemic cichlids are considered as a model to study adaptive radiation and rapid diversification. Because of the apparently high host specificity of gill monogeneans, phylogenetic studies using molecular data of these parasites offer an interesting additional approach to study their host's diversity, evolution and host-parasite interactions. Cichlids in Africa are known to host five different genera of dactylogyrideans, *Cichlidogyrus* being the most diverse with more than 95 species recorded from more than 70 cichlid species. Members of *Cichlidogyrus* are gill ectoparasites. To recognize different species of *Cichlidogyrus*, morphological data (sclerotized parts of haptor and male copulatory organs) in addition to molecular sequence analyses are used. The goal of this study is to investigate the phylogenetic affinities among the *Cichlidogyrus* species parasitizing the different Tanganyika cichlid tribes using different molecular markers (28S rDNA, 18S rDNA, ITS-1 and COX1). We described new *Cichlidogyrus* species parasitizing *Cyprichromis microlepidotus* and *Eretmodus marksmithi*, representatives of the tribes Cyprichromini and Eretmodini, which were not investigated for monogeneans until now. In addition, we focus on the host-parasite relationships of *Cichlidogyrus* species infecting two cichlid tribes: Haplochromini and Eretmodini. An evaluation of the phylogenetic relationships of cichlid mononeneans parasitizing the different Lake Tanganyika cichlid tribes may help us to elucidate the historic and ecological relationships between cichlid tribes and to determine the origin of *Cichlidogyrus* of Lake Tanganyika cichlids. ***Acknowledgments:*** This study was supported by *Czech Science Foundation*, project No. P505/12/G112 (ECIP).

SS-I-PP-04 The monogenean fauna of selected deepwater cichlids in Lake Tanganyika

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Lake Tanganyika is an aquatic biodiversity hotspot with the most diverse cichlid species assemblage of all African lakes. This makes it an important and remarkable study area for biologists. Whereas over 20 monogenean species were described from littoral cichlids, the biodiversity of these ectoparasitic flatworms in the depths is almost unexplored. Our host dataset comprised 82 individuals from 12 cichlid species belonging to four tribes (Bathybatini, Trematocarini, Benthochromini, Limnochromini) occurring in the deepwater habitat. Samples originated from localities throughout the lake. A wide range of techniques and analyses was used to describe their monogenean infection from a morphological as well as a genetic point of view. Finally, 849 monogenean individuals from 8 host species were collected. Three different species belonging to *Cichlidogyrus* were distinguished. Members of the Bathybatini are infected by a single species, *C. casuarinus*. According to previous studies, a decrease of parasite host specificity is probably correlated with lower host availability in the deepwater realm. Whereas significant differences in *C. casuarinus* morphology correlated with host preference, no incipient speciation was observed in the genetic part of the study. Moreover, analyses based on 42 mitochondrial COI fragments suggest a recent population expansion of *C. casuarinus*. The cichlids *Trematocara unimaculatum* and *Benthochromis horii* host two different *Cichlidogyrus* species, belonging to different lineages. Our study illustrates the potential of ectoparasites as a tool to reveal basic evolutionary principles as well as host species interactions. This research was supported by the Czech Science Foundation (P505/12/G112 - ECIP).

SS-I-PP-05

Adaptive divergence in East African cichlid fishes: a comparative approach

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Species that show replicate adaptation of divergent populations along the same environmental gradient are important model systems to address how new species are formed in natural populations. *Astatotilapia burtoni* is an East African haplochromine cichlid fish that occurs in both Lake Tanganyika (LT) and affluent rivers. Our previous study identified *A. burtoni* lake-stream population pairs in southern LT that rest at different stages of the 'speciation continuum'. Here we expand our ongoing study by including lake-stream population pairs from northern LT. In addition, we included another species, *Haplochromis stappersi,* which occurs in sympatry with *A. burtoni*. We first assessed the population structure and morphological differences in both species from northern LT and compared them to the populations from the southern part of the lake. Using microsatellite markers we detected no genetic differentiation between lake and stream populations from the northern LT. However, landmark based geometric morphometric analysis of body shape revealed the same morphological trajectories along the lake-stream gradient as previously identified in the southern *A. burtoni* populations. This indicates parallelism in adaptation, even across different cichlid species. Current work is now investigating the molecular basis of adaptation, by performing whole genome resequencing of lake-stream population pairs of *A. burtoni* and *H. stappersi*.

SS-I-PP-06

Phenotypic novelty is not associated with assortative mating preferences in a hybrid color morph of *Tropheus moorii*, Lake Tanganyika

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The genus *Tropheus* from Lake Tanganyika represents a model organism for geographic color pattern diversification, and hybridization seems to play an important role in these processes. Ancient lake level fluctuations created periods of separation and secondary contact. In phases of secondary contact, positive assortative mate preferences evolved in allopatry influence the degree of introgression between differentiated populations. The genome of yellow-to-orange colored populations of *T. moorii* in southern Lake Tanganyika is a mixture between adjacent red and blue morphs. Experimental crosses between bluish and red *Tropheus* produce offspring resembling the natural yellow populations. A hybrid origin of the yellow color variant is therefore likely and probably dates to a major lake level fluctuation at ~100,000 years BP. The novel hybrid color trait might offer a route to homoploid hybrid speciation, which would predict color assortative mating. Two series of two-way female choice experiments tested for reproductive isolation between females of the hybrid morph and males of each parental morph. Courtship behavior was used to assess mating preferences. The experiments demonstrated a lack of reproductive isolation between the hybrid and either parental morph. Individual females courted with either the homotypic or the heterotypic male or with both. There was no difference in the frequencies of homotypic and heterotypic courtship between experiments with red and bluish males. Our results suggest that the hybrid color morph has not yet started to evolve positive assortative mating preferences, and that color pattern diversity among the hybrid and parental lineages is contingent on their allopatric distribution.

SS-I-PP-07

The reproductive behavior of two sympatric *Ophthalmotilapia* species (Ectodini) from Lake Tanganyika

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Geographic isolation is a driving force of speciation, but recent studies have also demonstrated species formation in the presence of ongoing gene flow. In such systems, partner choice may act as a prezygotic barrier. Understanding the speciation process therefore requires information at the behavioral and the genomic level. The aim of this study is to determine whether two *Ophthalmotilapia* species, *O. ventralis* and *O. nasuta*, collected from a region where they live in sympatry differ in their reproductive behavior under controlled conditions. Although ecologically similar, the species differ in color patterns and snout morphology. *Ophthalmotilapia* species are maternally mouthbrooding cichlids endemic to Lake Tanganyika. They have large eyes and a pronounced sexual dimorphism: territorial males differ from females in coloration and in the size of their pelvic fins which are much longer and possess 'egg dummies' at their distal ends. In the lake, courtship takes place in a bower that is constructed and defended by the male. We described courting behavior by monitoring the events (e.g. egg laying) and displays (e.g. presenting the pelvic fins) observed during spawning bouts. Their occurrence and the time spent by the females inside the bower of the male were recorded using the free software BORIS (Behavioral Observation Research Interactive Software). In addition, a hydrophone was placed inside the tank to check for sound production during courtship and mating.

SS-I-PP-08

Polygenic sex determination in *Astatotilapia burtoni*

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The adaptive radiation of East African cichlid fish serves as a powerful model system for the study of evolution and development, and an astounding diversity of genetic sex determination systems has been revealed within the radiation from just a handful of studied species. In some of these species the interaction of multiple, independently segregating alleles determines sex, a phenomenon known as polygenic sex determination. The species *Astatotilapia burtoni* is an important model for sexually dimorphic physiology and behavior, and also serves as an outgroup to the adaptive radiations of cichlids in Lake Malawi and Lake Victoria. A better understanding of the basis of sex determination in this species will provide important context for behavioral studies within *A. burtoni*, as well as studies of the evolution of genetic sex determination and sexual conflicts in East African cichlids. Here we describe the mapping of sex determination loci in the species *A. burtoni*, using a combination of bulked segregant mapping and restriction-site associated DNA sequencing (RADseq) strategies. Mapping in many independent *A. burtoni* families demonstrates the presence of multiple, previously unidentified sex determination alleles, and thus strongly suggests the existence of polygenic sex determination in this species. Additionally, our genetic data provides insight into karyotype-level structural differences in *A. burtoni* relative to other East African cichlid species. We are currently working to understand the developmental outcomes of interactions between genetic sex determination alleles. Ultimately, we hope to reevaluate the rich behavioral data available in *A. burtoni* in light of complex sex genotype differences.

