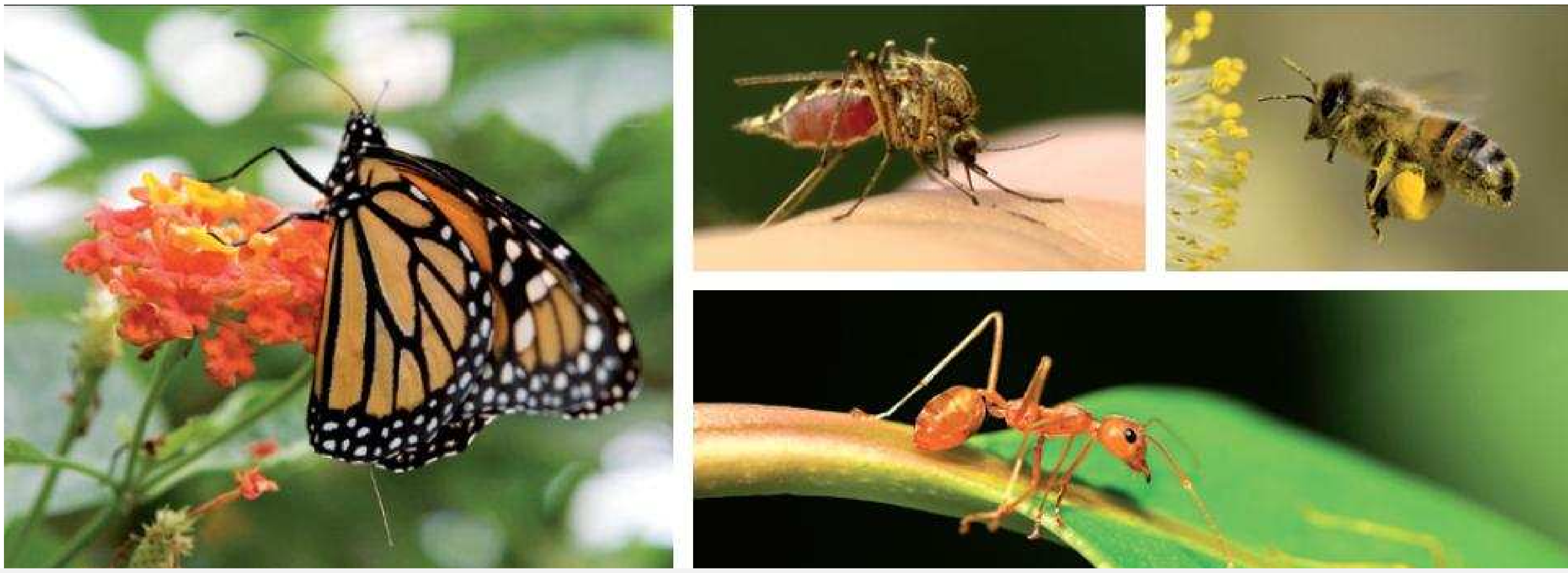

German Zoological Society 105th Annual Meeting

Abstract Volume

September 21 – 24, 2012
University of Konstanz, Germany

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SARSTEDT

Dear Friends of the Zoological Sciences!

Welcome to Konstanz, to the 105th annual meeting of the German Zoological Society (Deutsche ZoologischeGesellschaft, DZG) – it is a great pleasure and an honor to have you here as our guests!

We are delighted to have presentations of the best and most recent research in Zoology from Germany. The emphasis this year is on evolutionary biology and neurobiology, reflecting the research foci the host laboratories from the University of Konstanz, but, as every year, all Fachgruppen of our society are represented – and this promisesto be a lively, diverse and interesting conference. You will recognize the standard schedule of our yearly DZG meetings: invited talks by the Fachgruppen, oral presentations organized by the Fachgruppen, keynote speakers for all to be inspired by, and plenty of time and space to meet and discuss in front of posters. This year we were able to attract a particularly large number of keynote speakers from all over the world. Furthermore, we have added something new to the DZG meeting: timely symposia about genomics, olfaction, and about Daphnia as a model in ecology and evolution. In addition, a symposium entirely organized by the PhD-Students of our International Max Planck Research School “Organismal Biology” complements the program.

We hope that you will have a chance to take advantage of the touristic offerings of beautiful Konstanz and the Bodensee. The lake is clean and in most places it is easily accessed for a swim, so don’t forget to bring your swim suits.A record turnout of almost 600 participants who have registered for this year’s DZG meeting is a testament to the attractiveness of Konstanz for both scientific and touristic reasons. Our hope is that this year’s DZG meeting will contribute to a further strengtheningof the scientific standing of Zoology in Germany. We also hope that this conferencewill provide an opportunity in particular for young scientist to showcase their best research not only nationally, but also internationally.

We would like to thank the sponsors for their valuable financial contributions, the Deutsche Forschungsgemeinschaft for travel support, the DZG and in particular Sabine Giesslerfor help in organizing this event. The University of Konstanz provided substantial support in various forms without which this meeting would not have been possible - this is much appreciated. In particular, we would like to thank Mrs. Anne Zitzelsberger from our “events management” for her commitment and skills in organizing this meeting.

As local organizers we are glad to have you here, and we are looking forward to four days of excellent science! We hope that you will enjoy your stay in Konstanz and that you will be stimulated by the exciting researchthat you will be able to hear and see at this year’s meeting of the Deutsche ZoologischeGesellschaft.

Axel Meyer

1. *Key Note and Special Guest Talks*

Friday, September 21, 2012

Welcome address: A 600 / 18:30

Uli Burchardt (major of Konstanz), Ulrich Rüdiger (principal University of Konstanz), Hermann Wagner (chairman DZG)

Key Note: Chair - Axel Meyer A 600 / 19:00

Scott Edwards (Harvard University)

Molecular Ecology in the 21st Century: Genomic Foundations of an Integrative Science

Author: *Scott Edwards*[1]

Affiliation: [1]*Organismic and Evolutionary Biology, Harvard University, USA*

Molecular ecology in the 21st century is gradually transforming from a neutral-marker science, in which genetic markers were used to track lineages through time and space, into a functional marker science, in which the functions and expression of gene variants are studied in the context of ecology, behavior and field biology. Ironically, the vision of molecular ecology of linking variation in gene function to variation in phenotype and fitness is moving ever closer to goals long held by molecular biology, albeit with an emphasis on non-traditional model species in diverse natural and behavioral settings. As whole genomes, transcriptomes, other 'omes' and the computational tools to mine them are accumulated for diverse species, well-curated specimens and genome resources from diverse temporal, geographic, experimental and behavioral states will be key for continued progress. These transformations will be illustrated through recent research showing first how genes are used to track the evolution and spread of a bacterial pathogen, *Mycoplasma gallisepticum*, infecting songbirds in the US, and then how genomics is detailing the birds' rapidly evolving resistance to this pathogen.

Saturday, September 22, 2012

Key Note: Chair - Giovanni Galizia A 600 / 08:30

Christiane Weirauch (University of California-Riverside)

Bee killers and blood suckers – on the evolution of assassin bugs

Author: *Christiane Weirauch*[1]
Affiliation: [1]*Department of Entomology, University of California, Riverside*

With ~6,800 described and many undescribed species, Reduviidae, or assassin bugs (Insecta: Hemiptera: Heteroptera), are the largest clade of predatory non-holometabolous insects. Together with their remarkable morphological and behavioral diversity, an emerging phylogenetic framework, and their importance as diseases vectors, this makes Reduviidae an ideal group for studying the evolutionary history of a megadiverse group of predators and blood feeders. This talk outlines a research program embracing species discovery, molecular and morphological phylogenetic aspects ("Tree of Life"), and evolutionary research using Reduviidae and Heteroptera, the true bugs, as a model. Modern approaches to species discovery and lower-level phylogenetics are explored using the charismatic and diverse bee killer assassin bug genus *Apiomerus* Hahn as an example. At a higher systematic level, current efforts are on revealing relationships between the infraorders of true bugs and on relationships within the least known bug infraorder Dipsocoromorpha, the cryptic "litter bugs". Recent evolutionary research on assassin bugs in my lab has focused on the evolution of novel predation strategies. An example is "sticky trap predation" that evolved within the largest clade of predatory Reduviidae, the Harpactorini. A more infamous predation strategy is exhibited by the blood-feeding Triatominae, or kissing bugs, the vectors of Chagas disease. Our molecular analyses show Triatominae to be paraphyletic and we conclude that the evolution of blood-feeding may have occurred once or twice independently among predatory assassin bugs. Divergence time estimates indicate that kissing bugs are much younger than previously assumed.

Key Note: Chair - Giovanni Galizia A 600 / 09:30

Alison Mercer (University of Otago)

Social modulation of learning in honey bees

Author: *Alison Mercer*[1]
Affiliation: [1]*Department of Zoology, University of Otago, Dunedin, New Zealand*

Honey bees are highly social insects and chemical communication is critical for colony survival. Interestingly, chemical signals (pheromones) modulate learning behaviour in honey bees. Aversive learning in young worker bees (*Apis mellifera*), for example, can be suppressed by pheromone released by the honey bee queen[1], and pheromone released by guard bees inhibits appetitive learning in bees recruited for colony defense[2]. This talk will focus on recent attempts to explain why the effects of

pheromones on learning performance in honey bees are age- and state-dependent. It will outline what is known about mechanisms that support pheromone modulation of learning behaviour in the honey bee and also, discuss the possible adaptive value of social modulation of learning in this insect. One important question is whether a better understanding of pheromone communication can offer novel insights into cellular and molecular mechanisms that underpin learning and memory formation in the honey bee.

Supported by a grant from the Royal Society of New Zealand Marsden Fund (UOO0910)

[1.] Vergoz V, Schreurs HA, Mercer AR. (2007) *Science* 317:384-386
[2.] Urlacher E, Francés B, Giurfa M, Devaud J-M. (2010) *Front Behav Neurosci* 4:157

Special Guest Lecture: Chair - Giovanni Galizia A 600 / 11:00

Alistair McGregor (Oxford Brooks University)

Evolution of the regulation of cellular morphology in Drosophila

Authors: *Saad Arif*[1], *Sophie Murat*[2], *Maria D. S. Nunes*[1], *Isabel Almudi*[1], *James Currie*[1], *Elio Sucena*[3], *Eric Lai*[4], *Christian Schlötterer*[2], *Alistair P. McGregor*[1]
Affiliations: [1]Oxford Brookes University; [2]Vetmeduni Vienna; [3] *Instituto Gulbenkian de Ciencia*; [4]*Sloan-Kettering Institute*

A major challenge in evolutionary developmental biology is identifying the genetic changes underlying the evolution of animal morphology. Although great progress has been made in recent years in finding changes underlying differences in a number of traits, the contribution of standing genetic variation in natural populations to the evolution of differences between species remains poorly understood. To address this question we have investigated the genetic basis of leg trichome pattern differences within and between Drosophila species. *Drosophila simulans* displays a large portion of naked cuticle on the femur of the second leg called the 'naked valley'. However, in *D. melanogaster* the naked valley is extremely variable ranging from a small naked patch to approximately an area ten times larger like in *D. simulans*. It was previously shown that the Hox gene Ultrabithorax (Ubx) is involved in the 'naked valley' difference between these species. To determine if intra-specific differences in the 'naked valley' have a similar genetic basis we investigated the cause of variation in this trait in *D. melanogaster*. Our study has found a novel regulatory mechanism underlying variation in leg trichome patterns segregating in *D. melanogaster*, which provides new insights into the genetic regulatory network for trichome development, and the molecular basis of phenotypic evolution within and between species.

Welcome and introductory lecture: Konzil / 19:00

Axel Meyer and Peter Berthold
Geschichte der Biologie in Konstanz

Public Key Note: Chair - Giovanni Galizia Konzil / 19:30

Randolf Menzel (Freie Universität Berlin)
Wie ein kleines Gehirn aus Erfahrung lernt (Eine Reise in das Gehirn der Honigbiene)

Author: *Randolf Menzel*[1]
Affiliation: [1]*Freie Universität Berlin*

Small brains, like those of insects, are thought to control behaviour by hard-wired neural connections triggered by developmental programmes and external stimuli. The concept behind such an argument assumes that experience-dependent rewiring of networks is more demanding and thus more 'neuron-intensive', particularly if memory structures are built from combinations of stimuli. Recent studies in honeybees refute such a claim. They live in colonies and exhibit complex social, navigational and communication behaviours as well as a relatively rich cognitive repertoire. Because these relatively complex behaviours are controlled by a brain consisting of only 1 million or so neurons, honeybees offer an opportunity to study the relationship between behaviour and cognition in neural networks that are limited size and complexity. Recently, the honeybee has been used to model learning and memory formation, highlighting its utility for neuroscience research, in particular for understanding the basis of cognition**.** These studies are embedded in the long tradition of ethological research on sensory physiology, navigation and communication of this animal leading to 100 years of discoveries made by Karl von Frisch and his students and their students.

The cognitive dimensions of learning behaviour in bees reach far beyond simple stimulus associations, and include learning about stimulus categories, their sequences and combinations, and trends in changing reward values. These memory contents are embedded in a rich spatial and temporal context. Neural recordings during honeybee learning, memory formation and retrieval enable us to investigate the neural correlates underlying these cognitive faculties. Patterns of synaptic aggregates and single neurons that store components of a particular memory have been identified and characterized. The small size of the bee brain offers the opportunity to trace neural plasticity to specified neural nets and single neurons. I will present examples of the power and current limitations of the honeybee as a model of cognitive neuroscience focusing on studies that aim to unravel neural correlates of behavioural adaptation and social communication.

Sunday, September 23, 2012

Key Note: Chair - Axel Meyer A 600 / 08:30

Chris Jiggins (Cambridge University)

A butterfly genome offers insights into adaption and speciation

Author: *Chris Jiggins*[1]
Affiliation: [1]*University of Cambridg, UK*

Heliconius butterflies are a rapidly radiating neotropical genus widely used in studies of ecology, behaviour, mimicry and speciation. Closely related species typically differ in several aspects of their ecology and behaviour, and in particular their mimetic wing patterns. We sequenced the genome of Heliconius melpomene and compared it with other taxa to investigate chromosomal evolution in Lepidoptera and gene flow among multiple Heliconius species and races. Among 12,669 predicted genes, biologically important expansions of families of chemosensory and Hox genes are particularly noteworthy. Chromosomal organization has remained broadly conserved since the Cretaceous period, when butterflies split from the Bombyx (silkmoth) lineage. Using genomic resequencing, we show hybrid exchange of genes between three co-mimics, Heliconius melpomene, Heliconius timareta and Heliconius elevatus, especially at two genomic regions that control mimicry pattern. We infer that closely related Heliconius species exchange protective colour-pattern genes promiscuously, implying that hybridization has an important role in adaptive radiation.

Special Guest Lecture: Chair - Axel Meyer A 600 / 09:30

Hans Hofmann (University of Texas)

Variation on a Theme: Function and Evolution of a Vertebrate Social Decision-Making Network

Author: *Hans Hofmann*[1]
Affiliation: [1]*The University of Texas at Austin*

Animals evaluate and respond to their social environment with adaptive decisions. Revealing the neural mechanisms of such decisions is a major goal in biology. We analyzed expression profiles for 10 neurochemical genes across 12 brain regions important for decision-making in 88 species representing five vertebrate lineages. We found that behaviorally relevant brain regions are remarkably conserved over 450 million years of evolution. We also find evidence that different brain regions have experienced different selection pressures, because spatial distribution of neuroendocrine ligands are more flexible than their receptors across vertebrates. Our analysis suggests that the diversity of social behavior in vertebrates can be explained, in part, by variations on a theme of conserved neural and gene expression networks.

Special Guest Lecture: Chair - Giovanni Galizia A 600 / 11:00

James Poulet (Berlin)

Cortical Processing during Behaviour

Author: *James Poulet*[1]
Affiliation: [1]*Max Delbrück Center for Molecular Medicine Berlin-Buch.*

A prominent reflection of different behavioural states in the mammalian central nervous system are the distinct patterns of neocortical oscillations and synchrony. Such “cortical states” are thought to be fundamental mechanisms of neuronal computation underlying sensory perception, sensorimotor coordination and learning. In this talk I will present data showing cortical state change in the primary somatosensory cortex and thalamus in awake mice performing behaviour. The membrane potential of nearby cortical neurons undergo slow large amplitude fluctuations that are highly correlated during quiet wakefulness, but when mice start to move their whisker, to sense their local tactile environment, cortical neurons depolarise and undergo a change in state that reduces both the correlation between the neurons and the amplitude of membrane potential fluctuations, resulting in a desynchronised local field potential and electroencephalogram. The change in cortical state is generated internally within the brain as it is not the result of sensory feedback from the whisker pad and can be mimicked by thalamic optogenetic stimulation.

Boattrip MS Konstanz: Harbour / 19:45

Award of the “Werner-Rathmayer-Preis” and Posterprizes

Monday, September 24, 2012

Key Note: Chair - Axel Meyer A 600 / 08:30

David Reznick (University of California-Riverside)

Experimental Studies of the Interaction between Ecology and Evolution in a Natural Ecosystem

Author: *David Reznick*[1]
Affiliation: [1]*University of California-Riverside*

Our traditional perspective of the relationship between ecology and evolution is that ecology drives evolution. The environment defines a template and evolution by natural selection shapes the organism to fit that template. At the same time, the perspective is that evolution is so much slower than ecology that we can model ecological processes in a fashion that implicitly assumes that evolution does not occur; organisms are treated as constants. A different perspective that has emerged from some theory and laboratory studies, with limited support from nature, is that ecology and evolution are interacting processes that can reciprocally shape one another. I am my colleagues are evaluating this proposition as part of a multidisciplinary study of guppies on the island of Trinidad. Our work was inspired first by the observation that evolutionary interactions happen on time frames comparable to ecological interactions, which makes it more plausible that the two processes can interact. We were also inspired by the role that phenomena like density regulation or the indirect effects of predators appear to have played in shaping some aspects of guppy evolution. Our argument is that “density regulation” and “indirect effects of predators” are actually black boxes created by evolutionary biologists. These labels acknowledge how a process of interest is influenced by other ecological factors without attempting to name or characterize what those factors might be. Our current research includes replicate introduction experiments, modeled on those of the past, in which we are integrating ecosystems ecology with evolutionary biology in an attempt to characterize the mechanisms that underlie these labels. Our work also includes replicate, factorial experiments performed in artificial streams and the development of novel, adaptive dynamic theory that defines the consequences of the integration of evolutionary and ecological processes.

Special Guest Lecture: Chair - Giovanni Galizia A 600 / 09:30

Catherine Carr (University of Maryland)

Evolution of sound localization circuits

Author: *Catherine Carr*[1]
Affiliation: [1]*Department of Biology, University of Maryland*

In the vertebrate auditory system, the fossil record shows that tympanic ears evolved independently in mammals, reptiles, and amphibians. New tympanic ears would have conveyed sensitive responses to the brainstem auditory neurons, leading to the parallel evolution of the central targets of the auditory nerve. In this talk I will focus on the organization of sound localization circuits in Reptilia. Examination of these circuits in birds, crocodilians, lizards and turtles has revealed a suite of apparently convergent physiological and morphological features that contribute to temporal coding and localization. The appearance of these features in the different clades reveals the organizational principles of temporal coding circuits.

Public talk and award of the Karl-Ritter-von-Frisch-Medal: A 600 / 19:00

Laudator: Friedrich Barth
Laureate: Horst Bleckmann

Die Welt der Sinne

Tiere nehmen ihre Umgebung mit Hilfe der unterschiedlichsten Sinnesorgane wahr. Gut verstanden sind vor allem die Sinne, über die auch der Mensch verfügt. Dies sind neben dem Tast- und Geschmackssinn der Sehsinn, der Gehörsinn und der Riechsinn. In meinem Vortrag werde ich dagegen vor allem auf die Sinnessysteme und ihre Verhaltensrelevanz eingehen, über die der Mensch nicht verfügt. Dazu gehören die Strömungssinnesorgane der Fische und Amphibien sowie die verschiedensten mechanosensorischen Sinnesysteme bei Spinnen, Tintenfischen, Krokodilen, Seeschlangen und Seehunden. Weitere hochinteressante Sinnesorgane finden sich auch bei den Insekten. So können z.B. pyrophile (feuerliebende) Käfer Waldbrände nicht nur riechen, sondern diese auch mit Hilfe von hochsensitiven Infrarotorganen orten und gezielt anfliegen. Abschließen wird der Vortrag mit Informationen über die morphologischen und verhaltensphysiologischen Anpassungen die es Speikobras ermöglichen, aus bis zu drei Meter Entfernung die Augen eines Angreifers zu treffen. In dem Vortrag wird beispielhaft auch gezeigt werden, dass die vergleichende zoologische Forschung ein wichtiger Ideenlieferant für die bionische Forschung sein kann.

2. Behavioral Biology TALKS

Saturday, September 22, 2012

Invited speaker 1: Chair – tba A 703 / 11:00

Andre Ganswindt (University of Pretoria)

***Omnis amans amens* – Endocrine correlates of male reproductive behaviour in terrestrial megaherbivores**

Author: *Andre Ganswindt*[1/2]

Affiliation: [1]*Mammal Research Institute, Department of Zoology and Entomology, University of Pretoria*; [2]*Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria*

Androgens are considered ‘male sex hormones’, since they are mostly known for their virile and anabolic effects, including an increased probability of aggressive and competitive behaviour. The pivotal role of androgens on male reproductive behaviour is well documented, with males sometimes even undergoing androgen-dependent morphological changes during well-defined breeding seasons. Shifts to alternative reproductive tactics are also hypothesized to be under proximate hormonal control, but only limited data so far exist on the potential role of, and interaction between the hypothalamic-pituitary-gonadal and -adrenal axes in affecting behavioural tactics shown by terrestrial megaherbivores.

The ‘terrestrial megaherbivores' are a select group of mammals that exceed 1000 kg in mass as adults and in total consist of 9 species from the families Giraffidae, Elephantidae, and Rhinocerotidae. In this presentation, I will use a series of case studies to illustrate the reproductive tactics of male African and Asian elephants as well as Giraffe bulls by describing the physical, physiological, and behavioural characteristics associated with the different defined forms of sexual activity. The talk will elucidate the existing reproductive states of male African elephants (*Loxodonta africana*) and document that the different reproductive conditions are associated with quantitative differences in androgen and glucocorticoid metabolite excretion. The presentation will further address the behavioural characteristics and endocrine correlates of reproductive activity in Asian elephants (*Elephas maximus*), considering the phenotypic variation in secondary sexual characters, with respect to the presence of tusks, in this species. Finally, I will briefly report here new results on the endocrinological basis of the sexual active behaviour shown in different classes of giraffe bulls (*Giraffa camelopardalis*).

Chair – tba

☐1 Julie Duboscq A 701 / 16:00

Behavioural trade-offs in macaques: a within-species perspective

Authors: *Julie Duboscq[1], Antje Engelhardt[1], Bernard Thierry[1]*
Affiliation: [1]*German Primate Centre / Georg-August University Göttingen*

In animal societies, the need of individuals to balance the costs and benefits of social life creates numerous behavioural trade-offs. This is especially the case in societies as complex as those of non-human primates. Conflict management strategies are a good example of behavioural trade-offs where aggression is counter-balanced by for example submission and/or affiliation. Macaques (*Macaca sp.*) show a wide range of variation in these strategies despite a similar social organisation. The different species express, amongst others, varying degree of conflict intensity, conflict symmetry and conciliatory tendency. Accordingly, macaques are classified into a 4-grade scale of social tolerance (despotic/grade-1 to tolerant/grade-4). Cross-species comparisons have shown that patterns of conflict management co-vary with each other along the different grades: the degree of conflict intensity is inversely related to the degrees of symmetry and of conciliatory tendency. We were interested in further investigating these relationships within species. We studied the tolerant crested macaques, M. nigra, to test specifically whether the three social traits under investigation were interrelated and, if so, in the same way as in the inter-species analysis. As expected, conflict symmetry was positively related to conciliatory tendency but unexpectedly, conflict intensity was not negatively but positively related both to conflict symmetry and to conciliatory tendency. Our results support the hypothesis that the three investigated behavioural patterns form a set of interrelated traits, but also highlight species-specific social strategies. This study shows that the mechanisms responsible for the interrelation of behavioural traits at the proximate level may differ from those found at the evolutionary level.

☐2 Christof Neumann A 701 / 16:15

Stress levels, dominance rank and hierarchy dynamics in wild male crested macaques (*Macaca nigra*)

Authors: *Christof Neumann[1], Michael Heistermann[1], Muhammad Agil[1], Anja Widdig[1], Antje Engelhardt[1]*
Affiliation: [1]*German Primate Centre / Georg-August University Göttingen*

In many animal taxa there is evidence that high social status conveys reproductive benefits. In contrast, costs associated with high social status are much less studied and understood. In male primates, potential costs of high dominance rank are elevated stress levels. This relationship, however, is mostly expected if the social hierarchy is unstable. In this study, we therefore investigate the link between hormonally assessed stress levels and dynamics in rank relationships. On the individual level, we will determine whether changes in glucocorticoid levels differ between individuals that rise as opposed to decline in rank. On the group level, we will test whether during periods of instable hierarchies there is a positive relationship between glucocorticoid levels and dominance rank and whether in stable periods this relationship is reversed. The study was conducted in the Tangkoko Nature Reserve on Sulawesi, Indonesia, on males in two wild groups of crested macaques (Macaca nigra). Crested macaques are an ideal study system to address our study questions since rank changes are frequent as are migrations of males between groups and subsequent instable periods. We collected 662 fecal samples from 29 males over the course of 16 months (median: 26 samples per male, range: 1 - 43). Glucocorticoid levels were assessed by means of a recently validated 3alpha, 11beta-dihydroxy-etiocholanolone assay. Individual rank trajectories and hierarchy stability were derived from Elo-ratings, allowing for a novel way of quantitatively assessing hierarchy dynamics. We will discuss our results in the light of the increasing interest in the relationship between social status and stress physiology. Our results will thereby contribute to the growing body of data on benefits and costs of status and stress in social animals in general and primates in particular.

☐3 Oliver Schülke A 701 / 16:30

The evolution of coalitions among male primates - empirical test of a mathematical model

Authors: *Oliver Schülke[1], Andreas Berghänel[1], Annie Bissonnette[1], Bonaventura Majolo[2], Christopher Young[1], Julia Ostner[1]*

Affiliations: *[1]Courant Research Centre Evolution of Social Behaviour, Georg August University Göttingen, Germany; [2]School of Psychology, University of Lincoln, UK*

Male coalitions against other males, i.e. joint aggression of at least two males against a common target, can take several forms and have different adaptive functions. The dominance rank constellation in a coalition may be all-down when the allies rank above the target, all-up when the allies rank below the target and bridging when the target ranks between the allies. Coalitions may lead to changes in dominance ranks or may level the rank-related distribution of payoffs. A mathematical model by Pandit and van Schaik built to predict the occurrence of different form/function combinations considers the feasibility of coalitions (the degree of allies? added power exceeding the target's power) and their profitability (ratio of costs in terms of energy spent and potential injury to benefits in terms of increased reproductive success) and identifies the strength of contest competition among males as the main driver of variation in coalitionary behavior. Here we use predicted and observed male mating skew and paternity skew as measures of contest competition and use data on a captive group of Barbary macaques (*Macaca sylvanus*) from Affenberg Salem, Germany, two wild groups of Barbary macaques from Azrou, Morocco, and one wild group of Assamese macaques (*Macaca assamensis*) from Phu Khieo Wildlife Sanctuary, Thailand, to investigate predictions of the Pandit/van Schaik model. The model failed to reliably predict coalition formation. Between species contrasts were not predicted by the model. Despite similar contest potential patterns of coalition formation and adaptive contexts varied markedly within species and even within the same group across time. We conclude that the Pandit/van schaik model is incomplete and propose additional factors, i.e. male age, immigration status and female mating preferences, to be included in future models of coalition formation in primates.

Funding for this project was provided by the Max Planck Society and the German Initiative of Excellence to the University of Göttingen.

☐4 Julia Ostner A 701 / 16:45

Stable heterosexual friendships in promiscuously mating wild Assamese macaques (*Macaca assamensis*)

Authors: *Julia Ostner*[1]*, Linda Vigilant, Jyotsna Bhagavatula, Mathias Franz, Oliver Schülke*

Affiliation: [1]*Courant Research Centre Evolution of Social Behaviour, University of Göttingen*

Cercopithecine males frequently associate with females and their infants or individual immatures. Male-female(+infant) and male-infant associations have been interpreted as a male strategy to either increase the likelihood of future mating privileges with the respective females (mating effort hypothesis) or to increase the survival of their infants (paternal care hypothesis). Using behavioral and genetic data from our study group of Assamese macaques (*Macaca assamensis*) living in their natural habitat at Phu Khieo Wildlife Sanctuary, Thailand, we investigated male-female and male-infant association during a 5-year study period. Results revealed significant relationships between male-female spatial association and subsequent mating privileges, supporting the mating effort hypothesis. After birth, paternity significantly predicted the time a male and an infant spend together during the first three months of infancy, when infants are still closely associated with their mothers, as well as up to one year after birth. Thus, in our study system where females typically conceive only every other year, it seems that predictions from both hypotheses are met and male-female preferences are stable in the medium term. Further analyses on the relationship between mating history and male-female and male-infant behavior will illuminate the underlying mechanisms responsible for heterosexual associations and paternal care.

Funding for this project was provided by the Max Planck Society and the German Initiative of Excellence to the University of Göttingen.

☐5 Wolfgang Goymann A 701 / 17:00

Parental effort in socially monogamous white-browed coucals (*Centropus superciliosus*) and classically polyandrous black coucals (*C. grillii*)

Author: *Wolfgang Goymann*[1]

Affiliation: [1]*Max-Planck-Institut for Ornithologie*

The black coucal is the only altricial bird species with an obligate classical polyandrous mating system. In this mating system sex-roles are reversed resulting in female competition for territories (and access to males) and sole male parental care. It has been suggested that this unusual mating system is possible in black coucals, because - in contrast to closely related coucal species - this species relies on a temporally superabundant food resource, thus enabling females to quickly gather resources to lay a large number of eggs within a short period of time and at the same time allowing males to raise a brood without help from the female partner. I tested this idea by comparing the breeding phenology of black coucals with a close congener, the white-browed coucal. The white-browed coucal is socially

monogamous and both parents provide parental care at approximately equal rates. I compared the parental effort between black and white-browed coucals and conducted an experiment during which I temporarily removed one partner to investigate whether the remaining partner is able to compensate and adjust its feeding rate accordingly. The results of this study and its implications for current ideas regarding the evolution of sex-role reversal in black coucals and birds in general will be presented and discussed at the meeting.

☐6 Hanna Kastein A 701 / 17:15

Discrimination of individuals by vocal communication in a bat, *Megaderma lyra*

Authors: *Hanna Kastein*[1], *Rebecca Winter*[1], *AK Vinoth Kumar*[2], *Sripathi Kandula*[2], *Sabine Schmidt*[1]

Affiliations: [1]*Institute of Zoology, University of Veterinary Medicine Hanover Foundation,* [2]*Department of Immunology, School of Biological Sciences, Madurai Kamaraj University, India*

A discrimination of group members from unfamiliar conspecifics may be crucial for the fitness of individuals living in social groups. In mammals, vocalizations often carry individual signatures which are a necessary, though not sufficient, prerequisite for an acoustic discrimination and recognition of individuals. Bats are nocturnal, socially living mammals with rich vocal repertoires for communication. They constitute an outgroup to primates and are thus an ideal model for comparative studies on the evolution of vocal recognition in mammals. In isolation situations, *M. lyra* emits contact calls with individual signatures which may guide reunions with group members. We investigated the perception of contact calls from social partners, and unknown individuals of a different group in habituation-dishabituation experiments and analysed the acoustic features *M. lyra* uses for discrimination. The bats responded to any new stimulus used for dishabituation, but reactions were stronger to dishabituation stimuli from social partners and an unknown individual than to a novel stimulus from the same bat, suggesting a discrimination of individuals. After a dishabituation stimulus from a social partner, bats showed a release from habituation which may indicate a recognition of individuals. As in primates, vocal communication may thus be sufficient for a discrimination of individuals. A model reveales that *M. lyra* may separately evaluate the dissimilarity in the syllable frequencies, syllable durations and inter-call intervals with respect to learned memory templates for this discrimination.

Supported by the DFG SCHM 879/6-3.