SS-I-PP-09

Revealing the genetic basis of mouth asymmetry in the scale-eating cichlid *Perissodus microlepis*

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How polymorphism consisting of left-right asymmetries is produced and maintained in natural populations is an outstanding question in evolutionary biology. The scale-eating cichlid fish *Perissodus microlepis* from Lake Tanganyika (Africa) is a remarkable example of morphological and behavioral laterality. Its asymmetric mouth is accompanied by lateralized foraging behavior, where a left-bending morph preferentially feeds on the scales of the right side of its prey fish, while the opposite is true for the right morph. This striking dimorphism made this fish a textbook example of the astonishing degree of ecological specialization and negative frequency-dependent selection. Nevertheless, the mechanisms underlying this notable morphological and behavioral laterality remain elusive. With the aim of addressing this question, we investigated the genetic basis of mouth asymmetry through analyses of wild-caught fishes using high-throughput DNA sequencing data. A novel array of SNP markers was developed (i) *via* individual sequencing through double-digest Restriction Associated DNA (RAD) tags (ddRADseq) and (ii) *via* the creation of pooled DNA samples (PoolSeq). We obtained more than 150,000 SNPs using ddRADseq, and 1,300,000 SNPs with PoolSeq. Among these, we identified SNPs that are differentiated between the left and right morph. This, in turn, allowed us to uncover candidates genomic regions containing genes for this trait. This data will make an important contribution in understanding the genetic bases of left-right asymmetry and, ultimately, the evolutionary processes governing the long-term maintenance of intra-specific variation in animals.

SS-I-PP-10

Only true pelagics mix: Comparative phylogeography of deepwater Bathybatini cichlids from Lake Tanganyika

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Allopatric speciation is thought to be the predominant mode of speciation in East Africa’s spectacular lacustrine cichlid radiations, and indeed most cichlid species investigated thus far do show high levels of geographic population differentiation. This is particularly true for stenotopic littoral taxa. Only little is known about the population genetic structure of benthopelagic and pelagic cichlids, although it is widely assumed that these taxa form large panmictic populations. Here we present preliminary phylogeographic data for four highly mobile piscivorous species of the Lake Tanganyika deepwater cichlid tribe Bathybatini, all of which are prime targets of artisanal fisheries. Despite their old evolutionary age, which would have allowed for the accumulation of high genetic diversity, all species investigated show only very little intraspecific divergence and little genetic diversity, indicative for a fairly recent genetic bottleneck. Particularly low levels of diversity and a recent north/south divergence are observed in the benthopelagic species *Bathybates graueri* and *Hemibates stenosoma*, whereas the truly pelagic species *B. fasciatus* and *B. leo* exhibit somewhat higher levels of genetic diversity and no indication for population genetic structuring across the entire lake. Our findings indicate that (effective) population sizes in these taxa, especially the benthopelagic species, appear to be smaller than previously assumed and that only truly pelagic species constitute panmictic populations across the entire lake.

SS-I-PP-11

Evolution of Middle American cichlid diversity

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We combine molecular phylogeny with biogeographical and ecomorphological analyses to understand the reasons for the high diversity of cichlid fishes in Middle America. Seven molecular markers (three nuclear and four mitochondrial) with two nested taxon-samplings (*species-level* and *population-level* sampling) with 127 and 903 terminals, respectively, were analysed with Bayesian phylogenetic methods (MrBayes). The Bayesian approach to dispersal-vicariance analysis (S-DIVA) and fossil- and palaeogeography-calibrated beast molecular clock analyses were used to reconstruct and date the biogeography of the group in Middle America. Ecomorphological characteristics of the species were used to biologically interpret the results of the biogeographical analyses. Middle American cichlid diversity appears to be primarily derived from evolution in two river basins (the Usumacinta and the San Juan) and each of the two clades (crown-group herichthyines, amphilophines) still dominates its ancestral area. The two clades can be characterized as species flocks with widespread polyphyly of ecomorphologies. The evolution of the crown-group herichthyines in the Usumacinta river basin was gradual, while the amphilophine diversity originated by fast adaptive radiation in the San Juan river basin. The San Juan river basin is also the source of colonization of most areas of Middle America. Apart for providing evidence for the existence of two evolutionary centres of cichlids in Middle America we also provide for the first time an explanation for the depauperate fish faunas of the intervening area in northern Guatemala and Honduras due to extinctions caused by large-scale volcanic activity.

SS-I-PP-12

Diversification and trophic adaptation of external jaw morphology in East African cichlids

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In the three East African Great Lakes, independent adaptive radiations have produced a multitude of cichlid species. Similar environments in each lake have resulted in striking examples of convergent evolution - each lake contains species with a similar range of specialized trophic functions and corresponding structural similarities. This provides a rare opportunity to compare the morphology of multiple genetically distant but ecologically equivalent species. Ultimately, our goal is to better understand how changes in morphology are assimilated, specifically by examining differences in jaw shape in cichlid fishes. The unique jaw morphology of cichlids is a major factor facilitating their extensive radiation - having two sets of jaws allows each set to specialize for efficient performance of a specific function. Here, we present preliminary data on the external morphology of the cichlid feeding apparatus, for six cichlid species representing three trophic groups - carnivores, omnivores, and algae browsers - in Lake Malawi and Lake Tanganyika. We obtained three-dimensional images of the bones in cichlid heads using micro-computed tomography, and defined a set of homologous landmarks visible on the outer surface of the oral jaws. We used geometric morphometric techniques to compare the relative orientations of these landmarks between fish and to calculate the shape changes that best separated the different trophic groups, then visualized morphological differences in shape space and with deformation grids. Our results represent a preliminary analysis in preparation for a more detailed comparison of the three-dimensional morphology of the oral and pharyngeal jaw bones in cichlids from different radiations and trophic niches.

SS-I-PP-13

Geometric morphometric analysis of body shape changes in pond-bred *Tropheus* populations

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Lake Tanganyika´s rocky shoreline is populated by about 120 distinct populations of the Cichlid fish genus *Tropheus*. This array of populations and sister species represents an ideal model system for the study of evolutionary processes. To gain insight into morphological changes induced by captivity, pond breeding experiments with a standardized setup have been carried out since 2005. Altogether, four ponds were stocked, one containing fish of *Tropheus moorii* 'Nakaku', one with *Tropheus moorii* 'Mbita', and two ponds with their reciprocal hybrids. To prevent backcrossing the adult fish were removed after each year and F1, F2, F3 juveniles scanned periodically with a flatbed scanner to gain digital images of each individual. Overall morphology was assessed by means of geometric morphometric methods, defining a narrow size range of 3.5 - 6.5cm standard length to minimize the effects of allometry. Additionally, regression of size on shape was carried out to obtain size-corrected residuals for further analysis. In total 583 individuals from 4 populations and 3 generations were analyzed. Principal component analysis for shape variations showed that F2 and F3 generation offspring are more similar to each other than the F1 to both of them, suggesting strong selection from the pond environment, in addition to the effect from phenotypic plasticity in F1 published previously. As expected, the reciprocal hybrids were, and remained, more similar to each other than the ponds with Mbita- and Nakaku-*Tropheus*. Once again, deformation grids showed that most of the morphological variation occurred in the head region.