Sunday, September 23, 2012

Invited speaker 2: Chair – tba A 702 / 11:00

Jana Uher (Berlin)

Personality differences in nonhuman animals: Concepts, approaches, and methods of measurement

Author: *Jana Uher*[1]

Affiliation: [1]*Freie Universität Berlin*

Many animal species exhibit pronounced individual-specific behavioural phenotypes commonly construed as personality or temperament differences. Their relevance for ecological and evolutionary research questions is increasingly recognised, but the conceptual and methodological foundations needed for their empirical investigation are still not well established. I discuss three meta-theoretical core issues of personality research that I illustrate with empirical examples from my research on non-human primates. First, I elaborate three defining criteria needed to disentangle individual-specific patterns from random individual variation in behavioural data. Two principal perspectives on individuals can thereby be taken. Variable-centred analyses focus on populations and explore between-individual differences. Individual-centred analyses focus on the single individuals and their unique configurations of behavioural patterns. Both perspectives are needed to understand why cross-situational consistency of individual behaviour is often only moderate, and in which ways the individuals' responses to different situations can be individual-specific. Second, I discuss different methodological approaches used to decide which behaviours to study for meaningful individual differences, and discuss their advantages and limitations for comprehensive investigations of individuals. Third, I show how personality differences can be measured reliably in controlled experiments and group observations, and also discuss intuitive judgments by human observers that gain increasing popularity among some animal researchers. I highlight that their apparent advantages over ethological measurements, such as higher correlations among behaviours or across situations, may derive from biased perceptions and ascriptions of human observers that can, but need not accurately reflect the behavioural reality of animal individuals.

Chair: Neumann

☐7 Irene Maria van den Heuvel A 704 / 14:00

Land or Lover - Territorial defence and mutual mate guarding in a duetting songbird

Authors: *Irene M. van den Heuvel*[1]*, Michael I. Cherry*[1]*, Georg M. Klump*[1]

Affiliation: [1]*Carl von Ossietzky University Oldenburg*

Avian duets are joint acoustic displays where two birds, usually a pair, coordinate their songs with a remarkable degree of temporal precision. Several studies have been conducted to test the function of duets in different species and experimental evidence suggests that duetting serves a variety of functions. We investigated duetting in the Crimson-breasted Shrike Laniarius atrococcineus (Malaconotidae). The focus of our study was on two major functional hypotheses: the joint territorial defence (Land) and the mate-guarding (Lover) hypothesis. Both hypotheses predict increased duetting in response to conspecific playback; the critical distinction is in the relative threat posed by duets and same-sex solo intruders. If duets serve as mate-guarding, signaling of solo same-sex intruders will receive the strongest response, whereas if territorial defence is the main function, signaling of paired intruders will receive stronger responses than single intruders. The playback experiments revealed, that females answered their partner?s song to form duets significantly more often during female solo playback, suggesting that female duet contributions serve to guard their males from unpaired females. Males were equally aggressive towards male solo playback and duet playback, but they produced more solo song during male solo playback and showed more jamming during duet playback. Solos used in response to male- solo playback indicate that territorial males may guard their females from intruding males to prevent them from copulating with their mates. Males additionally perform territorial defence, mostly through solo song but get some support from their female who occasionally joins them to perform duets.

Study supported by a grant from the Deutscher Akademischer Austausch Dienst (DAAD)

☐8 Katja Heubel A 704 / 14:15

Bad choosiness? Female competition makes females picky

Author(s): *Katja Heubel*[1]
Affiliation(s): [1]*University of Tübingen*

Competition among females for access to mating opportunities and its effect on female mate choice decisions are poorly studied so far. Under natural conditions, female common gobies (Pomatoschistus microps) often compete for access to mates. The operational sex ratio is often female-biased and hence availability of nests and paternal care limited. Female-female competition can be expected to affect female decisions on mate choice and reproductive effort. With an increasing level of female competition for access to mates, there is a trade-off between choosing the best male and missed mating opportunities. I studied the effect of a female-competitive social environment on female mating decisions for male and nest quality. Female preferences and mating decisions for male size and nest size were tested either in presence or absence of competitive females. Surprisingly, females prefer males with larger nests regardless of the social environment. Preferences for male size, however, highly depend on the social context.

☐9 Inon Scharf A 704 / 14:30

Characterizing the collective personality of ant societies

Authors: *Inon Scharf[1], Andreas Modlmeier[1], Susanne Foitzik[1]*
Affiliation: [1]*Johannes Gutenberg University of Mainz*

Animal groups can show consistent behaviors like solitary animals. We studied the collective behavior of Temnothorax nylanderi ant colonies, including consistency in behavior and correlations between different behavioral traits. We focused on four collective behaviors (aggression against intruders, nest relocation, removal of infected corpses and nest reconstruction) and also tested for links to the immune defense level of a colony and a fitness component (per-capita productivity). Behaviors leading to an increased exposure of ants to micro-parasites were expected to be positively associated with immune defense measures and indeed colonies that often relocated to other nest sites showed increased immune defense levels. Besides, colonies that responded with low aggression to intruders or failed to remove infected corpses, showed a higher likelihood to move to a new nest site. This resembles the trade-off between aggression and relocation often observed in solitary animals. Finally, one of the behaviors, nest reconstruction, was positively linked to per-capita productivity, whereas other colony-level behaviors, such as aggression against intruders, showed no association, albeit all behaviors were expected to be important for fitness under field conditions. In summary, our study shows that ant societies exhibit complex personalities that can be associated to the physiology and fitness of the colony. Some of these behaviors are linked in suites of correlated behaviors, similar to personalities of solitary animals.

☐10 Jürgen Trettin A 704 / 14:45

Experimentally induced queen-queen aggression in low-skew populations of a socially polymorphic ant

Authors: *Jürgen Trettin[1], Thomas Seyferth[1], Jürgen Heinze[1]*
Affiliation: [1]*Biologie I, Universität Regensburg*

How reproduction is partitioned among members of animal societies varies widely among different taxa. Over the last decades, optimal skew theory has become the preferred framework to explain how the conflict over the amount of reproduction shared among group members can be solved. However, skew theory has been repeatedly criticized, as its numerous models make conflicting predictions and rely on untested assumptions. For example, models assume that individuals can freely choose whether to join or to leave a group or whether to share reproduction with group members or not. Thus, the question arises: is the observed variation in reproductive skew based on the decision of individuals, or are individuals genetically disposed to either fight, tolerate, or leave a rival reproductive? The answer to this question is of fundamental importance for the robustness and explanatory value of skew theory. We tested this basic assumption by experimental manipulation of socio-environmental factors in a social insect society. Here, we show that queen antagonism associated with high-skew in natural populations can be induced experimentally in colonies from low-skew populations. This indicates a response to environmental factors in behavioral rather than evolutionary time.

☐11 Taina Conrad A 704 / 15:00

The role of vibrational communication in mason bees

Authors: *Taina Conrad*[1], *Robert J. Paxton*[1], *Manfred Ayasse*[1]
Affiliation: [1]*Experimentelle Ökologie, Universität Ulm*

Vibrational signals are used by various species when communicating, and commonly play an important role in mating. Even though many bee species are known to emit vibrational signals during mating, there are almost no studies on the function of these vibrations. Vibrational signals are produced by bees through vibrations of the thorax, as in the precopulatory mating behavior of *Osmia rufa*. We hypothesized that a female might use these thorax vibrations to choose a suitable mate and, if these signals are species-specific, they can also be used as species isolation barriers. In order to investigate the function of these thorax vibrations, we measured and compared the accepted and rejected male vibrations during precopulation using a laser vibrometer. For the role as a pre-mating isolation barrier we investigated vibrations of O. rufa from England, Germany and Denmark and of the sister species *O. cornuta*.

Our results clearly showed that male vibration burst length was significantly longer in accepted than in rejected males (Conrad, Paxton et al. 2010). Vibrations may therefore indicate vigor and assure that the males selected by females are in fact the healthier ones. Furthermore we found significant differences in the frequency and modulation of vibrational signals between *O. rufa* and *O. cornuta* and between the subspecies of O. rufa, supporting our hypothesis that they might have an additional function as a pre-mating isolation barrier. Based on these results we conducted bioassays to further investigate how vibrational signals are used by the bees. For these we used an interesting new technique involving magnets and an inductor to experimentally change the bees vibrations.

We would like to thank the DBU for funding this project.

Conrad, T., R. J. Paxton, et al. (2010). Female choice in the red mason bee, *Osmia rufa* (L.) (Megachilidae)." Journal of Experimental Biology."

☐12 Hellena Binz A 704 / 15:15

Antipredator behavior in the wood cricket *Nemobius sylvestris* varies among distinct spider species and their biological traits

Authors: *Hellena Binz*[1], *Roman Bucher*[1], *Florian Menzel*[1], *Martin H. Entling*[1]
Affiliation: [1]*Johannes Gutenberg University Mainz*

Predators affect their prey not only via consumption, but also through non-consumptive effects. These effects, e.g. changes in prey behavior, often exceed effects through consumption. Spiders are dominant predators in almost all terrestrial ecosystems and prey on a wide range of arthropods. Therefore spiders can elicit strong antipredator behavior in insects and influence ecosystem functioning.

We investigated the occurrence and strength of antipredator behavior (APB) of the wood cricket *Nemobius sylvestris* towards 14 widespread and common hunting spider species by performing two different behavioral arena experiments. Mobility of crickets was recorded (1) either in presence or absence of spider cues in separate arenas to analyze behavioral changes per se, and (2) in one arena partly covered with spider cues, where the crickets could choose between cue-bearing and cue-less areas.

Crickets showed both strategies of APB (freeze or escape) which led to a significant difference in cricket mobility among the investigated spider species. If crickets were exposed to spider cues only, the magnitude of behavioral change increased significantly with increasing predator-prey body-size ratio. If crickets could choose between spider cues and control, their mobility was significantly higher on cues of diurnal spider species, and the change in mobility correlated significantly with spider abundance.

We assume that wood crickets can distinguish between their predator species and respective sizes resulting in predator-prey specific APB's. Astonishingly wood crickets tried to escape more often in the former presence of abundant and diurnal predators, suggesting the capability of olfactory memory for predation risk.

Monday, September 24, 2012

Chair: Duboscq

☐13 Dominic Kugel A 701 / 16:00

Early memory phases in *Nasonia vitripennis*

Authors: *Dominic Kugel[1], Daria Schurmann[1], Johannes Steidle[1]*

Affiliation: *[1]Universität Hohenheim*

During recent years, the wasp *Nasonia vitripennis*, a parasitoid of fly pupae became established as an important model organism for the study of learning and memory formation in parasitic wasps. Whereas longer lasting memory forms as long-term memory are relatively well studied in this species, nothing is known on earlier memory forms, like anaesthesia sensitive memory (ASM). The data obtained from this study suggest that there is a small time window of less than five minutes after training, where the reaction to a learned odour can be blocked up to 1 hour after training by exposing wasps to CO2. When applying CO2 at 5 or 15 minutes after training, the effect is still visible, but much less pronounced. This phase is most likely equivalent to ASM (anaesthesia sensitive memory), observed in other animals, which is replaced by a phase insensitive to CO2-treatment (ARM-anaesthesia resistant memory). ARM most likely ends at 45 to 60 minutes after training and is replaced by some form of medium term memory, which cannot be inhibited by hypoxia directly after training. Combined with earlier data, our study represents the first complete memory structure for olfactory learning in *N. vitripennis*.

☐14 Hanneke Poot A 701 / 16:15

Song learning and tutor choice in a multi-tutor environment

Authors: *Hanneke Poot*[1]*,Andries Ter Maat*[1]*, Lisa Trost*[1]*, Manfred Gahr*[1]

Affiliation: [1]*Max-Planck-Institute for Ornithology*

Male Zebra Finches sing repetitions of unique song motifs that consist of 3 to 14 syllables, which are learned by imitation of adult tutors during a sensitive phase in early life and do not change during lifetime. Wild Zebra Finches live and breed in large flocks with many potential song tutors, but it is assumed that juveniles imitate the song of their fathers rather than that of others. The aim of our study was to test whether juvenile Zebra Finches growing up in a controlled multi-tutor environment really prefer their (genetic/social) father's song for imitation, or prefer other song tutors. Songs of 40 young Zebra Finches from 4 different aviaries were recorded and analysed with several methods. It was found that these birds learned song syllables rather than complete song motifs. Furthermore, clear preferences for certain adult tutors were found, whereas some adult males were never learned from, although these males did not differ in any way (body size, behaviour, song quality) from the others.

We found that the preferred tutors were not necessarily the (genetic and/or social) fathers, and then tested various alternative hypotheses for tutor preferences. Furthermore, we posed the question whether juvenile Zebra Finches really choose a tutor; or rather choose a convenient song model, and how our results fit into the theory of song template learning.

☐15 Stefan Leitner A 701 / 16.30

Environmental and genetic control of brain and song structure in the zebra finch

Authors: *Stefan Leitner*[1]*, Joseph L. Woodgate*[1]*, Andrew T.D. Bennett*[1]*, Clive K. Catchpole*[1]*, Roswitha Brighton*[1]*, Katherine L. Buchanan*[1]*,*

Affiliation: [1]*Max Planck Institute for Ornithology, Department of Behavioural Neurobiology*

Birds and humans are unique in possessing brain regions dedicated to learned vocal communication, which has evolved through direct selection on these structures. The strength of selection is in part determined by genetic control of trait expression which ultimately determines fitness. In order to quantify the environmental and genetic control of song and brain structures in the zebra finch, we partially cross-fostered nestling zebra finches, raised under control conditions or conditions of nutritional restriction. We measured song structure and the volumes of key brain nuclei in the song control system of fathers and sons. We found low heritability of neuroanatomy and song structure, indicating that song does not signal heritable quality either directly or via heritable differences in susceptibility to developmental stress. HVC volume was uniquely susceptible to environmental regulation, highlighting the potential for song to provide an honest signal of phenotypic quality. Our study demonstrates the fundamental importance of environmental conditions for vocal learning and neural development in songbirds and suggests that selection acts on the genes determining vocal learning, rather than directly on the underlying neuroanatomy.

☐16 Ingo Rischawy A 701 / 16:45

Archerfish adjust a rapid motor decision to changed environmental laws

Authors: *Ingo Rischawy*[1], *Stefan Schuster*[1]
Affiliation: [1]*Animal Physiology, University of Bayreuth*

Archerfish (*Toxotes sp.*) shoot down objects from above the water level and secure it with their so-called predictive start: based on the initial motion of a dislodged target they infer its later landing point and trigger a fast-start to reach it before competitors are attracted by the splash. In the present study we experimentally shift the law that naturally connects the initial motion of a dislodged object (height, direction and velocity) to the point of impact on the water surface. Here we demonstrate that fish that responded correctly to all combinations of initial motion parameters under natural conditions made errors after the law was changed. Surprisingly this error decreased with increasing practice over time, showing a remarkable readjustment to the new conditions. This tuning of a complex motor decision suggests an outstanding degree of plasticity in the small circuit of identified neurons that triggers the predictive start of archerfish. It provides an ideal basis for further investigations on how dynamic environmental conditions are represented and stored in the vertebrate brain.

☐17 Anja Weidenmüller A 701 / 17:00

Nest temperature homeostasis in a social insect: How bumblebee colonies (*B. terrestris*) control the temperature of their brood

Authors: *Anja Weidenmüller*[1], *Marco Smolla*[1], *Mirta Jacobs*[1], *Christoph Kleineidam*[1]
Affiliation: [1]*Universität Konstanz*

Like many social insects, bumblebees are able to manipulate the climatic conditions inside their nests. Even under strongly fluctuating environmental conditions, brood temperature is maintained at around 30°C. This nest-temperature homeostasis is based on division of labor among the workers of the colony; it ensures rapid and safe development of the brood.

In order to understand how collective patterns like nest temperature homeostasis emerge, we need a solid understanding of the individual response-behavior underlying these patterns; and of the mechanisms that integrate the responses of the numerous workers of a colony into a functioning unit. Control of nest temperature in bumblebees is a good model system to address these questions. The two thermoregulatory measures employed by bumblebees are incubation (to increase temperature) and wing fanning (to increase evaporative cooling).

We analyze the stimuli involved in the individual response decision for thermoregulative behavior. Based on measurements within undisturbed colonies and experiments using temperature-controlled brood dummies, we show that both wax-temperature and olfactory cues modulate individual response behavior. We further show that thermoregulative behavior is adjusted to the age of the brood.

Workers within a colony differ in their thermoregulative response behavior. Such inter-individual variability is believed to be crucial for the emergence of nest-temperature homeostasis and of division of labor in general. We experimentally test this hypothesis by creating worker groups that differ in the degree of inter-individual variability in their fanning response; we show that response behavior in bumblebee workers is highly flexible and modulated by the social environment.