SS-I-PP-14

The transcriptional trajectory of parallel pharyngeal jaw evolution in African cichlids

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Cichlid fishes epitomise the most spectacular cases of adaptive radiation in vertebrates. These radiations are particularly dense in the Great African Lakes (Tanganyika, Malawi and Victoria). One of the major drivers of speciation in cichlids has been the key innovation of flexible and efficient oral and pharyngeal jaws, which facilitated trophic diversification. However, the transcriptional basis of cichlid oral and pharyngeal jaw development is sparsely resolved, with only a handful of genes implicated in this process. A striking facet of cichlid radiations is evolutionary parallelism of similar trophic morphologies, which presents an exciting opportunity to address fundamental questions regarding the genomics of adaptation. We hypothesise that the short diversification time makes it plausible that ecological adaptations may have primarily been brought about by changes in gene expression. With the aim of dissecting the regulatory network underlying pharyngeal jaw development to elucidate broader patterns of parallel evolution in African cichlid radiations we utilised a comparative mRNA-sequencing approach. Preliminary data analysis of differentially expressed genes in after yolk-sac absorption cichlids young from Lake Tanganyika with different trophic specialisations (algae browser, invertebrate feeder and piscivore) revealed a suite of differentially expressed genes, some previously implicated and some novel. A cluster of *c-fos* cichlids paralogues featured prominently in gene expression differences between algae browsers versus the carnivorous species. Gene ontology annotation of highly differentially expressed genes between the species revealed an enrichment of myoglobin and cytoskeleton ontology terms. In the future correlation networks of candidate genes will be elaborated to study broader developmental pathways.

SATELLITE SYMPOSIUM II:

PhD MEETING EVOLUTIONARY BIOLOGY: “EVOLUTIONARY BIOLOGY: FROM THE FIELD INTO THE LAB”

SS-II-IT-01

Dealing with temperature variation: Thermal adaptation in butterflies

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Anthropogenic climate change is considered a major threat to biodiversity, although all organisms possess mechanisms to deal with environmental variation. Due to the concomitant plastic and genetic capacities, predicting the responses of individual species to climate change is challenging. In my talk I will highlight a few issues which may complicate predictions, including effects of heat waves, indirect thermal effects, and the interference between inbreeding and stress resistance.

SS-II-IT-02

Evolvability of the cichlid jaw: Using cichlids to better understand the development and evolution of complex phenotypes.

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A major pursuit in evolutionary biology is to characterize the proximate molecular mechanisms that underlie adaptive phenotypic variation in the wild. While significant progress has been made toward understanding the genetic and developmental origins for many “simple” shifts in morphology (e.g., pigmentation switching), less is known about the basis for variation in more “complex” adaptive phenotypes, including the craniofacial skeleton. Cichlids have undergone extensive evolutionary modifications of their skull and jaws, providing a rich array of phenotypic variation for analyses. Moreover, their evolutionary history is characterized by recent origins and ongoing gene flow, making them especially amenable to genotype-phenotype mapping. Finally, cichlids are easily maintained and bred in the lab, making experimental embryology possible. This combination of evolutionary richness and experimental tractability provides excellent opportunities to address longstanding questions in evolutionary biology. In particular, we have used this system to address the nature of phenotypic evolvability - i.e., the potential for complex traits to evolve. Here, I will highlight recent work in the lab that sheds light into three specific questions: (1) what is the molecular nature of evolutionary change? (2) can we extend the current evo-devo paradigm from genotype à phenotype to genotype à resource use? (3) what is the genetic basis of phenotypic plasticity? In all I hope to underscore the power and utility of the cichlid system in modern evolutionary biology.

SS-II-IT-03

Chemical profiles of stingless bees: an evolutionary story of genes and trees.

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The highly social stingless bees (Apidae: Meliponini) are a species-rich group found in tropical and subtropical regions around the world. Like all bees they collect pollen and nectar, but they additionally gather large amounts of plant resins which they use for nest construction and defense. They further transfer resin-derived compounds to their body surfaces, thereby increasing the diversity and complexity of their chemical profiles. To investigate whether environment or relatedness drive variation in the cuticular chemistry of stingless bees, we collected species from three different continents (Asia, Australia and America), analyzed their cuticular chemical profiles and matched their chemistry with their genetical phylogeny. We found resin-derived compounds to be a predominant characteristic of evolutionary derived species. Moreover, geographic origin had a stronger effect on the bees' profiles than genetic relatedness with regard to both resin-derived and self-produced compounds, indicating that the local environment may be more influential in shaping bee surface chemistry than relatedness. To better understand the role of resin-derived compounds for stingless bees, we additionally compared resin foraging, the prevalence of resin-derived compounds in nest material, and protective properties of resin-derived compounds on the bees' body surfaces between two Australian bee species with different biogeographic origins: *Tetragonula* from Asia and *Austroplebeia* from Africa/America. While *Tetragonula* bees have a high proportion of resin-derived compounds in their chemical profiles, *Austroplebeia* bees are lacking such compounds. We found that species of the two genera strongly differed in their collection behavior and usage of resin and that *Austroplebeia* bees were more vulnerable to predatory attacks than *Tetragonula*. Our findings suggest that resin-derived compounds represent an important component in the chemical ecology of stingless bees.

SS-II-OP-01

Can coevolution with a parasite lead to emergence of cross-resistance in the host? A study on survival and gene expression upon infection

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Interactions between hosts and the parasitic microorganisms in their environment are intimate and highly prevalent across taxa and ecosystems. Such interactions have the potential to proceed along a variety of evolutionary paths. One such path is coevolution, characterized by reciprocal genetic changes in both the host and parasite. We investigated laboratory lines of the red flour beetle *Tribolium castaneum* that were coevolved to the general entomopathogenic fungus *Beauveria bassiana* for an evidence of cross-resistance. For our experiments we define cross-resistance as 'increased resistance to one novel parasite species but not another upon prior parasitic exposure'. We analyzed the survival patterns of coevolved *T. castaneum* upon infection with *B. bassiana*, *Bacillus thuringiensis* and *Pseudomonas entomophila*. The survival experiments were followed by examination of candidate host immunity-related gene expression via RT-qPCR. We observed no differences in mortality between coevolved and control lines of beetles upon infection with *P. entomophila*. However, coevolved beetle lines had similar survivorship upon infection with *B. thuringiensis as with the B. bassiana* they had coevolved with, providing evidence of cross-resistance. Gene expression results from RT-qPCR experiments also indicate similarity in the pattern of host's immune response upon infection with *B. bassiana* and *B. thuringiensis* but not upon *P. entomophila* infection. We hypothesize that the route of entry and the mechanism of infection of these *B. thuringiensis* and *B. bassiana* bring about the cross-resistance that we observe in the coevolved beetles.

SS-II-OP-02

Cooperative pathogen defence in fungus-farming ambrosia beetles

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Survival of highly-related members of social insect colonies strongly depends on their abilities to cope with pathogens. Not only are immune mechanisms within single individuals important, but also a wider so called social immune defense consisting of different behaviours which reduce pathogen abundance and hinders their spreading over the whole colony. This is especially important for fungus-growing social insects, because pathogenic fungi flourish in the humid nest environment and threaten the food fungi of the insects. The fruit-tree pinhole borer *Xyleborinus saxesenii* ("der Kleine Holzbohrer") is a native fungus-farming ambrosia beetle living in facultatively eusocial societies with division of labour between adult and larval workers. It lives in large colonies, which are founded by a single female in the wood of freshly dead trees. Young females inbreed with their brothers and delay their dispersal to help raising their sisters by grooming them and by tending of the fungus garden. Here we manipulated laboratory colonies by injecting pathogenic fungi and monitored changes of the social immune response. Adult females detected several different pathogens and enhanced grooming frequencies and cannibalism of (presumable infected) larvae. Furthermore, beetle presence significantly reduces pathogen spore load. Our results show that ambrosia beetles are a great model to investigate the evolution of social pathogen defense, as they show a wide range of social organization patterns ranging from subsociality to eusociality.