☐18 Jakob Krieger A 701 / 17:15

Giant Robber Crabs (*Birgus latro*) monitored from space GPS-based telemetric studies on Christmas Island

Authors: *Jakob Krieger*[1], *Ronald Grandy*[2], *Michelle Drew*[2], *Susanne Erland*[2], *Marcus S. Stensmyr*[2], *Steffen Harzsch*[1], *Bill S. Hansson*[2]

Affiliation: [1]*Ernst Moritz Arndt University of Greifswald, Zoological Institute and Museum, Cytology and Evolutionary Biology*; [2]*Max Planck Institute for Chemical Ecology, Department of Evolutionary Neuroethology*

The giant robber crab *Birgus latro* (Linnaeus, 1767) (*Anomura, Coenobitidae*) is the largest land living arthropod and its populations are distributed over small Indo-pacific islands as for example Christmas Island (Indian Ocean). Although, many anatomical, physiological, and ecological studies on *B. latro* exist, behavioral analyses of these animals are surprisingly rare. To investigate the migratory behavior in *B. latro*, GPS-based telemetric studies on an arthropod were conducted for the very first time. The experiments were carried out in Christmas Island's rain forest during the wet seasons in 2008 and 2010, and during the dry season in 2011. In total, we equipped 56 male robber crabs with GPS-tags along a defined transect and data were sampled constantly. Besides territorial behavior with small-distance excursions, our data show large-distance migrations of robber crabs between the coast and the rain forest further inland as well. Large distance migrations occurring mainly during the wet season are likely related to mating, but can also be food and saltwater directed. A subgroup of twelve specimens was translocated to different directions showing that animals were capable of homing over large distances. By displacement induced searching behavior, our data indicate at least two possible navigation strategies including route following and path integration.

3. Behavioral Biology POSTERS

♦1 Karl Radtke

Transient response to early life stress in a poeciliid Fish

Author: *Karl M. Radtke*[1/2], *Helen M. Gunter*[2/3], *Axel Meyer*[2]
Affiliation: [1]*Department of Psychology, University of Konstanz and Center for Psychiatry Reichenau*; [2]*Lehrstuhl für Zoologie und Evolutionsbiologie, Department of Biology, University of Konstanz*; [3]*Zukunftskolleg, University of Konstanz*

Human personality traits and their associated behaviors are believed to be established through a combination of genetic and environmental factors. In particular, early life stress (ELS) i.e. stress during sensitive periods of development can have lifelong effects on behavior and mental health. Recent studies suggest, that also animals, such as rodents, display a sustained behavioral response to ELS. Our research focuses on the influence of ELS on behavioral traits along the boldness-shyness continuum in a teleost model, the poeciliid fish Heterandira formosa. We simulated predator stress in juvenile *H. formosa* through daily chasing with a net. Boldness related behavior was then quantified immediately after completion of the treatment and after four additional weeks through applying an open field and an emergence test paradigm. ELS strongly reduced boldness related behavior as stressed fish displayed less exploratory behavior and greater latencies to emerge compared to the unstressed control group. However, four weeks after the removal of the stressor the effect was no longer observed. The transience of this predator-induced shyness might reflect the dynamic ecological conditions of the freshwater streams inhabited by wild populations of *H. formosa.*

♦2 Anthi Apostolopoulou

Neuronal output from different subsets of Mushroom Body Kenyon Cells is necessary for different types of associative olfactory learning

Authors: *Anthi Apostolopoulou*[1], *Andreas Thum*[1]
Affiliation: [1]*University of Konstanz*

The Mushroom Body of *Drosophila melanogaster* was shown in flies and larvae to be the centre of associative olfactory learning and memory. However, it is largely unknown how the conditioned and the unconditioned stimulus are processed within this higher order brain region. Using Drosophila larvae as a model I have analyzed how neuronal output of mushroom body Kenyon Cells is necessary for associative olfactory learning reinforced by sugar, salt and electric shock. Taken together,neuronal output from different subsets of mushroom body Kenyon Cells is necessary for each type of learning. This distinction doesn´t only occur between appetitive and aversive reinforced olfactory learning but likely goes even further to distinguish between different types of aversive associative olfactory learning.

◆3 Lars Lewejohann

Spatial Learning and Corticosterone Stress Response in 5-HTT Knockout Mice

Authors: *Lars Lewejohann*[1], *Sandra Grauthoff*[1], *Rebecca Heiming*[1], *Sylvia Kaiser*[1], *Angelika Schmitt*[1], *Norbert Sachser*[1]
Affiliation: [1]*Dept. of Behavioural Biology, University of Muenster*

Serotonin transporter (5-HTT) knockout mice display a number of phenotypic changes especially regarding anxiety related behavior. 5-HTT is highly expressed in cortical areas involved in cognitive functions, implying also an important role in learning and memory. Moreover, cognitive processes are strongly influenced by emotionality and are modulated by stress-related hormones. In the present study we evaluated whether spatial memory is affected by 5-HTT genotype and differences in the aversiveness of testing conditions. Therefore 5-HTT knockout mice, heterozygous 5-HTT mice, and wild-type controls have been subjected to a 5-day series of repeated trials in either a water maze (WM) or a barnes maze (BM). An additional group of mice was used to measure plasma corticosterone concentrations (CORT) related to the different testing procedures.

5-HTT knockout mice performed significantly worse compared with heterozygotes and wild-types in the WM but not in the BM. Both learning tests led to significantly increased CORT. CORT measured after the WM did not differ from CORT measured after the BM in heterozygotes and wild-types but CORT of 5-HTT knockout mice was noticeably higher after the WM. We suggest that this exaggerated stress reaction contributes to the performance differences between the genotypes that were found in WM learning.

This study was supported by the German Research Foundation (SFB/TRR58, Project A1).

◆4 Annekatrin Widmann

High resolution setup for olfactory learning experiments in Drosophila larvae

Authors: *Annekatrin Widmann*[1], *Andreas Thum*[1]
Affiliation: [1]*Universität Konstanz*

Drosophila flies and larvae have a given repertoire of behavioral strategies in order to interact with their environment. In order to react properly to external stimuli they have to plan behavioral goals and break them down into a sequence of smaller tasks. Even past experience influences the planning of such behavioral goals, thereby introducing an additional variable into the system. By combining associative olfactory learning and high-resolution behavioral tracking in Drosophila larva we are analyzing the behavioral changes that occur during olfactory learning that finally lead to the expression of a particular sequence of smaller task in order to achieve a behavioral goal. In detail, we have focused on the molecular basics of learning and memory by using the two classical learning mutants amnesiac and radish that show a significant impairment in associative olfactory learning. In the longer run our result may lead to an initial understanding of the molecular pathways that organize a sequence of task relevant for learning and memory.

♦5 Nicole Prinz

The influence of Δ9-tetrahydrocannabinol administration on retrieval of spatial memory in the zebrafish (*Danio rerio*)

Authors: *Nicole Prinz*[1]*, Tim Ruhl*[1]*, Gerhard von der Emde*[1]
Affiliation: [1]*Institute of Zoology, Department of Neuroethology/ Sensory Ecology, University of Bonn*

While spatial memory has been intensely investigated in mammals, such as in mouse or in rats, little focus was set on the spatial memory of lower vertebrate, such as fish.
Spatial memory in teleost fish is thought to be located in the dorsolateral area of the caudal telencephalon. This area appears to be homologue to the hippocampal formation, which has been identified as the center of spatial memory formation in mammals. In these regions, the density of ?9-tetrahydrocannabinol (THC) sensitive CB1 receptors is very high in both fish and mammals. CB1 as well as CB2 receptors belong to the endocannabinoid system of vertebrates and are activated by cannabinoids. We therefore conclude that the endocannabinoid system might influence spatial memory in fish, like it does in mammals.
We used the tropical freshwater fish, Danio rerio, and examined the influence of the pharmacologically-active substance THC on this fish`s spatial memory.
Fish had to learn the position of a small food item in an open-field maze by using an ego-allocentric orienting strategy. With termination of the acquisition phase and memory consolidation, THC was administered and its effect on retrieval of memory was tested. Within 14 days, the latency to find the reward decreased from an average of about 90s to about 10s, indicating that the fish had learned the position of the reward. Two hours in water with THC (0,0314µg/l) led to an increase in search times to about 50s, i.e. near pre-training levels. Thus we conclude that the activation of CB1 receptors has a strong influence on retrieval and functional aspects of spatial memory in zebrafish.

♦6 Theodora Fuss

Do sharks have a cognitive spatial map?

Authors: *Theodora Fuss*[1]*, Horst Bleckmann*[1]*, Vera Schluessel*[1]
Affiliation: [1]*Universität Bonn, Institut für Zoologie, Abteilung für vergleichende Neurobiologie*

This study assessed spatial learning and memory in the grey bamboo shark (*Chiloscyllium griseum*) and the coral cat shark (*Atelomycterus marmoratus*). As complex spatial memory functions, including a cognitive spatial map, had already been described in stingrays (*Potamotrygon motoro*, Schluessel & Bleckmann 2005) it was hypothesized that sharks can also learn and apply an allocentric orientation strategy. Eight out of twelve sharks reached the learning criterion of 70% correct choices on three consecutive sessions in a two choice alternative spatial task based on allocentric strategies. Seven different types of Transfer tests revealed that sharks predominantly used visual cues to complete the task, thereby constructing a cognitive spatial map of their surroundings. These results correspond to earlier studies on stingrays (Schluessel & Bleckmann 2005), goldfish (Carassius auratus, Salas et al 1996) and mammals (O'Keefe & Nadel 1978, Gallistel 1990). Assuming that ablation of the medial pallium would cause similar impairments in spatial learning and memory functions as lateral pallial ablations cause in goldfish (Salas et al 1996), sharks were expected to be impaired in solving a task based on allocentric strategies. Experimental results confirmed this.

In summary, bamboo sharks (1) possess some form of spatial memory, since they can remember a fixed feeding location; (2) can construct cognitive spatial maps of their environment, as most animals in this study were able to approach the feeding location irrespective of single landmarks and altered geometric shapes of the setup and (3) use the visual system to orient. Furthermore, the telencephalon seems to be involved in processing information on allocentric orientation strategies.

♦7 Caroline Reinel

Archerfish can accurately determine three-dimensional distance in less than 100 ms

Authors: *Caroline Reinel*[1], *Stefan Schuster*[1]
Affiliation: [1]*Lehrstuhl für Tierphysiologie der Universität Bayreuth*

Archerfish are well known for their unique hunting-technique: They shoot down aerial prey, e.g. flies with a precisely aimed jet of water. Moreover the marksman or another schooling member subsequently predict the later point of impact of their falling prey merely on the basis of its initial direction, velocity and height, sampled within a very short interval of less than 40-100 ms. Surprisingly, prior information - such as the initial position of the fly or the direction of the shot - have no bearing on the fish?s accuracy or latency. Because all previous experiments were carried out at just one height level it is unclear if the fish would also not need prior information regarding the initial height of their prey. This appears unlikely because the brief sampling interval would seem to prevent usual mechanisms of estimating three-dimensional distance.

To specifically test if the fish could also determine distance without a priori information we create a novel experimental design: In this an initially invisible fly can be sent on a ballistic path from various intial height levels, positions, speed and directions. This prevents the fish from using any a priori information. The arrangement was such that errors in the estimate of initial height would have led to readily detectable errors in the fish's initial aim. Surprisingly archerfish cope with this novel demanding task just as well as with the simple setups: neither latency nor accuracy were impaired. Accordingly archerfish are also able to determine the starting height of falling prey in less than 100 ms.

♦8 Stefan Müller

Tracking program reveals rapid switching from open-loop to closed loop in hunting archerfish

Authors: *Stefan Müller*[1], *Stefan Schuster*[1]
Affiliation: [1]*Department of Animal Physiology, University of Bayreuth*

Archerfish are famous for their hunting strategy. They down prey, e.g. flies, with a jet of water and catch it at the water surface. After a successful shot they have to be fast in order not to lose their food to competitors. Based on a brief sampling of the initial motion of their falling prey they launch an open-loop start that accurately aims right at their prey's later point of impact on the water surface and leads them there even when no further information is available. In our experimental setup we challenged this open-loop strategy: prey moved initially on a ballistic path but then is reflected from an aerial obstacle, so that its aerial trajectory is drastically changed at a defined time. Using a program written in Matlab we could accurately determine the position and orientation of each fish to detect even slight deviations from the initially chosen bearing and thus to work out the time needed as well as the nature of the course corrections after a deflection. Surprisingly archerfish can rapidly detect if their open-loop course will be in error and change not to a new open-loop course but switch to closed-loop guidance.

◆9 Tim Ruhl

The endocannabinoid system and color discrimination in the zebrafish (*Danio rerio*)

Authors: *Tim Ruhl*[1], *Alessandro Clausen*[1], *Gerhard von der Emde*[1]
Affiliation: [1]*Institute of Zoology, Department of Neuroethology/Sensory Ecology, University of Bonn*

The zebrafish (*Danio rerio*) is one of the most important model organisms in developmental genetics and it is increasingly important in behavioral studies. Lesion experiments with other cyprinid fish (Goldfish - *Carassius auratus*) indicate that memory of associative color discrimination is stored in the medial pallium (MP) of the teleost dorsal telencephalon, an area with a high density of cannabinoid receptor 1 (CB1) in the zebrafish. In a two-alternative choice paradigm animals were taught to discriminate between two colors, namely to avoid green and swim towards red. Fish learned to associate different colors either with a reward or a mild punishment. Learning was divided into an acquisition phase, which was finished after seven days of training, followed by memory consolidation for another period of maximal seven days. Learning was indicated by a decrease of the time needed for a decision and by an increase of number of correct choices. After memory consolidation the influence of acute activation of CB1 on memory retrieval was tested by administration of receptor agonist THC (?9-tetrahydrocannabinol). We could show that pharmacological treatment did not impair behavioral performance of zebrafish. Those findings are absolute in agreement with results taken up from investigations done in mammals, which displayed that THC does not disrupt performance of rats in visual two-figures nor in black-white discrimination tasks.

Our data indicate that not only neurochemical anatomy, but also psycho-physiological working mechanisms of endocannabinoid system are highly conserved among vertebrate species.

◆10 André Steiner

Responses of fishes to Kármán vortex streets and artificial fish generated wakes

Authors: *André Steiner*[1]*, Horst Bleckmann*[1]
Affiliation: [1]*University of Bonn, Department of Comparative Neurobiology*

Fish can detect hydrodynamic stimuli with their mechanosensory lateral line. Lateral line information is used for spatial orientation, predator avoidance, schooling and for inner-specific communication. Furthermore, lateral line information is important for Kármán gaiting, i.e. for swimming and remaining in the vortex street caused by a stationary object exposed to running water. Rheophilic fish seek out Kármán vortex streets to save locomotive energy during station holding. In addition some fish use the lateral line to track the vortices caused by the undulatory swimming movements of another fish. We investigated whether fishes (*Rutilus rutilus, Chondrostoma nasus, Onchorynchus mykiss*) can be trained in a two alternative forced choice task to discriminate between laminar flow and flow that contained a vortex street. Under daylight conditions 7 out of 16 R.rutilus, 4 out of 9 *O.mykiss*, and none out of 4 *C.nasus* learned the task if a Kármán vortex street was presented. Two out of the 7 R. rutilus also performed well under infrared illumination. If a vortex street was presented that was generated with an artificial tail fin, only the 4 *O. mykiss* learned the task under daylight conditions. However, no individual was able to track the vortex street in the dark. Although fish can easily be conditioned to respond to the water motions generated by a vibrating sphere only individuals of *R.rutilus* were able to detect a Kármán vortex street in the dark.

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◆11 Sarah Schumacher

Discrimination of object shape during active electrolocation in the weakly electric fish Gnathonemus petersii

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Gnathonemus petersii is a weakly electric fish, which orients in its environment by detecting changes in a self generated electric field caused by objects. They generate electric signals with an electric organ located in the tail and perceive the resulting electric images with epidermal electroreceptors. G. petersii is able to detect properties of object such as position, distance, size, volume, capacity and resistance. During electrolocation, G. petersii is able to discriminate between two objects with different volumes up to a distance of about 4 cm, as shown by previous experiments. In this project, we tested how well Gnathonemus petersii is able to detect the shapes of objects of equal volume. Discrimination performance was assessed by determining up to what distance a fish was able to discriminate between a sphere and either a cube or an ellipsoid. These object shapes were chosen under consideration of physical experiments in order to allow conclusions about the mechanisms of shape recognition. Our results show that the distance threshold for discriminating between a sphere and an ellipsoid is with 2.75 cm about 1 cm further away than for a sphere and a cube with 1.76 cm. Under consideration of the physical background these results imply that instead of using only single electrical 'snapshots' of an object, fish have to make use of temporal modulations of a series of electric images caused by movement to reliably detect object shape.