SS-II-OP-03

How to smell worse: phenols in the defensive secretions of julid millipedes (Julida, Diplopoda)

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Juliformian diplopods (Spirobolida, Spirostreptida, Julida) are known to produce odoriferous benzoquinone-rich secretions in serially arranged defensive glands ("quinone millipedes"). However, an increasing number of non-quinonic secretion constituents has meanwhile been elucidated. One particularly awful smelling class of such non-quinones is the phenols: so far only reported from a parajulid species, we here focused on the occurrence of phenolic compounds in the defensive secretions of julid millipedes. Chemical screening of secretions from 29 species of different tribes of the Julidae showed that phenols were much wider distributed than hitherto assumed. In 5 species (= 17% of the julids herein investigated), phenolic secretions based on p-cresol (=4-methyl-phenol) were detected. This was true for the cylindroiulines *Styrioiulus pelidnus* and *S. styricus* as well as an undetermined *Cylindroiulus sp.*, the brachyiulines *Brachyiulus lusitanus* and *Megaphyllum fagorum*, and a yet undescribed *Typhloiulus* species (Leptoiulini). Biosynthetically, benzoquinones and phenols are supposed to share a common pathway, leading from aromatic precursors to phenols and finally to benzoquinones. Phenolic secretions in diplopods are indeed well known from close juliformian outgroups such as Callipodida, Stemmiulida, and Polydesmida. We thus hypothesize that phenolic secretions already evolved early, possibly in a common ancestor of Nematophora, Merocheta, and Juliformia, and that phenols in the Juliformia represent remnants of an ancient biosynthetic pathway.

SS-II-OP-04

Do major urinary proteins (MUPs) function as a sexual attractant in the wild house mouse (*Mus musculus musculus*)?

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The urine of the wild house mice (*Mus musculus musculus*) contains a large amount of major urinary proteins (MUPs), which are synthesized in the liver and excreted with the urine. MUPs function as pheromones and pheromone-shuttles for volatile ligands and have various priming effect on female physiology. It has been shown that male mice up-regulated MUP excretion when housed with females and down-regulated after a social defeat (‘quality indicator hypothesis’). So far, it is not known whether or how such changes in MUP production affect attractiveness of male scent. In this study, we investigated (i) the effect of different urine stimuli on MUP production in male mice and (ii) female preference for urine from unstimulated vs stimulated males in an olfactory two-choice preference test. We will report results and discuss implications for function of MUPs in a social context.

SS-II-PP-01

Influence of local adaptation on intraspecific phenotypic variation in *Daphnia galeata*

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Species adaptation to environment occurs at the population/habitat level, and thus can greatly increase the intraspecific variance of both genotypic and phenotypic traits. However, in evolutionary experiments on *Daphnia* species the population dimension is often missing, a few clonal lineages acting as representatives for a whole species. The importance of the intraspecific variation for adaptive potential is therefore rarely addressed. To understand the genetic background of rapid adaptation to environmental changes in *Daphnia galeata*, I will use a combined approach of ecological and genomic techniques. In common garden experiments under specific environmental factors life history traits such as growth rate, age of maturity, clutch size, neonate size, survival, survival of offspring will be recorded in four different European populations of *D. galeata* maintained in the lab. Each population is represented by 5-6 genotypes. To identify the molecular basis of phenotypic variance and its distribution in *D. galeata*, fitness traits and gene expression of differently expressed genes will then be checked for correlation. This poster presents the framework of my PhD project. The aim of the project is to provide answers to following questions: (i) How is the variance in life history traits distributed within and among populations? (ii) Are gene expression profiles correlated with the fitness of individuals? (iii) Is there a correlation between differentiation at the genotypic and phenotypic level?
Key words: local adaptation, *Daphnia galeata*, phenotypic plasticity, genetic variation, life history traits

SS-II-PP-02

Simulating effects of heat periods on different life stages in a tropical butterfly

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Climate change, especially increases in extreme weather events such as heat waves, has the potential to strongly affect biodiversity and poses a significant challenge to all natural systems on Earth. Their effects though are poorly understood due to a lack of empirical data. Therefore, we here explored the sensitivity of a tropical ectotherm, which are in general believed to have a low warming tolerance, to experimentally simulated heat periods of 24 hours across seven different life stages. We simulated five different heat periods of 36°C, 37°C, 38°C, 39°C and 40°C. Increasing temperatures had strong effects on the survival of all life stages in the butterfly *Bicyclus anynana.* In larvae mortality rates increased from 2-3% at 36°C to 100% at 40°C. In contrast, eggs (52%), hatchlings (24%) and adults (15%) suffered substantial mortality at 36°C already, while pupae were most heat resistant (61% mortality at 40°C). Thus, survival rates varied between different life stages in reaction to high temperatures. Heat periods substantially reduced survival even in this plastic and widespread butterfly, exemplifying the potentially dramatic impact of extreme weather events on biodiversity. Furthermore our results underline the importance of the developmental stage and the timing of extreme weather events on the survival of insects.

SS-II-PP-03

The invasive freshwater jellyfish *Craspedacusta sowerbii* - occult polyps and conspicuous medusae

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The rising introduction of non-native species into new ecosystems is a consequence of increased human mobility. The freshwater jellyfish *Craspedacusta sowerbii* is one example of a recently globally distributed species with original source populations in China. First reports in Germany are from 1905, today the species is widespread in standing and slow-flowing waters. *C. sowerbii* has a metagenetic life cycle, including a tiny sessile polyp and a conspicuous free-swimming medusa, both feeding on zooplankton. As gelatinous predator the medusa occupies a specific ecological niche and the introduction of this species created a new functional guild within freshwater plankton communities. Although mass occurrences of medusae have been recorded and effects on aquatic food web dynamics are likely, the consequences of *C. sowerbii* being introduced to aquatic systems has not been analyzed yet. Field mesocosm experiments will be designed to identify the trophic position of medusae, the cascading effects down to phytoplankton, and pelagic-benthic fluxes of energy and organic matter mediated by jellyfish. In laboratory experiments food selectivity, assimilation and ingestion efficiencies of medusae and polyps will be determined, in order to evalute competitiveness. To test for population structure and evolutionary dynamics, genetic and sexual diversity will be quantified using molecular markers in field samples. Evidence for multiple introductions and the association between genotype and sex will be identified by genetic analyses. Combined analyses of the genetic diversity and the ecological function of this species will allow a better understanding of cause and effect relationships within aquatic food webs exposed to invasions.

SATELLITE SYMPOSIUM III:
NEUROETHOLOGY / BEHAVIORAL NEUROBIOLOGY

SS-III-OP-01

Anatomical and functional organization and connectivity of sensory maps in electrolocation

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In many vertebrates parallel processing in topographically ordered maps is essential for efficient sensory processing. In Mormyrids active electrolocation sensory input is processed in two parallel hindbrain maps, the DLZ and MZ, where phase and amplitude information are somatotopically mapped. Behavioral and physiological data indicate that these maps need to be merged to enable optimal processing of the active electrosensory input and indeed interzonal projections between both zones have been found [Fechler 2008, this study]. A likely candidate for the merging is the midbrain torus semicircularis (TS), one of several toral nuclei. Preliminary physiological and anatomical data indicates that the detailed somatotopic representation from the ELL is lost, while a crude rostro-caudal mapping may be maintained [Finger et al. 1981]. In our study we investigated the projections between the ELL and the NL in more detail, using tracer injections into the ELL and the TS. Our qualitative and quantitative analyzes showed that information from the MZ of the ELL terminates in a topographic manner within the TS. Furthermore, we specifically focus on the presence of functional connectivity leading to merged sensory processing of phase and amplitude information in the NL. Injections into the DLZ indicate that information from corresponding regions within both zones of the ELL is processed within the same area in the TS. This suggests that electrosensory information about amplitude and phase information converges and is processed together in the TS. The ELL injections will also be used to investigate which neurons in the ELL convey inter-zonal connectivity and how this may be used to enhance parallel sensory processing.

SS-III-OP-02

Neuronal innervation of defence glands in stick insects

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Many insects use defence mechanisms to repel predators by startling behaviour, chemicals, or sound production. Stick insects (Phasmatodea) have a so-called-defence gland located in the prothorax, which commonly stores and releases repellent chemicals (allomones) for defence. These glands differ in size between species. So far, the neuronal innervation and control has not been studied in detail. The innervation in *Carausius morosus* was documented by the transverse nerve with additional nerve branches. Here, the innervation is investigated by axonal tracing comparing four species of stick insects including *C. morosus* and *Sipyloidea sipylus*. Several nerves are identified which are potentially innervating the prothoracic glands. These nerves were tested for morphological contacts on the gland surface by axonal tracing. Individual tracing experiments reveal a complex innervation pattern by several nerve branches. In addition, the neurons which send axons trough the respective nerves are studied by retrograde tracing of selected nerves. In the central nervous system of all species, about 3-4 different neuron types are identified which likely innervate the defence gland, as well as adjacent muscles. The neuron types are conserved in the species studied, but some interspecific variation occurs in the combination of neuron types. In some species, individual neurons have more prominent somata in the CNS, which appears to correlate to the size of the defence glands.