◆12 Michael Blum

The electric eel economizes on its electric organ discharges, required to paralyze prey until it is swallowed up

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The electric eel (*Electrophorus electricus*) is well known for its ability to generate strong Electric Organ Discharges (EODs) for self-defense and hunting. The electric eel is an obligate mouth breather and dies when access to water surface is denied. Accordingly its mouth mucosa is extremely thin and strong supplied with blood, so it is sensitive and susceptible to injury. To minimize this risk, *Electrophorus electricus* paralyzes its prey with strong EODs. It seems reasonable to think that the shocks are maintained as long as the prey is swallowed up, perhaps as a simple reflex that generates EODs while prey is in its mouth.

Here we show, that *Electrophorus electricus* just uses its strong EODs until the prey is paralyzed, then it switches them off and just restarts pulsing if the prey starts moving again. So the strong EODs are just used when required.

The obvious benefit of this tactic is that the electric eel is able to conserve energy. Furthermore there is another advantage. While the prey is getting shocked, its muscles contract thus fins erect, which could hurt the highly sensitive mouth cavity, especially if the prey has fin rays. So, its economic discharging behavior also keeps *Electrophorus electricus* from worrying about, if prey has fin rays or not.

◆13 Sabine Feyl

Orientation in electric fields: More than line-following in electrosensory predators?

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In contrast to almost all other sensory systems the electrical sense does not seem to allow easy localisation of the sender. A number of thorough studies have convincingly shown that territorial electric fish approach discharging conspecifics by following the current lines and initially without knowing distance and direction to the source of the discharges.

This strategy is safe but useless when the sender deactivates its discharges and it requires more time than a direct approach. Both may be important in a hunting context. According to this we asked if the ability to localise sender position efficiently is better developed in fish that hunt on the basis of electric signals. Such a situation is known for the electric eel *Electrophorus electricus* that preys on the weakly electric fish *Gymnotus carapo*. By mimicking the discharges of Gymnotus we analyse if Electrophorus can take a direct approach to the sender and detect it even when it goes silent.

♦14 Gerhard von der Emde

Electrocommunication behaviour in two species of pulse-type weakly electric fish (Mormyridae, Teleostei)

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Weakly electric fish generate and receive low-voltage electric signals (electric organ discharges, EODs) to sense objects in their close vicinity and for electrocommunication. With epidermal electroreceptors fish can perceive the highly stereotyped species-specific EOD waveforms of conspecifics and thus can recognise each others presence and identity. In addition, pulse-type weakly electric fish can vary the inter-discharge intervals (IDIs) and create temporal situation dependent discharge patterns for electrocommunication.

The current study compared electrocommunication behaviour in two homogeneous groups of freely swimming weakly electric fish of two species. Each group consisted of four individuals of either Marcusenius altisambesi or Mormyrus rume. During different situations such as resting, foraging and aggressive encounters, we searched for behaviourally caused temporal IDI-patterns. Depending on the fish? positions in the experimental tank, it was possible to assign each recorded EOD to an individual sender fish. Thus, we could study the electro-communicative behaviour of every single member in a group. The analysed sequences showed that both species performed complex situation-specific communication patterns, such as synchronised discharging, signalling in a fixed order or echo-responses. By comparing the communication patterns of the two species, we found similarities, e.g. in fixed-order-signalling, as well as differences, such as different IDI-pattern during resting or during aggressive encounters.

♦15 Nadja Grap

Nile crocodiles respond to water surface waves

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Nile crocodiles (*Cocodylus niloticus*) hunt at night, waiting half submerged for large ungulates that approach the water for drinking. In contrast juvenile crocodiles feed on insects that have fallen into the water. The aim of our study was to find out, whether juvenile Nile crocodiles can sense water surface waves, produced by blowing air onto the water surface. Using operant conditioning, juvenile Nile crocodiles were trained to respond to water surface waves. If rewarded with food the crocodiles even in complete darkness responded to a 15 Hz surface wave stimulus by swimming towards the wave source. Threshold amplitude (peak-to-peak water displacement) was 10 ?m at a stimulus frequency of 15 Hz. Most likely the responses were mediated by the dome pressure receptors that are known to be highly sensitive to mechanical stimuli.

◆16 Philipp Krupczynski

Archerfish and the changing world: temperature affects latency but not accuracy of the predictive start

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Archerfish are not only renowned for shooting down aerial insects with powerful jets of water but also for their ability of predicting their prey's later point of impact. Shortly after the prey is dislodged the fish initiate a quick C-shaped turn towards where the prey will later land and move on a straight line towards that position. Archerfish live in mangrove areas from Southeast Asia to Australia. This complex biotope enforces the fish to cover considerable distances in their search for hunting grounds. Thereby the fish may face dramatic and rapid changes in light conditions, salinity and temperature over the course of a few hours. Here we show that the time needed from the onset of prey movement to initiating the C-start (latency) increases strongly with decreasing temperature. However, the precision of their predictive start is not affected by temperature at all. This is surprising, because all underlying circuitry involved in monitoring prey motion, selecting and carrying out the appropriate motor pattern is strongly dependent on temperature. Given the high competition, but also the predation risk of starting archerfish, mechanisms must be at work to ensure that starts are only released when they are appropriately aimed.

◆17 Etienne Campione

Brightness discrimination in the hunting spider *Cupiennius salei*

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Cupiennius salei is a nocturnal spider with eight eyes, divided in two principal and six secondary eyes, which differ morphologically and functionally. They are extremely sensitive (< 0.001 lux) and the spectral sensitivy of the spider range from 365 nm to 675 nm, due to three different types of photoreceptors. In behavioural experiments, however, the animals are shown to be colour blind. On the other hand, the three photoreceptors might be used to provide a good brightness discrimination ability, necessary in the dim habitat of *Cupiennius salei* to discriminate preys and predators. We tested this hypothesis by presenting the spiders square-shaped flickering stimuli on a stationary background, both with variable brightness. The principal eyes have two muscles each whose activity increases when the spider detects a visual stimulus. Thus, when the spider perceives a visible contrast between the stimulus and the background, its principal eye muscle activiy should increase. This activity could be recorded in vivo through a special telemetric device. Our results show that *Cupiennius salei* has a quite good ability in brightness discrimination, a contrast of 0.25 is sufficient to elicit a significant response, except with very dark stimuli, where the minimal contrast needs to be higher. We were also able to calculate the Weber's fraction in order to compare the brightness discrimination ability of *Cupiennius salei* with others animals.

◆18 Paul Anthony Stevenson

Video-tracking movement analysis predicts a cricket's aggressiveness and win chances

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We aim to develop a reliable system for quantifying the aggressiveness of individual animals (crickets). Aggressiveness can normally only be quantified by observing the interactions between animals. However, the resultant scores, such as escalation level and fight duration, give little information on the potential aggressiveness of the individual contestants before they interact. Using an experimental set up similar to that used to quantify the gregarious and solitarious behavioural phenotypes of locusts (Cullen et al., J Insect Physiol. 56:937-42, 2010), we employed the Ethovision video-tracking system (Noldus) to record the activity of adult male crickets moving freely in an arena (27 x 13.5 cm). For each trial we selected 4 similarly sized crickets (weight difference < 5%) and isolated them for two day days, after which time all known effects of social interactions on aggression would have subsided. Each individual was then video-tracked for 5 min, after which the crickets were matched to fight. Winners (W) of the first fight were matched against each other in a second fight, as were the losers (L). This regime resulted in a WW that won twice, a WL that first won and then lost, a LW that lost first and then won, and a LL that lost both contests. Retrospective evaluation of over 40 sets of tracking data revealed highly significant differences between future WWs and LLs, but no significant differences to WLs and LWs. The future WWs, for example, were more active (i.e. total distance moved, total meander and mean velocity all greater) and spent more time in the vicinity of a small group of other male crickets placed behind a clear screen at one end of the arena. The LLs by contrast tended to avoid the other crickets and visited the edges of the arena more frequently. The results show that the win chances of a cricket in an aggressive contest can be predicted from simple behavioural measures, and suggest further that the expression of aggressive behaviour in crickets is inherently different between individuals.

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◆19 Manuela Zapka

Alarm pheromones and their effects on anxiety and escape behaviour in larval zebrafish (*Danio rerio*)

Authors: *Manuela Zapka*[1], *Lisa Täubner*[1], *Marina Kretzschmar*[1], *Stefan Schuster*[1]
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In adult zebrafish alarm pheromones released from injured skin (i.e. during predator attack) trigger a characteristic alarm response in nearby swimming conspecifics. The alarm response is an antipredator behaviour causing a dramatic change in locomotion. This response is characterized by increased shoal cohesion, faster

swimming with spontaneous rapid turns and at least markedly increased bottom dwelling.

So far, many studies described the effects of alarm pheromones on anxiety related behaviour and physiological changes in adult zebrafish but almost nothing is known about the effects on the behaviour in larval zebrafish. Therefore 5-10 days old larvaes were individually exposed under two different experimental conditions to alarm pheromones isolated from adult zebrafish.

First, since anxiety is strongly related to exploration behaviour in adult as well as larval zebrafish, locomotion and exploration were evaluated. Second, to examine a potential effect on escape behaviour, escape responses were triggered and recorded by digital highspeed video. Subsequently latency and duration of the escape responses were analyzed.

The alarm response provides a helpful tool to examine innate fear in a vertebrate system. Moreover this context dependent response can be used to investigate mechanisms of attention and decision making.

♦20 Francesca Santostefano

Linking personality traits, mating behaviour and colouration in the guppy Poecilia reticulate

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In recent years, it has become widely recognized that animals exhibit consistent individual differences (CIDs) in behaviour. However, we have a poor understanding of how these behavioural types are related to an individual's fitness - either survival or reproduction. Because activities such as predator escape, habitat exploration, courtship, etc. are energetically costly, physiological constraints may underlie personality traits and link behaviours across different contexts.

The purpose of this study was two-fold: 1) examine how CIDs in behaviour relate to mating behaviour in males, and 2) test whether colouration can predict behavioural types.

We repeatedly measured the behaviour (activity, feeding, boldness) of isolated male guppies to characterize each individual. We then observed the males interacting with females to assess their energy allocation to displays, sneaky copulations and chasing. We also measured male colouration, a secondary sexual trait, to link personality to phenotype and male quality.

By developing a better understanding of how CIDs in behaviour affect different aspects of individual fitness, we can begin to explore the evolutionary implications of personality.

♦21 Ana Catarina Miranda

Urbanization and the nature of animal personalities: a common garden experiment assessing novelty reactions in the Eurasian blackbird (*Turdus merula*)

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Coping with environmental challenges might have important evolutionary consequences, and individuals within populations often exhibit specific behaviours when dealing with novel situations. Nowadays, coping with urban habitats is a challenge for many animal species, and it is essential to understand how being born in a city can influence animal personalities (behaviours correlated across time and contexts). Many studies report behavioural differences between rural and urban conspecifics from the wild, but it remains unclear whether such differences result from habituation to the urban environment, or from inherent differences between individuals in rural and urban habitats. Using blackbirds (*Turdus merula*) collected from a rural and a nearby urban area and raised under common-garden conditions, we investigated two independent reactions towards novel objects: neophilia (approach) and neophobia (avoidance). These behaviours were consistent over time and across contexts, reflecting the existence of personalities. Blackbirds from the urban population were more neophobic and seasonally less neophilic than blackbirds from the nearby rural area. These inherent differences are likely the result of genetic differences suggesting selection against neophilia and favouring neophobia in the urban habitat.

♦22 Anastasia Krasheninnikova

The parrot and the string: how you eat is what you are?

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Problem-solving tasks such as string-pulling and string-choice tasks are often used to analyse the advanced cognitive abilities in animals, as it requires a large number of different motions in a very precise order to solve a problem never previously encountered, along with the ability to monitor the string. In birds only corvids and parrots seemed to understand the logical structure in the task and solve it without trial-and-error learning. However, inconsistent performances across parrot species suggest different socioecological factors driving success in the string-pulling test. I presented two closely related Australian parrot species the Galah (*Eolphus roseicapilla*), and the cockatiel (*Nymphicus hollandicus*), with a set of string-pulling and string-choice tasks. While both species forage on the ground, only the Galah uses its feet while foraging which was suggested a requirement for the string pulling problem. The performance of the cockatiels demonstrated that for the fine coordinating motor skills it is not necessary to use the feet during foraging. While both species performed equally well in simple string-pulling tasks, the galahs outperformed the cockatiels in 4 out of 5 choice tasks. Performance at the individual level suggests that some birds of both species were able to grasp the logical structure of the tasks, and to visually determine the presence of physical continuity between the string and reward. However, three Galahs but no cockatiels were able to inhibit their preference for a shorter string when it was not connected with the reward. Considerable inter-individual and inter-species differences in task performance are discussed.

♦23 Johanne Martens

Naturalized Amazon parrots in Stuttgart

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Yellow-headed Amazon parrots (*Amazona oratrix oratrix*) have been breeding successfully in the city of Stuttgart since 1986, thus being established Neozoa. In 1999, the first Blue-fronted Amazon parrot (*Amazona aestiva xanthopteryx*) was sighted. Hybrids of the two species exist and produce fertile offspring. The parrots use a broad range of food plants, available in parks, graveyards and gardens. A total of 62 food plant species of 24 plant families, 36 of which are endemic in Europe are known to be used by the parrots. Poisonous plants like Common Yew (*Taxus baccata*) are also taken. The parrots feed on different plant parts such as bark, leaves, shoots, flowers, seeds and fruit. Only some parts of the plucked food are used. The population size at the roost site was counted throughout the year 2011. Just before and during the breeding period, the population size decreased. In some weeks, the nonbreeders were gone as well. One breeding pair consisting of a hybrid male and an *A. o. oratrix* female was observed during their whole breeding period. Copulation, feeding times and the behaviour of the offspring before leaving the breeding cavity were documented. Breeding started at the end of May, one young parrot left the cavity in the end of August. Breeding behaviour was similar to the behaviour known from Amazon parrots kept in captivity.

♦24 Sven Krackow

Automatic dominance hierarchy determination in the IntelliCage

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The IntelliCage consists of 4 corners offering two water bottles each, access to which is controlled by the experimenter. Corners can be visited by mice from a group housed in the IntelliCage. Individual behavior is tracked and corner responses are applied based on RFID transponder identification. A simple competition test revealed social dominance hierarchies between females kept in groups during drinking sessions, as access to water proved to by strongly competed for at start of sessions and access sequences were found to be stable over time and after access point shifts.

While social dominance hierarchies are well known to govern female mouse behavior as well as male, it is notoriously harder to determine. So this first automatic social dominance determination system may be highly valuable for many lab rodent studies that would benefit from social hierarchy determination.

♦25 Madlen Ziege

Let's talk about... different things! Communication within and among sexes in Farasan gazelles

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Mammalian scent marking in localized defecation sites (latrines) has often been interpreted in the context of (male) territory defense. Still, latrines could have different functions in males and females, especially where territorial males monopolize groups of females with stable social alliances that show pronounced home range overlap. We investigated the communicatory significance of latrines in wild ranging Arabian gazelles (Gazella arabica) and hypothesized that latrines serve territory defense in males, but simultaneously function as communication centers amongst female group members. We assessed the spatial distribution of latrines within home ranges, as a function for territory demarcation should favor a pattern where more latrines are situated in peripheral home range sections, or overlap zones between adjacent home ranges, where latrines are more likely to be detected by neighbors. However, latrine density was highest in the center of female group home ranges, and urine marks were less frequent in peripheral home range sections. When considering male home ranges, latrine densities were higher, and more tracks detected in latrines situated in non-overlap zones, seemingly contradicting a territorial function. This pattern, however, appears to be largely caused by more females than territorial males per given area establishing latrines. Indeed, a subsequent survey of latrine utilization by males and females, based on camera trapping, suggests that males use latrines for territory defense: males visited latrines in overlap zones disproportionally more often than females, and successions of two males prevailed. Our study thus highlights that male territorial marking can be masked when males and females use the same marking system for different purposes.

♦26 Yuki Henselek

Are horses sensitive to reward contingency in a numerical competence task?

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Numerical competence is the ability to understand the relation between quantities and is present in a wide range of species. Yet, many subjects commit a surprisingly large number of errors even in simple discriminations such as 1 vs. 3, despite their general ability to solve such tasks. It had been suggested that this is a result of the use of edible items as stimuli, which then serve simultaneously as choice and as reward. Therefore, Schmitt and Fischer conducted a task in which monkeys had to

discriminate between different quantities of inedible stimuli, but were rewarded with edible rewards. In another condition, they had to discriminate between edible items and were rewarded in with other edible rewards. In both conditions, the monkeys were highly successful, indicating that their poor performance when tested and rewarded with the same edible items was caused by a lack of mental separation of the choice-stimuli and the reward-stimuli. We here investigated if the same effect can be found in a non-primate species and replicated the experiment with horses. Horses are known to discriminate between quantities up to four. Unexpectedly, we found only weak evidence for numerical competence and no effect of the type of stimuli. These findings are not only in stark contrast to our previous work on monkeys, but also to other studies on horses. We suggest that numerical competence may only be of minor importance for horses and highlight the influence of experimental conditions on the outcome of cognitive tests.