SS-III-OP-03

Processing of sky-compass information in the central complex of bees

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Honeybees are able to exploit sky-compass cues, like the solar azimuth, the sky polarization pattern or the chromatic gradient of the sky for spatial orientation and navigation. This fascinating ability has been the subject of a large number of behavioral studies, but the underlying neuronal mechanisms are virtually unknown. In recent years, accumulating evidence suggests that the central complex in the insect brain serves a pivotal role in spatial orientation and holds a neuronal representation of spatial directions. In locusts, crickets and monarch butterflies the central complex has been involved in coding of sky-compass signals. Here I used intracellular recordings to investigate neuronal responses in the central complex of the bumblebee (*Bombus terrestris*) to dorsal polarized and lateral unpolarized light stimuli. Neurons in the central complex were sensitive to the plane of polarized light as well as to the azimuth of a green or an ultraviolet light spot moving around the head of the animal. The responses to unpolarized light were largely insensitive to the elevation of the presented stimulus, suggesting that these neurons are able to code for solar azimuth independent of solar elevation. The experiments show that the central complex of bees is involved in sky-compass signaling.

SS-III-OP-04

Colour learning and memory in bumblebees

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Among Hymenoptera, bees historically have elicited enormous amounts of scientific attention, because of their conspicuous pollination behaviour, intriguing social systems, learning skills and importance as suppliers of honey and wax. One hundred years ago, Nobel laureate Karl von Frisch demonstrated that colour vision, a sensory capacity which was thought to be a unique character of higher vertebrates including humans, is also present in a small insect, the honeybee. Since then, the honeybee, and more recently the bumblebee, became insect model systems for understanding visual learning and cognition in non-vertebrates. I will summarize our recent findings on colour learning and memory in the buffed-tailed bumblebee. Free-flying bumblebees were individually trained to discriminate a rewarded from an unrewarded colour stimulus and tested for memory retrieval 2 hours (mid-term memory, MTM) and 1, 3, and 7 days (long-term memory, LTM) later. Bees' memory performance increased with training length and decreased with increasing time between training and testing and colour similarity between stimuli. The appetitive visual conditioning of the proboscis extension response (PER) in restrained bumblebees was used to test whether protein synthesis is necessary for colour MTM or LTM formation. Bees were conditioned to a monochromatic colour stimulus and subsequently injected with a transcription inhibitor (actinomycin D) or ringer solution (control group). Memory retention did not differ after 6 hours but was significantly reduced in the actinomycin D group after 3 days compared to the control group, suggesting the presence of a protein synthesis-independent MTM and a protein synthesis-dependent LTM.

SS-III-OP-05

Nestmate recognition in ants

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The ability to recognize nestmates (members of the same colony) and discriminate against conspecific individuals from foreign colonies is a fundamental ability of social insects. It is crucial for the emergence of colony coherence and ultimately benefits colony fitness. Colony coherence is based on individual decisions of the colony members in encounters with other ants. At the individual level, recognition and discrimination is based on colony specific profiles of cuticular hydrocarbons (CHC label) that are represented in the olfactory centers of the ants' brain. I will present our latest results on the neuronal mechanisms underlying nestmate recognition and the amazingly fast classification of complex and changing colony odor cues and how they relate to results from behavioral studies. I will present examples, illustrating context specificity of aggressive acts, and how individual behavior can be modulated. Finally, I will discuss the neurobiological basis of individual recognition of complex colony odors and discrimination abilities in light of behavioral results and theoretical approaches, aiming to better understand the integration of the individual decisions into the collective recognition /discrimination abilities of the colony.

SATELLITE SYMPOSIUM IV: SOCIAL BEHAVIOUR AND SELF-REGULATION IN INSECTS, SWARMS AND ALGORITHMS

SS-IV-IT-01

Organization of work via the “common stomach”

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A social insect colony operates without a unit of central control, in consequence, individuals cannot assess pieces of global information at one specific place or from one specific nestmate. Social insect colonies can self-regulate as a collective. These collectives can evaluate their surroundings, process information, and make decisions. The limitations of individual workers (local information, simple behavioral rules) strongly contrast with the diversity of colony level reaction to environmental changes and challenges these colonies face. We propose a mathematical model for describing task partitioning in ant and wasp colonies. The model is based on the organizational capabilities of a ‘‘common stomach’’ through which the colony utilizes the availability of a natural substance as a major communication channel to regulate the income and expenditure of the very same substance. This communication channel has also a central role in regulating task partitioning of collective hunting behavior in ants and construction behavior in wasps is a supply and demand driven manner. The saturation of the common stomach provides accessible information to individuals so that they can adjust their behavior accordingly by engaging in or by abandoning in different tasks. The common stomach is able to establish and to keep stabilized an effective mix of workforce to exploit the resources and to ensure uninterrupted flow of material between the subtasks. This system is also able to react to external perturbations in a de-centralized homeostatic way, and the common stomach itself also used as a buffer for smaller perturbations. The model is compared to previously published models and its predictions are compared to field data.

SS-IV-IT-02

Collective motion modeled by a perception-based stochastic model

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Collective motion is one of the most ubiquitous behaviours displayed by social organisms and has led to the development of numerous models. In these models, individuals are assumed to adjust their velocity and orientation by a resulting vector computed as a function of their neighbours’ position, speed and/or orientation. These rules produce structured groups travelling cohesively in the same direction. While the most astonishing collective motion patterns are displayed by highly aligned groups, numerous species show cohesive behaviour without presenting high order or only occasionally. In this context, we present a new stochastic model based on a probability distribution function to move in targeted directions rather than on a summation of influential vectors as most models classically assume it. We describe the sensory perception field of each individual to determine the different stimuli that it perceives. Each perceived stimulus increases locally the probability for the focal agent to move towards it. Then, the focal individual adjusts its trajectory by choosing a direction according to this custom probability distribution function. With this new model, we simulated group of fish freely swimming in a homogeneous bounded tank and compared our theoretical results with experimental data obtained with groups of fish. Our results show that this stochastic perception-based approach can simulate the collective motion of social species showing not only schooling behaviour but also a wide range of loosely ordered patterns in heterogeneous environment.

SS-IV-IT-03

Honeybee-inspired models and swarm (robotic) algorithms

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Honeybee colonies exhibit sophisticated, complex and smart behaviours in collective decision-making and distributed homeostasis. On the one hand, those capabilities require mathematical and agent-based modelling to be fully understood. On the other hand those collective mechanisms offer a rich source of inspiration for computer algorithms: Honeybee foraging, food storage, resource allocation and task selection are closely intertwined with colony population dynamics. This issue has been researched several times with mathematical and agent-based models, e.g., HoPoMo, HoFoReSim, FlowerSim and TaskSelSim. This ultimately inspired several swarm-robotic algorithms, like the “vector-based swarm strategy“, the „trophallaxis-inspired algorithm“, the “social inhibition algorithm” and BEECLUST, which have been researched in computer simulations and which have several incarnations in real-world robot swarms on land and in the underwater domain. The next step will be to further develop those algorithms in the project subCULTron in artificial „cultures“ which closely resemble colony systems on a functional level, just that they are built by 130+ animal-inspired robots instead of natural animals. However, those „artificial animals“ will draw inspiration from various sources in their morphology and in their behavioural physiology. Thus, instead of simply bio-mimicking one natural species, they will represent novel social species of bio-inspired robots.

SS-IV-OP-01

Biohybrid swarms: A new way to examine collective behaviours

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Collective decision making processes, in which not a single individual is making a choice but all individuals of a group contribute to the outcome, are common in social insect societies. These self-organised processes enable groups of social insects to collectively choose e.g., a nest site, the shortest path to a food source or an aggregation site. Studying the underlying mechanisms of these processes is challenging, as various communication channels and cues can be involved. For example, although every young worker bee is able to sense local temperatures, single tested individuals do not locate themselves at their preferred temperature in a complex thermal gradient, whereas groups of bees tested in the same environment aggregate at the optimal place. The bees even collectively discriminate it from a suboptimal alternative and choose the optimal temperature. Although this behaviour is quite robust, experiments have shown that the bees can be manipulated into choosing the suboptimal temperature by introducing an additional stimulus, e.g., confined bees, in the suboptimum. In the EU-funded project ASSISIbf we now aim to develop a novel method to further study the fundamental mechanisms of such collective behaviours. We are developing a bio-hybrid system, consisting of honeybees and an array of autonomous stationary robotic devices, able to sense and change the local environment. By emitting various physical stimuli these devices will be able to interfere with group decisions. The stationary robots will learn to autonomously interact with the animals and adapt by evolutionary algorithms. With this system we aim to examine the underlying mechanisms of the self-organised processes from within the bio-hybrid society.

SS-IV-OP-02

Shimmering in Giant honeybees (*Apis dorsata*) is directed to mob wasps away from the nest

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The open nesting behaviour of giant honeybees (*Apis dorsata*) accounts for the evolution of a series of defence strategies to protect the colonies from predation. In particular, the concerted action of the shimmering behaviour is known to effectively confuse and repel predators (Kastberger et al. 2008 PLoS ONE). In shimmering, bees on the nest surface flip their abdomens in a highly coordinated manner to generate Mexican wave-like patterns. The first 200-300 ms of a shimmering wave form a flash-like visual signal with the capacity to repel a preying wasp. Depending on the distance from the nest and the velocity of the threatening wasp, the shimmering waves vary in the repetition rate and in the recruitment of nest mates. Lastly, a startle reflex is initiated in the preying wasp, which makes her turn around and fly away from the bees' nest. This paper documents a further-going capacity of this kind of collective defence (Kastberger et al. 2014 Naturwissenschaften): the visual patterns of shimmering waves align regarding their directional characteristics with the projected flight manoeuvres of the wasps when preying in front of the bees' nest. The honeybees take here advantage of a threefold asymmetry intrinsic to the prey-predator interaction: (a) the visual patterns of shimmering turn faster than the wasps on their flight path, (b) they "follow" the wasps more persistently (up to 100 ms) than the wasps "follow" the shimmering patterns (up to 40 ms) and (c) the shimmering patterns align with the wasps' flight in all directions at the same strength, whereas the wasps have some preference for horizontal correspondence. The findings give evidence that shimmering honeybees utilize directional alignment to enforce their repelling power against preying wasps. This phenomenon can be identified as predator driving which is generally associated with mobbing behaviour (particularly known in selfish herds of vertebrate species), which is, until now, not reported in insects.

SS-IV-OP-03

Robustness and distributed learning in bio-hybrid societies

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Our research aims to better understand collective behaviours in social animals, through the use of decentralised robot populations that manipulate environments of animals, the robots themselves reacting to the behaviours of the animals. In this way, we hope to create conditions in which animals and robots can together "choose" how to manipulate their own environment. A central goal is for the robots to interact with animal populations in a harmonious way, developing novel insights into factors that can influence and steer collective behaviours. Within this framework, we are building simulation models of these "mixed animal-robot societies" to generate hypotheses that are testable with real animals and robots. We are currently investigating the robustness of mixed societies to exogeneous perturbations, and the extent to which the robot population is able to enhance robustness. We are interested in how sub-dividing the animals and robots into several distinct groups (each of which comprises animals and robots) can influence robustness. Here, between-group communication is facilitated solely via the robots and while this restricts the set of cues that can be transferred between animals, it offers high observability. Interestingly, the robot--robot interactions can also be adaptive, allowing the mixed society to exhibit (distributed) memory that may aid in system-level responses to perturbation. This work also leads towards using different types of robots as mediators within systems that comprise multiple species.

SS-IV-OP-04

Interdisciplinary mechantronics: from social animals to swarm robotics and vice versa

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Most of the research activity in swarm robotics, swarm intelligence or biology of swarms is mono-disciplinary. Computer scientists or roboticists copy the bits of nature they understand, develop algorithmic solutions to more or less complex problems, focusing on performances, scalability and robustness of the approach. In parallel biologists analyze their animals joking about the knowledge in biology of their colleagues in engineering, struggling with data acquisition and analysis. Ideally this field should be fundamentally multidisciplinary, with engineers, computer-scientists, biologists, chemists and many other disciplines interacting together. Within swarm robotics itself, we are far from taking advantage of all aspect or robot design. If one look to swarm of insects, fish or other animals, many mechanisms take place at the physical and not at the algorithmic level. It is therefore critical to address the design of swarm of robots at the mechatronic level and not at the algorithmic level only. This presentation gives an overview of a set of interdisciplinary projects were both biologists and engineers were involved, where the engineering part covered all mechatronic disciplines and where both biologists and engineers took advantage of it. Some example will be taken from the project Swarmbots, Swarmanoid, Leurre and ASSISIbf.

SS-IV-OP-05

Comparative analyses of plasmodial networks of different slime molds (Myxogastria)

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Several plasmodial slime molds (Myxogastria) form a phaneroplasmodium during their lifecycle. This large single cell relies on pulsatile contractions to distribute for instance food particles or chemical messengers across its network. Its most prominent member *Physarum polycephalum* has emerged as a model organism to study biological fluid dynamics and foraging behavior. The analogy with transportation networks also stimulated research on adaptive network topology and self-organisation. Studies of network formation by other Myxogastria are required for a broader understanding of plasmodial organisation but are so far underrepresented. We have isolated several phaneroplasmodia-forming slime molds, established stable laboratory cell cultures and identified them using taxonomic and phylogentic approaches. Growth characteristics and chemotactic responses of the organisms were recorded using custom-made optical setups. Images of plasmodial networks were analysed and compared with respect to growth velocity, network topology and stimuli responses. Differences in the network formation were found among the strains, suggesting genetically fixed search strategies and variations in behavioural ecology. The significance of the results will be discussed, also in relation of using slime molds for network modeling.

SS-IV-OP-06

Collective biohybrid systems: challenges and ambitions

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Collective biohybrid systems represent new and challenging field of technological and biotechnological developments. Goals targeted by these approaches vary from creating advanced sensing systems, up to establishing interfaces between natural and artificial ecologies. In many cases biological parts are microbiological systems, plants, insects and animals; technological parts are represented by mobile and stationary robots, complex sensors networks, swart artefacts. Current developments demonstrate appearance of such biohybrid systems in micro- and macro- ranges and in different organizational forms: from swarms and networked systems up to distributed computational networks. This work provides an overview over biohybrid developments in various scales as well as discusses challenges and potentials of this approach.

SS-IV-PP-01

Speeding up social waves in Giant honeybees (*Apis dorsata*)

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Shimmering is a defence behaviour in giant honeybees (*Apis dorsata*), whereby bees on the nest surface flip their abdomen upwards in a Mexican wave-like process. However, information spreads faster than can be ascribed to bucket bridging. We identified (Kastberger et al 2014 PLoS ONE) a saltatoric process that speeds up shimmering by the generation of daughter waves, which subsequently merge with parental waves, producing new wave fronts. Motion patterns of individual focus bees (n >10k) and their shimmering-active neighbours (n >459k) were measured with high-resolution video recording and stereoscopic imaging (Kastberger et al 2011 Frontiers in Zoology). Three types of shimmering-active surface bees were distinguished by their communication status: 75% of all bees (= bucket-bridging agents) affected 88% of their neighbours, and transferred information at a velocity of v = 0.32 ± 0.02 m/s. 9% of bees (= chain-tail agents) were activated by 6% of their neighbours, but did not motivate others to participate in the wave. Lastly, generator agents comprised 16% of bees, showed abdominal flipping before the arrival of the main wave front, and initiated daughter waves. They affected 7% of their neighbourhood and speeded up the compound shimmering process compared to bucket bridging alone by 42% to v = 0.52 ± 0.02 m/s. The main direction of shimmering was reinforced by 36% of agents, whereas the contribution of the complementing agents was fuzzy. The saltatoric process could enable the bees to instantly recruit larger cohorts to participate in shimmering and to respond rapidly to changes in flight direction of preying wasps. At a distance of up to three metres from the nest shimmering could notably contribute to the startle response in mammals and birds.