♦27 Elfriede Kalcher-Sommersguter

Long-term evaluation of abnormal and affiliative social behaviour in adult re-socialised chimpanzees (*Pan troglodytes*)

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Impoverished early rearing conditions inevitably cause behavioural aberrancies and social deficiencies in juvenile chimpanzees. We investigated the development of abnormal and affiliative behaviour, i.e. social grooming and play, in 18 adult ex-laboratory chimpanzees over three years starting with the period subsequent re-socialisation. The chimpanzees had spent about 20 years in solitary confinement before being re-socialised into one of three different social groups. According to their age at onset of deprivation the individuals could be assigned to two different deprivation classes: early deprived subjects (ED, N = 10) had a mean age of 1.2 years and late deprived chimpanzees (LD, N = 8) of 3.6 years upon arrival at the laboratory. We expected and found that the abnormal behaviour had become habituated in this study population and, accordingly, did not change significantly over the three sample periods neither in ED nor in LD chimpanzees. Moreover, subsequent to re-socialisation ED and LD individuals did not differ in their mean percentage of scans spent on abnormal behaviour. However, within the two years after re-socialisation, EDs increased their levels of abnormal behaviour which were significantly higher than that of LDs. By contrast, LDs significantly exceeded EDs with respect to their mean levels of affiliative behaviour immediately after re-socialisation as well as in the following two years. Our study revealed that infantile deprivation causes persistent behavioural aberrancies and early deprivation within the first two years of live additionally compromises the ability to affiliate with other conspecifics. Thus, re-socialisation, though successful, does not change differences between early and late deprived individuals.

♦28 Claudia Radler

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

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Japanese macaques, *Macaca fuscata*, are seasonal breeders and live in groups containing several female matrilines and unrelated males which are the dispersing sex. Groups are structured according to a despotic dominance hierarchy and from free living populations it is reported that most offspring is sired by high-ranking males. We investigated the distribution of paternity in a large semi-captive group of Japanese macaques (n= 140 individuals in 2010) containing an unusually high number of sexually mature males to females (32:41). The group originates from a founder population of 40 individuals imported to the Affenberg Landskron, Austria, in 1996. No transfer of individuals occurred since then except for one male who was integrated into the group in 2004.We collected hair samples from 104 mature and immature individualsand extracted the DNA in 5%-Chelex-Solution containing also Proteinase K. We used eight primers for genotyping ? five human primers (D5S820, D6S493, D6S501, D12S67, D19S582) and three macaque specific primers (MFGT5, MFGT24, MFGT25). Paternity could be dissolved in 45 individuals. Results show that high ranking maleswere not more likely to father offspring than low ranking males ($?^2$=3.00, DF=2, p=0.223). With the exception of two individuals, parents were not closely related, i.e. r<0.125. Our results indicate that high ranking males are not able to monopolize paternity probably due to the high number of adult males to females in this population.

♦29 Sarah Kieper

Effects of supplementary bird feeding during breeding: a study on great and blue tits

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Supplementary feeding of garden birds is a widespread household activity. However, if and how supplementary feeding affects bird individuals and populations is controversially discussed. For example, the provision of artificial and thus unsuitable food for nestlings has been suggested as a negative consequence. Only few studies so far have tried to estimate the impact of supplementary feeding on successful breeding in birds and it is yet largely unknown if and to which extent parents supply their young with food from bird feeders. Here, we studied the effects of supplementary feeding during reproduction on an urban population of great and blue tits. We mimicked feeding activities of households by providing a bird population a mixture of suet and grains and compared breeding behaviour to another non-fed population. The supplementary provided food was labelled isotopically with N15 during the nestling period. Isotope analysis allowed us to test whether and to which extent parents provide artificial food to their nestlings.

We hypothesized that supplementary feeding has a positive effect on the time course of breeding, on reproduction success and on nestling condition. Isotopic analysis revealed that parents indeed provided nestlings with supplementary food. We could detect an increase in clutch size and body measures of nestlings fed with artificial food, but we found negative effects on hatching rates resulting in a dramatically reduced reproductive success, particularly in supplemented great tits. We discuss possible causes and consequences of our findings and recommend further studies to investigate the complex effects of supplementary feeding on bird reproduction.

♦30 Eva Heeb

Context-specific colony defense in the red wood ant *Fromica rufa*: Social interactions modulate aggressive behavior

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Colony defense requires reliable discrimination of colony members (nestmates) from members of other colonies (non-nestmates). Nestmate recognition in ants is based on chemical recognition of cuticular hydrocarbons (CHC) that originally served as protection against desiccation. The CHC profile of a colony (colony-label) is uniformed through trophalaxis and frequent exchange of CHCs between nestmates. This promotes colony cohesion and chemical separation of neighboring colonies, which consequently are treated as ?aliens? that evoke aggression (Wallis D.I. (1964) Animal Behaviour). The ants? aggressive response is negatively correlated to the distance to its own nest: Ants show a lower level of aggression when they are further away from their nest (Wilson E.O. (1971) The Insect Societies). Furthermore, a relation between path integrator information and aggression to non-nestmates has been described for desert ants (Knaden M. and Wehner R. (2004) Science). However, it is unclear whether indeed information of the path-integrator, as suggested, or more direct measures, like e.g. (reduced) social interactions between nestmates is used to modulate aggressive responsiveness.

We addressed the question how separation form colony members versus recent and frequent social interactions affect aggressive responsiveness to non-nestmates. In behavioral tests, we separate workers and groups of workers of Formica rufa for different time spans and subsequently test their aggressive responsiveness under laboratory conditions and in the field. In addition, we use dummies, loaded with extracts from the postpharyngeal gland (containing the CHCs) to investigate the ants’ response under highly controlled experimental conditions that also allow a detailed analysis of the behavior based on high speed video recordings.

♦31 Harald Wolf

Assessment of food sources and food search strategies in desert ants *Cataglyphis fortis*

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North African desert ants, *Cataglyphis fortis*, assess and return to rich feeding sites. Their decision to return to a feeder and the organization of food searches has been little studied, however. Here we present our recent findings on these aspects.

Two parameters determine the ants' assessment of food site quality, namely, the amount of food available and the reliability of food encounter on subsequent visits. The amount of food appears to be judged by the concentration of items on the spot of food uptake. Initially, the amount of food in a feeder dominates the foragers? decision to return, while learning about reliability takes precedence in the course of a few visits.

The location of a worthwhile site is determined by the animals' path integration system. In particular, the distance of a feeding site is memorized as the arithmetic average of the (beeline) distances covered during the previous outbound and homebound journeys.

Feeding sites that are small and inconspicuous cannot be approached directly with sufficient certainty, due to inevitable inaccuracies of the path integrator. Desert ants instead steer downwind of the goal to encounter the odor plume emanating from the food, and they follow this plume upwind to safely arrive at the feeder. The angle steered downwind reflects the animals' maximum navigation error and is adjusted with experience. This downwind distance may be readjusted if the feeding site relocated.

In summary, food searches of desert ants provide a wealth of features that may advance our understanding of search, navigation and decision strategies. There are several points that warrant further scrutiny, for instance, (i) whether or not a typical meandering outbound path influences how the food site vector is determined, (ii) whether or not navigation accuracy is influenced by environmental parameters such as the structure of the walking substrate, substrate grip etc..

♦32 Philip Schmitz

Habitat use of *Bison bonasus* in a low mountain range enclosure

Authors: *Philip Schmitz*[1], *Stephanie Caspers*[1], *Klaudia Witte*[1]
Affiliation: [1]*Dept. Chemistry-Biology, Research Group Ecology & Ethology, University of Siegen*

In the E+E-Project 'Wisente im Rothaargebirge' (Germany, NRW), a herd (1,6,0) of European Bison (*Bison bonasus*) is managed in an 88 ha area in a low mountain range habitat with beech, pine and alder forest, grasslands and creeks. The animals are prepared for the reintroduction as a free-living herd in an intensively used working forest. We investigated habitat use, foraging behaviour and habitat preferences of the animals. We measured the home range size during 19 month using minimum convex polygone (MCP) and kernel with fixed bandwith (kernel href), as well as the factors that shape the habitat use. As the animals do not use the whole area during summer and are able to attain their required food, we conclude that an 88-ha enclosure is suitable for this herd regarding the nutritional and ethological requirements during summer. As additional feeding is provided during winter, the animals limit their home range size to a core area of < 1,1 ha.

We also tested for correlations between habitat use and environmental factors. We found the strongest correlations between ground coverage by grasses and total grass biomass available. The animals avoided beech forests, prefer pine forests and open areas as well as the respective shrub habitats. We found no correlations with the overall shrub-coverage, although the animals feed on several taxa.

We additionally categorized the area in eight habitat types and calculated the modified Jacob's index for each season (vegetation-time versus non-vegetation-time). This revealed the animals avoid beech forests and prefer pine forests, storm damaged areas and grasslands. All other habitat types are used at random. The feeding site used frequently in both seasons.

This leads to the conclusion that the nutritional requirements are crucial for the habitat preference of *Bison bonasus* and most important for shaping their home ranges.

♦33 Peggy Gerullis

Activity of fins ensures a stable position during the focussing phase of the archerfish shot

Authors: *Peggy Gerullis*[1]*, Stefan Schuster*[1]

Affiliation: [1]*Universität Bayreuth – Department of Animal Physiology*

Archerfish are well-known to shoot down a variety of different prey by means of a precisely aimed water jet released from their mouth. As soon as the water is released resulting forces should lead to a backward movement of the fish which could influence the shot. However, archerfish fully compensate this recoil and keep their position and orientation surprisingly stable during the complete focussing phase of the jet. Using high-speed-video recordings, we show that this stability is ensured by means of an ingenious activation of the fins. Here, a key factor is the movement pattern of the pectoral and pelvic fins, which in turn is perfectly coordinated with the jet.

♦34 Ruben Andres Berthé

Body posture control in *Drosophila* during aerial maneuvering

Authors: *Ruben Andres Berthé*[1]*, Fritz-Olaf Lehmann*[1]

Affiliation: [1]*BioFuture Research Group, Institute of Neurobiology, University of Ulm*

Elaborate neuromuscular support for body posture control is a key feature of most animals. Especially in flying animals such as birds, bats, and insects, wing control requires a finely tuned underlying motor system during aerial maneuvering. Since wing flapping must also support the animal’s body weight, many animals steer by employing only subtle changes in wing motion. Moreover, animals typically employ several redundant motor control systems that synergistically enhance overall locomotor performance.

Besides wing control, the nervous system of the flying fruit fly supports control of abdomen and hind leg movements. These changes potentially inform aerial steering by wings in two ways: by a shift in the fly's center of mass and by changes in total aerodynamic drag on the body. We determined turning moments in freely flying animals by three-dimensional reconstructions of body posture and wing motion, including *in vitro* measurements of aerodynamic drag coefficients on body and legs, and eventually scored the dependencies between body and leg/abdominal movements. We found surprisingly small contributions (2-3%) of mass shift and drag alterations to turning moments generated by wings. Leg and abdominal steering thus appears to be a motor system for fine control rather than for redundancy.

The benefit of leg and abdominal steering might lie in its ability to produce constant moments compared to the pulsating moments generated by oscillating wings. The resultant reduction in body posture fluctuations ultimately helps to avoid retinal image blur during flight and thus, for example, to enhance early triggering of evasive maneuvers during predation

◆35 M. Nazri M.Nasir

Body posture control in freely flying house flies during aerial perturbations

Authors: *Mohd Nazri M.Nasir*[1], *Fritz-Olaf Lehmann*[1]
Affiliation: [1]*BioFuture Research Group, Institute of Neurobiology, University of Ulm*

Flying animals such as birds, bats, and insects, typically stabilize their body during flight by subtle changes in wing motion. In contrast to terrestrial animals, however, body posture control in flight is much prone to aerial perturbations from the environment such as fluctuations in cross and side winds. These fluctuations cause body instabilities due to fluid momentum transfer, retinal image blur, and also metabolic cost due to drag on body and wings.

We determined posture recovery strategies in freely flying house flies by tracking wing and body motion at high-speed during take-off behavior, while perturbating the animals with an impulsive laminar jet of air over a period of 200 ms. Data from 120 flies show that the body's roll, pitch and yaw stability predominantly depends on the direction of the flow. The fly's roll axis is most sensitive to changes in wind speed, causing high roll angles in 62% of the tested animals. Flies minimize jet-induced drag on body and wings by an interruption of wing motion or a significant reduction of stroke angle for approximately 15 ms, and typically turn into the direction of flow.

Collectively, posture recovery behavior in house flies leads to both higher body stability during flight and a reduction in body displacement, while the fly beneficially employs jet-induced flow components over the wings to maintain vertical lift. The observed sequence of complex behaviors emphasizes the complexity of sensorimotor control behavior for flight, which depends on both the visual and fluid dynamic structures of the animal's environment.

♦36 Gerhard von der Emde

Spatial coding and receptive field properties of neurons in the electrosensory lateral line lobe of *Gnathonemus petersii* stimulated by real objects

Authors: *Gerhard von der Emde*[1]*, Simone Gertz*[1]*, Jacob Engelmann*[1]

Affiliation: [1]*Universität Bonn*

The weakly electric fish *Gnathonemus petersii* explores its environment by active electrolocation, during which they emit electric signals and perceive the resulting electrical field with epidermal electroreceptors. Objects within the electric field project ‘electric images’ onto the sensory surface of the fish. Analyzing these images enables the fish to discriminate between different object parameters. The focus of the present study is to understand how information about objects is processed in the first central stage of the ascending electrosensory pathway, the electrosensory lateral line lobe (ELL). Thus, we relate the sensory input caused by objects to the neuronal response. We recorded extracellularly from single neurons while presenting either a plastic or a metal cube within their receptive fields (RF). The responses of the neurons were analyzed for the parameters discharge rate, first spike latency and the PSTH pattern. Further we used Receiver-Operating characteristic to compare the quality of the coding strategy. The RF organization was analyzed with respect to the two cell classes found in the ELL, I(inhibitory)- and E(excitatory)-cells. We recorded neurons with RFs in all body regions, Schnauzenorgan, head and trunk. We propose that at the level of the ELL, both spike rate and first spike latency are used for coding, either separately or as mixed coding. There were neither significantly differences in RF size between the two cell classes nor in the different body regions, but the structural organization increases in complexity from rostral to caudal along the fish’s body.

♦37 VerenaGrün

Influence of housing on blood T cell subsets in pregnant sows

Authors: *Verena Grün, Sonja Schmucker, Volker Stefanski*

Affiliation: [1]*Behavioural Physiology of Farm Animals, University of Hohenheim*

Mixing of unacquainted animals or social isolation can lead to an activation of physiological stress systems that affect various immune functions and may result in increased disease susceptibility. Allthough these factors may cause economical disadvantages in agricultural industry, the question whether or not common housing conditions affect the immune functions in pregnant sows is poorly studied, especially with respect to T cells which represent crucial regulatory elements of the adaptive immune system. The aim of this study was therefore to investigate the influence of two different housing systems on numbers of T cells and their main subsets in pregnant sows (German landrace). From four weeks after insemination until one week before parturition sows were either housed in a social group, n=22 (as required by EU guidelines (2001/88 EG) by 2013) or in single crates, n=11 (most common housing condition in sows worldwide). Blood samples for physiological measurements were taken 7, 6, 4 and 2 weeks before parturition by jugular vein puncture. Numbers of leukocytes and lymphocyte subpopulations were determined by flow cytometry using monoclonal antibodies for subset identification (CD3, CD4, CD8, CD172a). Preliminary results show that the number of blood T cells and the number of important subsets (CD3+CD4+CD8-/+ and CD3+CD4-CD8+) was significantly higher in group-housed sows at most sampling points. These first results show that housing systems can have substantial effects on regulatory immune cells in pregnant sows and might therefore affect the capacity of the organism to fight infection.