SS-IV-PP-02

Evidence for convection funnels in giant honeybee (*Apis dorsata*) nests

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The Southeast Asian giant honeybees (*Apis dorsata*) build single-comb nests in the open, which make this species particularly prone to environmental conditions. Long-term infrared imaging (Waddoup 2014 Master thesis Graz) documented cooler spots on the bee curtain ($N = 207$, > 20 nests) distinguished by a steep temperature gradient ($\Delta T < -3$°C) at their borders. Their occurrence correlates with ambient temperature and daytime, they were generated within minutes, variable in size (A), position, and faded away minutes after emergence. Their spatial and thermal properties displayed autonomous features despite their link to ambience. The main ($P > 0.97$) $\Delta A/\Delta T$ parameters correlated positively, which can be understood as a Ventori effect (that an airflow through restricting apertures lowers the temperature of the flowing medium). Thus, the cool nest spots are likely to represent funnels with an inward airflow. The $\Delta A/\Delta T$ plots also exhibit rare ($P < 0.03$) but repetitive events of negative proportion, which are presumably caused by ventilation in the course of an “inhaling” / “exhaling” cycling. The “breathe-in” process would suck ambient air through the funnels (whereby the conjunct fall of pressure in the nest lumen could be caused by collective enlargement of the cavities between bee curtain and comb). It is followed by a relaxation of the bee curtain, which would press warm nest-borne air through the leaking mesh structure outwards. Both, infrared imaging and vibrometry (Kastberger et al 2013 Naturwissenschaften) support these presumptions of the ventilation hypothesis and give evidence that cool nest spots depict low-resistance convection funnels for maintaining thermoregulation and thus also for restoring fresh air in the nest.

SS-IV-PP-03

Intraspecific Aggression in Giant Honey Bees (*Apis dorsata*)

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We investigated intraspecific aggression in experimental nests ($expN_1$, $expN_2$) of the giant honey bee *Apis dorsata* in Chitwan (Nepal), focusing on interactions between surface bees and two other groups of bees approaching the nest: (1) homing “nestmate” foragers landing on the bee curtain (Kastberger et al. 2011) remained unmolested by guards (Breed et al. 2004); and (2) supposed “non-nestmate” bees, which were identified by their erratic flight patterns (Winston 1987) in front of the nest, such as hovering or sideways scanning and splaying their legs from their body, and were promptly attacked by the surface bees after landing. These supposed non-nestmate bees only occurred immediately before and after migration swarms, which had arrived in close vicinity (and were most likely scouting for a nesting site). In total, 231 of the “nestmate” foragers (fb) and 102 approaches of such purported “non-nestmate” scouts (sc) were analysed (total observation time $expN_1$: 5.43 min) regarding the evocation of shimmering waves (sh; Kastberger et al. 2008). During their landing the “nestmate” foragers provoked less shimmering waves (${}_{rel}n_{sh}[fb] = 23/231 = 0.0996$, ${}_{rel}n_{sh}[sc] = 75/102 = 0.7353$; $p < 0.001$, $\chi 2$-test) with shorter duration ($D_{sh}[fb] = 197 \pm 17$ ms, $D_{sh}[sc] = 488 \pm 16$ ms; $p < 0.001$; t-test) than “non-nestmates”. Moreover, after having landed on the nest surface, the “non-nestmates” were attacked by the surface bees ($expN_1$, $expN_2$: observation time >18 min) quite similarly to the defensive response against predatory wasps (Kastberger et al. 2008). Hence, the surface members of settled colonies respond differently to individual giant honey bees approaching the nest, depending on whether erratic flight patterns are displayed or not.

SS-IV-PP-04

Antbots: A feasible visual emulation of pheromone trails for swarm robots.

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We present an experimental setup to model the pheromone trail based foraging behaviour of ants using a special phosphorescent glowing paint. To do this, we have built two custom addons for the e-puck robot that allow for trail laying and following on the glowing floor, as well as a way for the robots to mimic the ants capability of using polarization patterns as a means of navigation. Using simulations we show that our approach allows efficient pathfinding between nest and potential food sources. Experimental results show that our add-on boards for trail laying and sun compass navigation are accurate enough to allow a single robot to lay and follow a trail repeatedly.

SS-IV-PP-05

ASSISIbf: Honeybees and robots form a bio-hybrid society

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In the EU-funded project ASSISIbf we will investigate how different stimuli types, e.g., vibration and temperature, can trigger specific individual and collective behaviours in bees. These findings will have impact on the development of robotic devices that are capable to interact with bees autonomously. The main goal of ASSISIbf is to enable novel communication between animals and robots, creating a mixed, bio-hybrid, and self-organising society of animals and machines.

SS-IV-PP-06

Evolving Collective Behaviors With Diverse But Predictable Sensor States

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There are multiple different ways of implementing artificial evolution of collective behaviors. Besides a classical offline evolution approach, there is, for example, the option of environment-driven distributed evolutionary adaptation in the form of an artificial ecology and more generally there is the approach of embodied evolution. An other recently reported approach is the application of novelty search to swarm robotics. A concept of our interest is an information-theoretic analogon to thermodynamic (Helmholtz) free energy. The assumption is that the brain is permanently trying to predict future perceptions and that minimizing the prediction error is basically inherent to brains. This is defined by the 'free-energy principle'. The struggle for prediction success requires a complementary force that represents curiosity and exploration. Here we present a method called diverse prediction that rewards not only for correct predictions but also for each visited sensory state. This proves to be a better approach compared to the method prediction that was reported before.

SATELLITE SYMPOSIUM V:

WEITERBILDUNGS-WORKSHOP ZU TIEREXPERIMENTELLEM ARBEITEN

SS-V-IT-01

Tierschutzrechtliche Bestimmungen für Tierversuche – das novellierte Deutsche Tierschutzgesetz und seine Verordnung

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Die Umsetzung der Richtlinie 2010/63/EU in nationales Recht erfolgte in Deutschland im Juli 2013. Das Tierschutzgesetz wurde für den Bereich Tierversuche an europäisches Recht angepasst und durch eine Verordnung ergänzt. Die Richtlinie ist für die Mitgliedsstaaten bindend und dient einer innereuropäischen Harmonisierung und Stärkung des Tierschutzes. Das grundsätzliche Ziel der 2010/63/EU ist es, zukünftig Tierversuche weitestgehend durch Alternativmethoden zu ersetzen. Für Deutschland wurden neben Änderungen im Antrags- und Anzeigeverfahren und der Erweiterung des Begriffs Tierversuche auch umfangreiche Regelungen zur Qualifikation des Personals sowie zur Belastungseinstufung im Versuch vorgenommen. Auch die Dokumentationspflicht wurde deutlich umfangreicher. In den letzten zwei Jahren führten die Neuerungen zu regional sehr unterschiedlichen Verfahrensabläufen und zu einem bürokratischen Mehraufwand für die Forschungseinrichtungen und Forscher. Von den Neuregelungen betroffen ist auch die Freilandforschung; hier gelten jetzt nicht nur die artenschutzrechtlichen Bestimmungen, sondern auch die tierschutzrechtlichen Vorgaben für Tierversuche. Der Vortrag gibt über die Neuerungen einen Überblick, die anschließende Diskussion soll helfen Unklarheiten zu beseitigen.

SS-V-IT-02

Belastungsmodelle und -einschätzungen sowie Abbruchkriterien in Tierversuchen bei Vögeln

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Für das Experimentieren ist die Gesundheit der Tiere eine wichtige Voraussetzung für den Erhalt von vertrauenswürdigen Daten. Genauso erfordert die Haltung von Tieren eine laufende Gesundheitskontrolle. Neben Blutuntersuchungen stellen Verhaltensdaten wichtige Kriterien bei der Einschätzung des Gesundheitszustandes eines Tieres dar. Die Tierschutz - Versuchstierverordnung schreibt folgendes Vorgehen vor „….mindestens einmal täglich das Befinden der Tiere durch direkte Inaugenscheinnahme …. überprüft werden“ (§1, Absatz 1). Diese Vorschrift trägt der Tatsache Rechnung, dass aus dem Verhalten eines Tieres etwas über seinen Gesundheitszustand ausgesagt werden kann. Die Ethologie hat für das Gesamtinventar des Verhaltens eines Tieres den Begriff Ethogramm entwickelt. Tierhalter und Tierexperimentatoren sollten also das Ethogramm einer Tierart kennen oder ein Ethogramm der von ihnen gehaltenen Tierart erstellen. Dieses Ethogramm sollte neben dem Normalverhalten auch vom Normalverhalten abweichende, auf Krankheitszustände hinweisende, Verhaltenselemente enthalten. Im Tierversuch stellt sich die Frage nach den Schmerzen und Leiden, denen ein Tier bei der Haltung und während eines Versuchs ausgesetzt ist. Deshalb sind solche Verhaltenskriterien wichtig, die etwas über Schmerzen und Leiden eines Tieres aussagen. Der Gesetzgeber verlangt bei der Einreichung eines Antrags auf Genehmigung von Tierversuchen als Anlage Belastungstabellen und Scoresheets. Unter letzteren versteht man Einstufungskriterien, die als Grundlage für einzuleitende Maßnahmen verwendet werden. In einer gemeinsamen Aktion vieler Halter von Vögeln an deutschen Hochschulen wurden solche Tabellen und Scoresheets entwickelt. Diese sollen vorgestellt und erläutert werden.

SS-V-IT-03

Investigating neuroendocrine mechanisms of seasonal adaptations: Surgical interventions, anaesthesia and analgesia in small mammals

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Seasonal mammals have evolved manifold strategies to deal with the reoccurring environmental changes over the course of the year. Djungarian hamsters originate from the steppes of Kazachzstan and show extreme physiological and morphological adaptations to seasonal environmental changes. They change in fur colour and thermogenic capacities, reproductive activity, body weight and during winter they show daily torpor, a state of hypometabolism and hypothermia. We are interested in the neuroendocrine mechanisms of these processes, in particular in the regulation of daily torpor. To investigate these phenomena we routinely measure and manipulate different physiological in- and outputs. This involves surgical interventions in the periphery as well as of the central nervous system. This presentation focuses on preparation and implementation of surgical methods in small mammals.

SS-V-IT-04

Tierversuchsfreie Verhaltensdiagnostik für neuropsychiatrische Tiermodelle

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Abstract not available.

SS-V-IT-05

Anästhesie bei biomedizinischen Experimenten mit Mäusen

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Die Maus ist die heute am häufigsten eingesetzte Versuchstierspezies in der biomedizinischen Forschung. Bei Mäusen werden häufig Eingriffe vorgenommen, die betreffend der Belastung von niedrigen Schweregraden wie beispielsweise bei einer einfachen Probennahme zum Zweck der Genotpyisierung, bis zu hohen Schweregraden, wie beispielsweise bei Transplantationen oder open-chest Eingriffen reichen. Bei der Anaesthesie derart kleiner Säugetiere (das Körpergewicht erwachsener Labormäuse liegt i.d.R. bei 17-30 g), die zudem meistens genetisch modifiziert sind, können die etablierten Methoden, wie sie bei grösseren Tieren oder beim Menschen üblich sind, nur eingeschränkt angewendet werden. Als weitere Einschränkung kommt die Interferenz der Anaesthetika und Analgetika mit dem Versuchsziel hinzu, die schon bei der Planung von Experimenten bedacht werden muss. Es werden die Einschränkungen und Möglichkeiten der Anaesthesie von Mäusen im Labor auf der Basis der Grundprinzipien der Anaesthesie und der Besonderheiten der Tierart ausgeführt. Häufig angewendete Anaesthesie-Protokolle werden gezeigt und einige Effekte und Nebenwirkungen werden diskutiert.

SS-V-IT-06

Nicht-invasive stoffwechselphysiologische Datenerhebung im Feld

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Abstract not available.

SS-V-IT-07

Grundsätze der Aus-, Fort- und Weiterbildung in der Versuchstierkunde

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Mit der Umsetzung der EU Tierschutzrichtlinie (Richtlinie 2010/63/EU) und der daraus resultierenden Novellierung des Tierschutzgesetzes (TierSchG) haben sich die Anforderung an die Aus-,Fort- und Weiterbildung des mit Versuchstieren arbeitenden Personals geändert. Neben dem Sachkundenachweis, der für alle Personen erforderlich ist, die mit Versuchstieren arbeiten oder diese töten sollen, fordert der Gesetzgeber eine kontinuierliche Weiterbildung des Personals, vom Tierpfleger zum Versuchsleiter. Bisherige Ausbildungsprogramme haben sich auf die Ausbildung von Experimentatoren fokussiert (FELASA B), vorzugsweise mit dem Schwerpunkt zu Arbeit mit Kleinnagern. Neue Empfehlungen und die Themenvorgabe der Tierschutzversuchstierverordnung (TierSchVersV) erfordern umfangreiche Anpassungen an vorhandene Ausbildungsstrukturen oder die Etablierung neuer Programme, die den verschiedenen involvierten Disziplinen gerecht werden. Die BMBF und DFG geförderte Plattform „Laboratory Animal Science interactive“ (las-interactive.de, vormals „Versuchstierkunde online“) kann Einrichtungen bei der Etablierung entsprechender Ausbildungsprogramme unterstützen. Zusätzlich bietet die Plattform die Möglichkeit einer Vernetzung verschiedenster Anwendungsbereiche und Ansätze der tierexperimentellen Forschung. Der Vortrag wird kurz die rechtlichen Grundlagen sowie die Aus- und Weiterbildungssituation in Deutschland und der EU beleuchten und die online Plattform LAS interactive vorstellen.

SS-V-IT-08

Schmerzvermeidung in Experimenten mit Crustaceen

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Wirbellose besitzen Nozizeptoren, aber eine Verarbeitung der Informationen dieser Rezeptoren zu einer Empfindung, die wir Menschen als "Schmerz" beschreiben, konnte bisher nicht nachgewiesen werden. Es gibt eine Anzahl von Publikationen, die auf ethologischer Ebene die Reaktionen von Wirbellosen und Wirbeltieren auf "schmerzhafte" Reize miteinander vergleichen und eine Reihe von Übereinstimmungen gefunden haben. Daher kann nicht ausgeschlossen werden, dass die Wirbellosen und insbesondere die wohl am höchsten entwickelten Vertreter der Krebse und auch Weichtiere Schmerz empfinden. Solange keine anderen Befunde vorliegen, sollte bei Fang, Hälterung bzw. Zucht und experimenteller Verwendung bzw. Zubereitung für die menschliche Ernährung daher eine Schmerzvermeidung analog zu der Behandlung bei Wirbeltieren in Betracht gezogen werden. Die Frage ist, wie dieses im Laboralltag umgesetzt werden kann. In Bezug auf Betäubung und Tötung von höheren Krebsen (Hummer und Flusskrebse) werden im Vortrag aktuelle Erkenntnisse über folgende Betäubungs- und Tötungsmethoden vorgestellt: Abkühlung auf Eis/in Eiswasser, Elektrobetäubung, Einleitung von CO2 in das Hälterungswasser, Zugabe 10% MgCl2 zum Hälterungswasser, langsame Erwärmung (1°/min), schnelle Erwärmung (Überführung in 100°C). Zusammenfassend kann festgestellt werden, dass aktuell keine Betäubungsmethode empfohlen werden kann. Zur Tötung sind eventuell eine langsame Erwärmung oder eine "Elektrobetäubung" mit anschließender Überführung in kochendes Wasser geeignet, aber bei diesen Verfahren müssen noch einzelne Aspekte weitergehend untersucht werden.

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