♦37a Marjolein Kruidhof

The influence of habitat complexity on parasitoid foraging behaviour

Authors: *H.M. Kruidhof*[1/2], *A. Roberts*[1/2], *T.S. Hoffmeister*[1]
Affiliation: [1]*Institut für Oekologie, Universitaet Bremen, Fachbereich 2, Bremen*;
[2]*Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, The Netherlands*

Parasitoids play a key role in structuring and organizing communities in terrestrial food webs. They often parasitize herbivorous insects, on which their offspring develops, and as such are used as biological control agents of agricultural pests. *Cotesia glomerata* parasitoids, which parasitize early-instar *Pieris* caterpillars, use indirect odour information from their hosts' food plants, so-called herbivore-induced plant volatiles (HIPVs), to locate their inconspicuous hosts. Differences in quality of the hosts' food plants can also create differences in host quality and thus affect parasitoid performance. As choosing a poor host in the presence of more suitable hosts can be highly detrimental to parasitoid fitness, it is expected that natural selection will favour mechanisms that increase the capacity of the females to discriminate against inferior quality hosts. We are investigating the extent to which *Cotesia glomerata* can distinguish between cues related to the presence of high and low quality host-insects in habitats of varying complexity. This will be an important addition to our current knowledge, as most studies on tritrophic interactions involving plants, insect herbivores and their parasitoids are based on simple agricultural systems studied under laboratory conditions.

4. Developmental Biology TALKS

Saturday, September 22, 2012

Chair: Nico Prpic-Schäper

☐19 Jennifer Schmidt A 704 / 16:00

The regulatory network of FoxN3 during *Xenopus laevis* head development

Authors: *Jennifer Schmidt*[1], *Lennart Olsson*[1]
Affiliation: [1]*Institut für Spezielle Zoologie, FSU Jena*

In *Xenopus laevis* little is known about the underlying genetic control mechanisms determining the correct development of neural crest cells. FoxN3 a member of the fork head/Winged Helix family of transcription factors is required for craniofacial development in *X. laevis*. Based on a morpholino knock-down of FoxN3 we found that FoxN3 has a direct effect on the development of neural crest derived cartilages, the jaw joint formation and an indirect effect on cranial muscle development. The articulation between the infrarostral and Meckel´s cartilage were lost as well as the jaw joint. Moreover we found a delay in the development of the neural crest derived cartilages and an incomplete fibre development in cranial muscles. We studied the molecular process that led to the delayed and distorted development by analysing the expression of different maker genes using whole mount in situ hybridisation and qRT-PCR. We found that the functional knock-down of FoxN3 leads to a decrease in the expression of different bagpipe genes like zax and Xbap, of cartilage makers like Runx2 and col2a1 and of muscle makers like MyoD and MHC. We show that FoxN3 is embedded in a complex gen network and the knock-down leads to a decrease in expression of different genes which has been reported to be important for a proper head development in *X. laevis*. Furthermore we are now analysing the effect of FoxN3 knock-down on joint development as well as possible changes in the expression of cell adhesion genes.

☐20 Nathalie Feiner A 704 / 16:15

Molecular phylogenetic, comparative genomic and expression analyses of Pax10, a novel sister gene of Pax4 and Pax6

Authors: *Nathalie Feiner*[1], *Axel Meyer*[1], *Shigehiro Kuraku*[1/2]
Affiliation: [1]*Laboratory for Zoology and Evolutionary Biology, Department of Biology, University of Konstanz, Germany;* [2]*present address: Genome Resource and Analysis Unit, RIKEN Center for Developmental Biology, Kobe, Japan*

The prerequisite for comparative molecular biological analyses is an accurate orthology/paralogy assignment. However, this is often obscured by incomplete sequence identification, secondary gene loss or difficulties in reconstructing molecular phylogenies. While Pax6 is present in all vertebrates analyzed to date, Pax4

and Pax10 show mosaic phylogenetic distributions: Pax4 has been found so far only in mammals and teleosts, while a careful survey of publicly available databases revealed the presence of Pax10 only in a few non-mammalian vertebrates. Pax10 is characterized by a paired-type homeodomain, but lacks the paired domain that is present in all other Pax genes (Pax1-9). Despite the lack of the paired domain, a molecular phylogenetic analysis unambiguously placed Pax10 genes within the Pax4/6 subgroup. To tackle the question about the origin of Pax10 we established both intra- and inter-genomic comparisons of chromosomal regions containing Pax4, -6 and -10 in vertebrate model organisms. We found conserved synteny indicating that the origin of Pax10 was part of a large-scale duplication event. Thus, Pax10 is presumably the third identified member of the original gene quartet generated by the two rounds of whole-genome duplication that occurred in the ancestral vertebrate genome. An analysis of the expression patterns of Pax10 genes in zebrafish, Xenopus and anole lizard using in situ hybridizations and quantitative RT-PCR showed that Pax10 expression patterns differed between three different vertebrate classes and revealed secondary changes in developmental roles between the three sister genes Pax4, -6 and -10.

☐21 Peter Lesny A 704 / 16:30

Transcription factors from the parasitic barnacle *Sacculina carcini* (Crustacea: Rhizocephala) identified by transcriptomic analyses

Authors: *Peter Lesny*[1]*, Andreas Vilcinskas*[2]*, Lars Podsiadlowski*[1]

Affiliations: [1]*Inst. Evolutionsbiologie & Ökologie, Universität Bonn*; [2]*Inst. Phytopathologie & Angew. Zoologie, Universität Giessen / Fraunhofer Projektgruppe "Bio-ressourcen", Giessen*

Rhizocephala are endoparasitic barnacles with a highly aberrant adult morphology, predominantly parasitizing decapod crustaceans. Adults are barely recognizable as crustaceans or even arthropods. They grow inside the host in form of a simple branched rootlet system, built of out of two cell layers. With complete lack of appendages, gut, brain and complex sensory organs the adult rhizocephalans rather resemble a fungus than an arthropod. Besides molecular sequence data only the cypris larva point to their inclusion into *cirriped crustaceans*. *Sacculina carcini* is an abundant parasite of the shorecrab, *Carcinus maenas*. Its internal rootlet tissue infiltrates and destroys the gonads and part of endocrine glands, nervous system and other tissues. Mature parasites grow an breeding pouch out of the hosts body, receiving male larva and subsequently breeding new larvae. We obtained mRNA preparations from breeding pouches of *S. carcini* and produced a normalized cDNA library to enhance the coverage of rare transcripts. High-throughput sequencing was performed with the Illumina HiSeq 2000 yielding a total of 180 mio bp raw data. 5732 contigs >500 bp were assembled from that primary data, with almost 50% of these sequences showing significant similarities to a set of all protein sequences from eight arthropod species (six insects, tick and water flea). Here we present preliminary comparative analyses of transcription factors with putative roles in development identified in the transcriptomes of Sacculina and non-parasitic barnacles.

☐22 Franziska AnniFranke A 704 / 16:45

Study of segment polarity genes in Onychophora (velvet worms): Insights into the evolution of segmentation in Panarthropoda

Authors: *Franziska Anni Franke*[1], *Georg Mayer*[1]
Affiliation: [1]*Animal Evolution & Development, Institute of Biology, University of Leipzig*

Organisation of the body into serially repeated units or segments is found in several distantly related animal groups, including chordates, annelids and arthropods. The evolutionary origin of body segmentation in these groups is under debate and it is unclear whether segmentation has evolved once, twice, or several times among bilaterians. Gene expression studies in one of the closest relatives of arthropods, the Onychophora, might help to clarify this issue since the onychophoran body shows both segmental and non-segmental features. To assess whether onychophorans and arthropods share a common segment patterning mechanism, we analysed the expression pattern of the segment polarity genes engrailed, hedgehog, wingless and cubitus interruptus, which play a major role in the segmentation process of the arthropod embryo. Our data show that despite differences there are also similarities in the segmentation process of the onychophoran embryo to that in arthropods, suggesting that the subdivision of the body into repeated, antero-posterior genetic units predated the evolution of externally visible segmental boundaries in the panarthropod lineage.

☐23 Reinhard Schröder A 704 / 17:00

FGF signalling organizes extraembryonic membrane formation and integrity in the red flour beetle *Tribolium castaneum*

Authors: *Reinhard Schröder*[1], *Rahul Sharma*[1], *Anke Beermann*[2]
Affiliations: [1]*Universität Rostock*; [2]*Universität Tübingen*

Fibroblast growth factor (FGF) signalling plays a key role in cell proliferation and differentiation in both vertebrates and invertebrates. To gain insight into FGF signalling in an arthropod, we functionally characterized the Fgf1 ortholog in the beetle *Tribolium* that is not represented in the Drosophila genome. Tc-fgf1 RNA-interference results in asynchronous nuclear division seen already during blastoderm formation. Tissue-specific marker genes analysis reveals a loss / severe reduction of extra-embryonic membranes in the affected embryos. As a consequence, secondary phenotypes develop later during embryogenesis such as (I) mispositioning of the germ anlage resulting in a novel “floating embryo” phenotype, (II) completion of embryogenesis around the posterior pole resulting in a curved embryonic axis and (III) impairment of dorsal closure. We discuss whether these phenotypes might be caused in part by changes of the expression level of Tc-dpp in Tc-fgf1-RNAi embryos. This is the first study reporting the functional characterization of Fgf1 outside the vertebrate system.

☐24 Eileen Knorr A 704 / 17:15

Post-embryonic functions of HSP90 the model beetle *Tribolium castaneum*

Authors: *Eileen Knorr*[1], *Andreas Vilcinskas*[2]
Affiliation: [1]*Fraunhofer Institute for Molecular Biology and Applied Ecology Project Group "Bioresources"*; [2]*Institute of Phytopathology and Applied Zoology, Justus Liebig University of Giessen*

Heat shock protein 90 (HSP90) belongs to a highly conserved family of molecular chaperons with pleiotropic roles in development and stress associated signaling. Its known functions in insects are associated with spermatogenesis, oogenesis and embryogenesis in insects. In this study, we analyzed the role of HSP90 in the red flour beetle Tribolium castaneum. Gene expression analysis of HSP90 using real-time RT-PCR revealed a transiently upregulation of HSP90 during larval development, and higher levels in female pupae and adults compared to males, suggesting putative role in gametogenesis. Silencing of HSP90 via RNA interference was lethal within 10 days at all developmental stages. Titration experiments showed that larvae were more susceptible than pupae or adults. Furthermore, knock-down in final instars arrested development at the prepupal stage and prevented the development of compound eyes. Our results provide evidence that HSP90 functions can be expanded beyond insect embryogenesis to include roles in post-embryonic development, particularly in compound eye formation.

Monday, September 24, 2012

Invited speaker 1: Chair – Monika Hassel A 701 / 11:30

Kristin Tessmar-Raible (Wien)

Shedding Light on Rhythms

Author: *Kristin Tessmar-Raible*[1]
Affiliation: [1]*Max. F. Perutz Laboratories, Austria*

Since the dawn of life the marine ecosystem is governed by a multitude of environmental cycles. In accordance with these cycles, marine species evolved various biological rhythms, ranging from circadian to circalunar and seasonal rhythms. For instance, many marine species synchronize their reproductive cycle with the photoperiod, the lunar cycle and to a specific time of the day. Yet, despite the fundamental nature of these light-controlled 'marine' rhythms, we have very limited knowledge about their molecular basis. The reproductive cycles of the annelid *Platynereis dumerilii* are synchronized by the interplay of a circadian and a circalunar clock, which are synchronized by sun and moon light, respectively.

We have started to dissect the molecular mechanisms that govern light-dependent circadian and circalunar rhythmicity in the marine annelid *Platynereis dumerilii*. Our analysis covers three areas: (i) the measurement of light spectra and intensities that the animals receive in their natural environments over the lunar cycle.

(ii) the characterization of candidate lunar light sensors and their spectral sensitivity
(iii) the analysis of circadian clock components and their regulation under light regimes that mimic different phases of the lunar cycle.
Our results suggest that lunar and circadian clocks are molecularly connected, and provide new molecular entry points into the study of light-dependent marine rhythms.

Invited speaker 2: Chair – Nico Prpic Schäper A 702 / 12:00

Benjamin Altenhein (Mainz)

Glial cell development in *Drosophila*: from cell fate specification to function

Author: *Benjamin Altenhein*[1]
Affiliation: [1]*Institut für Genetik, Universität Mainz*

The nervous system of vertebrates and invertebrates comprises two major cell types, neurons and glial cells. In *Drosophila* both cell types are generated by common precursors or neural stem cells, the so called neuroblasts (NB). At the end of gastrulation, these NB delaminate from the neuroectoderm into the embryo and divide in a stem cell mode, thereby generating stereotyped cell clones of neurons and/or glial cells. The binary choice between neuron and glia as well as further cell fate specification in the developing nervous system is achieved by a combination of positional information of the NB already in the neuroectoderm, temporal specification within each NB lineage, and asymmetric distribution of determinants during mitosis. Recent work in our lab revealed that nearly all glial cells within an abdominal hemineuromere of the fly embryo represent individual cell identities as reflected by a combinatorial code of marker gene expression and a stereotyped positioning, the latter being a consequence of an individual migratiory behaviour of these cells. Specification eventually results in functional diversification of the entire glial population which again is reflected by differential gene expression accompanied by morphological and physiological changes. The genetic and molecular program underlying such glial cell specification however, is poorly understood. I will present our recent approaches towards a better understanding of these specification steps, though not yet fully unravelled. Furthermore, I will show that differential expression of particular genes already early in glial development regulates glial function in the larval and adult nervous system. These functions influence cell-cell connections between glia and neurons, neurons and muscles, and among neurons or glia themselves. Loss of function of these glial genes results in structural and/or physiological deficits of the flies, which will be demonstrated by different approaches. After all, a clear understanding of glial cell specification and the resulting functional diversification of these cells will help to better understand the functionality of the nervous system in its entity (not only in *Drosophila*).

Chair: Reinhardt Schröder

☐25 Anika Lidke A 704 / 14:00

Estradiol promoted effects on the development of primordial germ cells in the polychaete *Platynereis dumerilii*

Authors: *Anika Lidke*[1], *Nicole Rebscher*[1]
Affiliation: [1]*Philipps Universität, spezielle Zoologie*

The steroid hormon estradiol is involved in reproductive processes like gametogenesis, estrous cycle, induction of vitellogenesis, maturation of sexual organs or proliferation of primordial germ cells (PGCs). For a long time estrogen signaling was considered to be vertebrate specific, unless recently an estrogen receptor was found in the *mollusk Aplysia* (Thornton et al., 2003) which however was not able to bind estradiol. Later an estradiol receptor activated by estradiol was found in the polychaete *Platynereis dumerilii* (Keay and Thornton, 2009) and biochemically and phylogenetically characterised. Since there are no data available in vivo on the function of estrogen in this species, we examined the effect of estradiol on PGC development in the polychaete *Platynereis dumerilii*. Embryos were incubated with estradiol at different concentrations and periods and were allowed to develop until the age of six days post fertilisation. Larvae were then fixed and numbers of PGCs were assessed by immunohistochemistry against the Vasa protein. After treatment with estradiol excessive PGCs were found as compared to the control group. The effect of estradiolon the PGCs seems to be concentration dependent.

Reference:
Thornton,J.W., Need,E., and Crews,D. 2003. Resurrecting the Ancestral Steroid Receptor: Ancient Origin of Estrogen Signaling. Science 301: 1714-1717.

☐26 Beate Mittmann A 704 / 14:15

Embryonic development and staging of the cobweb spider *Parasteatoda tepidariorum* C. L. KOCH, 1841 (syn.: Achaearanea tepidariorum; Araneomorphae, Theridiidae)

Authors: *Beate Mittmann*[1], *Carsten Wolff*[2]
Affiliations: [1]*Institut für Biologie III, Neurogenetik, Albert-Ludwigs-Universität* Freiburg; [2]*Institut für Vergleichende Zoologie, Humboldt-Universität zu Berlin*

The cobweb spider Parasteatoda tepidariorum (C. L. KOCH, 1841; syn.: Achaearanea tepidariorum) has become an important study organism in developmental biology and evolution as well as in genetics. Beside Cupiennius salei, it has become a chelicerate model organism for evo-devo studies in recent years. However, a staging system taking into account the entire development, and detailed enough to apply to modern studies, is still required. We describe the embryonic development of P. tepidariorum and provide a staging system which allows easy recognition of the distinct stages using simple laboratory tools. In addition to fluorescent stainings, schematic drawings of all stages are provided to ease stage recognition. Furthermore, we described and filmed the cocoon production of P. tepidariorum and provide movies of developing eggs. As the genom of P. tepidariorum is just being sequenced, our staging will provide a useful basis for near evo-devi-studies.

Keywords: Achaearanea tepidariorum, Parasteatoda tepidariorum, embryonic development, staging, embryogenesis, morphogenesis.

☐27 Joris Bressan A 704 / 14:30

Comparative analysis of the *Cardiocondyla obscurior* brain

Authors: *Joris Bressan*[1]*, Robert Knüppel*[2]*, Lukas Schrader*[2]*, Simon G. Sprecher*[1]*, Jan Oettler*[2]
Affiliations: [1]*DepartDepartment of Biology, University of Fribourg, Switzerland*;
[2]*Biologie I, Universität Regensburg, Germany*

The brain of insects is organized of lineage related neuropile compartments. Several aspects of neuropile compartmentalization have been suggested to be evolutionarily conserved. However, compartments vary dramatically between different insects and in general reflect functional differences. In contrast to most ants, the ant genus *Cardiocondyla* (Formicidae: Myrmicinae) contains two male castes with distinct behaviors and roles in the colony in addition to queens and workers. Thus *Cardiocondyla* offers the unique opportunity to study brain plasticity in a social insect. We here describe patterns of brain compartmentalization during metamorphosis and in adults. We concluded a comparative analysis between the Drosophila brain and the *Cardiocondyla* worker brain to identify the main different compartments of the central brain and generated a descriptive 3D model of the whole brain. We identified conserved neuropile compartments and major axon scaffolds. We then constructed 3D models to measure compartment volumes in developing larval brains. At an early stage of the 3rd (last) instar the brain size was similar across castes. At the late 3rd instar brains of the winged castes are distinct in size from the wingless castes. Some compartments in the early 3rd instar brain are already differentiated in both winged castes, whereas in the wingless morphs these compartments started to differentiate in late 3rd instars. This study will be the backbone of our future collaborative work combining behavioral and neuroanatomical plasticity in *Cardiocondyla obscurior*.

☐28 Christina Schulte A 704 / 14:45

A transposon-mediated germline transformation system for the honeybee *Apis mellifera*

Authors: *Christina Schulte*[1]*, Martin Beye*[1]
Affiliation: [1]*Heinrich-Heine-University, Institute of Evolutionary Genetics*

We established a system for stable germline transformation in the honeybee *Apis mellifera* by using piggyBac, a transposon discovered in the lepidopteran Trichoplusiani. The transformation system has been widely used in nonsocial insects and consists of the piggyBac inverted terminal repeats flanking the 3xP3 promoter and a reportergene. We utilized rubia as reportergene that encodes a red fluorescence protein. We in vitro synthesized mRNA encoding the piggyBac transposase in order to catalyze the transposition. The transposon was coinjected with this mRNA into female honeybee embryos which were reared to queens. We found G1 individuals positive for Rubia protein and integration of the transgene into

the genome. We confirmed the presence of the inverted terminal repeats of piggyBac and the characteristic TTAA sequence of the insertion site suggesting precise transposition events. Our results showed an efficient method of stable gene transfer in a hymenopteran insect. We are currently testing different honeybee specific promoters that will allow us to manipulate genes in a particular tissue or developmental stage. Our method offers new opportunities to study the interesting social phenotypes of the honeybee by stable genetic manipulation.

☐29 Inga Nissen A 704 / 15:00

Molecular control of sex determination in honeybees

Authors: *Inga Nissen, Martin Beye*
Affiliation: [1]*Heinrich-Heine-Universität Düsseldorf, Institute for Evolutionary Genetics*

Molecular analysis of the diversity of sex determination systems can contribute in our understanding of how and why pathways and gene functions evolved. Sex in the honey bee (*Apis mellifera*) is determined by heterozygosity of the complementary sex determiner (csd) gene. This sex-specific signal is realized by a cascade of genes that involves the feminizer (fem) and the highly conserved Am-doublesex (Am-dsx) gene, which is found across the order of insects. We have previously reported that Csd proteins control the female-specific processing of the fem transcript encoding the Fem protein, while Fem proteins are required to promote female specific Am-dsx splicing. However, it is still unknown whether Fem proteins are direct regulators of Am-dsx pre-mRNA splicing and how this process is molecularly regulated. To analyze the molecular control of female and male Am-dsx splice regulation, we developed an in vivo splice assay in Sf21-cells. To mimic sex-specific Am-dsx splicing we constructed an Am-dsx-minigene and co-expressed beside Fem proteins, the RNA-binding protein Am-Tra2 as potential co-factor of Am-dsx splice regulation. Analysis of Am-dsx splicing products showed that both proteins are direct regulators of alternative Am-dsx-minigene splicing. Fem and Am-Tra2 proteins activate the splice donor site of the female exon that requires an evolved exonic splice enhancer sequence upstream of the splice donor site. Our study showed that the molecular control of sex-specific dsx splicing substantially diverged compared to *Drosophila melanogaster*.

☐30 Monika Hassel A 704 / 15:15

MAPK signaling is necessary for the final phase of bud detachment and correlates with Sprouty expression

Author(s): *Monika Hassel*[1], *Christian Hasse*[1], *Ellen Lange*[1], *Ashwini Suryawanshi*[1],
Affiliation: [1]*Spezielle Zoologie, Morphology and Evolution of Invertebrates, Philipps University Marburg*

Signaling by the Hydra FGFR Kringelchen is essential for the establishment of the boundary between parent and bud (1), where it likely acts upstream of Notch (2). Overexpression of the full length FGFR variant in Hydra.induces autotomy of the body column and indicates a role of FGFR signaling in tissue separation.

Downstream of Kringelchen, three alternative pathways may be targeted, one of them is the Ras/MAPK pathway. Analysis for presence of dpERK-positive cells showed a transiently detectable signal in cells clustering at the bud base in stage 9. This signal accompanies tissue separation. A potential role of MAPK signaling in this late phase is further corroborated by treatment with the MAPK inhibitor UO126, which delays bud detachment in stage 9 by about two days.

FGFR-induced MAPK signaling is known to induce the negative regulator Sprouty. By expression analysis, we found one of the three Hydra Sprouties expressed at the bud base at a time correlating with MAPK activation.

We conclude that FGFR signaling is able to start a program of tissue separation possibly by targeting MAPK signaling and Sprouty in the final step(s) of bud detachment.

(1) Sudhop et al., 2004; (2) Münder et al., 2010

We thank Bert Hobmayer and Thomas Bosch and their groups for help with transgenesis and the DFG for support

5. Developmental Biology POSTERS

♦38 Yvette Kühnel

Hemocyte Identification in Embryos and Larvae of *Manduca sexta* L 1763 (Lepidoptera, Sphingidae)

Authors: *Yvette Kühnel*[1]*, Christoph-Rüdiger von Bredow*[1]*, Tina Trenczek*[1]
Affiliation: [1]*Institut für Allgemeine und Spezielle Zoologie, Justus-Liebig-Universität Gießen*

In lepidoptera five different hemocyte types can be observed: Prohemocytes (PHC) plasmatocytes (PL), granular cells (GR), spherule cells (SP) and oenocytoids (OE). PLs and GRs are the most abundant hemocytes (Beetz et al. 2002). The hematocytopoiesis in *M. sexta* is expected to be divided in the occurance of GR and PL in the embryo (Nardi 2004) and the larval hematopoiesis, which is partial accomplished by the hematopoietic organs (HO) (Nardi et al. 2003). The source of OE and SP remains totally unclear.

In this work embryonic hemocytes and larval hemocytes were identified with a panel of mAbs raised against larval hemocytes by Willot et al. 1994. Free embryonic hemocytes were identified with GR specific mAbs MS#7 and MS#21. Presumable GRs were found at about the middle of embryonic development. PLS were detected with mAbs MS#75, MS#13 and MS#34. In late embryos wing disk associated cell clusters were observed. These are probably the HOs which are described for the *M. sexta* larvae. In caterpillars the surface protein Neuroglian 3B11 is present on the surface of coherent HO cells which do not readily leave the HO (Nardi et al. 2003). Therefore it is likely that these cells are PHC which resemble precursor cells (Gardiner and Strand 1999, 2000) for PLs in this case. Double staining with the lectin PNA from Arachis hypogaea and the mAb anti NG3B11 (raised by Nardi 1993, provided by DSHB) showed clearly that PNA stains cells which are NG3B11 negative. Therefore, the glycosilation recognized with PNA appears to be a marker for differentiation of the HO cells. Double staining of HO cells with different PL specific mAbs (mAb MS#77 and MS#75, MS#77 and MS#13) also reveals that different PL subpopulations and/or differentiation stages are present in the HO. Moreover, antimicrobial activity of HO cell extracts like lysis of bacterial cell walls was observed.

◆39 Jeanette Woopen

Immunohistochemical investigations of retinoid receptors in different developmental stages of the locust *Locusta migratoria*

Authors: *Jeanette Woopen*[1]*, Jeyathevy Sivalingam, Jörg Mey, Peter Bräunig, Katrin Göbbels*

Affiliation: [1]*Institute for Biology II, RWTH Aachen University*; [2]*Hospital Nacional de Parapléjicos, Toledo*

Retinoic acid (RA), the active metabolite of vitamin A, plays an important role during development and regeneration in vertebrates, including patterning of the nervous system and neurite outgrowth. Some effects of retinoic acid seem to be conserved between vertebrate and invertebrate species. In the fresh water snail *Lymnaea stagnalis* a RA plays an important role in development, e.g. formation of the eye. Furthermore, it induces positive growth cone turning in regenerating neurons in vitro. In the grasshopper *Locusta migratoria*, the presence of RA and a retinoid X receptor was shown throughout embryogenesis. Locust RXRs bind 9-cis RA and all-trans RA with high affinity, similar to human RXRs. Previously we showed a positive effect of RA treatment on cell viability and neurite outgrowth of embryonic locust neurons in vitro. However, the localization of the retinoid receptor remained unknown. In the present study we have investigated the distribution of the retinoid X receptor in different developmental stages of *Locusta migratoria*. Therefore, the central nervous system of both embryos and first and second larvae were dissected free or taken out and stained immunohistochemically as whole mount material. Interestingly, the antibody bound to only a few neurons in the entire nervous system, including a few peripheral neurons, neurons in the optic lobes, and a pair of neurosecretory cells with axonal collaterals in all ganglia of the CNS. The physiological function of this specific cellular distribution of RXR in the locust remains to be investigated.

6. Ecology TALKS

Invited speaker 1: Chair – Gerlind Lehmann A 702 / 11:30

Kathrin Lampert (Bochum)

Does it have to be sex? Ecological and evolutionary success of a clonal vertebrate, *Poecilia formosa*

Author: *Kathrin Lampert*[1]

Affiliation: [1]*Ruhr University Bochum*

Sexual and clonal reproduction have very different advantages and disadvantages. While clonal reproduction ensures very high reproductive rates, sexual reproduction produces genetically variable offspring that is highly adaptable to changing environmental conditions. Depending on the environment one reproductive strategy should therefore have a higher fitness than the other one and a co-existence of clonal and sexual reproduction should not be possible.

Despite these theoretical considerations there are a few cases where a close co-occurrence of sexual and clonal species with very similar ecological requirements can be observed. One example is the clonal Amazon molly (*Poecilia formosa*) that, due to its gynogenetic reproductive mode, depends on a close co-existence with one of its sexually reproducing parental species, *Poecilia mexicana* or *Poecilia latipinna*. I am investigating the advantages and disadvantages of both reproductive strategies and try to understand which environmental and genetic factors allow their co-existence.

Sunday, September 23, 2012

Chair: Axel Hochkirch

☐31 Holger Goerlitz A 702 / 12:00

Functional impacts of global warming on prey detection ability of echolocating bats

Authors: *Holger R. Goerlitz*[1], *Jinhong Luo*[1], *Klemen Koselj*[1], *Sándor Zsebek*[1], *Björn M. Siemers*[1]

Affiliation: [1]*Max Planck Institute of Ornithology, Sensory Ecology Group, Germany*

Many studies on climate change predicted shifts in the future distribution range of plants and animals. Here we take a more functional perspective and explore the idea that a rise of average temperature can affect the foraging efficiency of echolocating bats in present day communities. Ambient temperature affects sound attenuation, which determines the maximum distance over which bats can echolocate insects. Sound attenuation is a non-linear function of both temperature and sound frequency and is especially pronounced for high frequencies, such as bat echolocation. Hence, the prey detection ability and foraging efficiency of bats might be affected by global temperature rise through climate change. Using projected temperature rises of the 21st century, we modelled this effect for the entire range of bat echolocation call frequencies and for biome types around the globe. We found that, depending on call frequency, global warming will result both in a decrease and in an increase of prey detection ability. Those species within local species assemblages using calls above a cut-off frequency will lose and those using lower frequencies will gain foraging efficiency. The magnitude and cut-off frequency of this shift in competitive balance depends on the local climate conditions and can amount to 40% prey search volume and vary from 10 to 100 kHz call frequency, respectively. Global warming will thus affect bat species directly through changes in their prey detection ability and indirectly through shifts in the balance of competitive interactions and predator-prey dynamics.

☐32 Rudy Jonker A 702 /12:15

Climate change and common buzzard survival: a complex case

Authors: *Rudy M. Jonker*[1], *Nayden Chakarov*[1], *Oliver Krüger*[1]
Affiliation: [1]*Dept. of Animal Behaviour - University of Bielefeld*

The effect of changing climatic conditions on wild populations has received ample attention in the past decade. However, most attention has been on direct effects of climate changes on species of lower trophic levels and on negative consequences of climate change. Here we analysed the survival of 670 male and 669 female common buzzards *Buteo buteo* over the period 1989 to 2011, a period in which our study population quadrupled. We used mark-recapture survival analysis of individual resightings of breeding adults using the program MARK and AIC comparison to test what environmental factors best explained survival. Our study shows that a decrease in North Atlantic Oscillation index, with colder winters with more snow and less rain, surprisingly increased survival of buzzards. This relationship might be due to higher vole *Microtus arvalis* survival in drier conditions and under snow cover. Buzzard survival increased slightly more for males than for females, presumably due to males being more sensitive to winter food availability than females because of their smaller size. Our results also show a slightly higher survival for buzzards of the intermediate morph, as compared with the light and dark morph. Also, survival was higher in years with intermediate rainfall in spring. This study shows that climatic changes in one season, which may be different from changes in other seasons, can have positive effects on species of higher trophic levels via an interaction with their prey.

Chair: Kathrin Lampert

☐33 Hannah Burger A 702 / 14:00

An arthropod deterrent attracts a specialized bee to its host plants

Authors: *Hannah Burger*[1], *Stefan Dötterl*[1], *Christopher M. Häberlein*[1], *Stefan Schulz*[1], *Manfred Ayasse*[1]

Affiliation: [1]*University of Ulm, Institute of Experimental Ecology*

Oligolectic bees are specialized on few closely related plant species for pollen foraging. At the beginning of the flight season newly emerged, naïve females have to find and recognize their specific host-plants to reproduce successfully.

To investigate the importance of floral cues for host-plant finding and recognition in oligolectic bees, we chose Hoplitis adunca (Megachilidae), a solitary bee species which is highly specialized on the flowers of Echium spp. (Boraginaceae). We hypothesized H. adunca to use Echium-specific signals to recognize their host-plants. To test the hypothesis, we used a combination of chemical (GC-MS) and electrophysiological (GC-EAD) analyses, spectral reflection measurements and bioassays.

Our investigations showed that the interplay between visual and olfactory cues of Echium flowers is essential for host-plant finding and recognition by H. adunca females. Colour cues of the flowers attract the bees, while the olfactory cues, which are highly specific floral scent compounds only known from the host-plants of H. adunca and as arthropod deterrent, are used by the bees to recognise their host plant and discriminate it from non-host plants.

Burger, H., Dötterl, S. & Ayasse, M. 2010. Host-plant finding and recognition by visual and olfactory floral cues in an oligolectic bee. Funct. Ecol., 24: 1234-1240.

Burger H., Dötterl S., Häberlein C.M., Schulz S. & Ayasse M. 2012. An arthropod deterrent attracts specialised bees to their host plants. Oecologia 168: 727-736

☐34 Christian von Hoermann A 702 / 14:15

The attraction of newly emerged *Nicrophorus vespilloides* females (Coleoptera: Silphidae) to odour bouquets of large cadavers (Sus domesticus) in different stages of decomposition

Authors: *Christian von Hoermann*[1], *Sandra Steiger*[1], *Josef K. Müller*[1], *Manfred Ayasse*[1]

Affiliation: [1]*Institute of Experimental Ecology, University of Ulm*

The burying beetle *Nicrophorus vespilloides* (Coleoptera: Silphidae) feeds and reproduces on small carcasses which are buried under the ground as food for their offspring. For a long time it has been postulated and confirmed that large cadavers (too big for burying) are important food sources especially for newly emerged females. Therefore, in a forensic chemo-ecological approach, we have investigated a potential preference of newly emerged *N. vespilloides* females for odour bouquets of piglet cadavers in five different stages of decomposition (fresh, bloated, post-bloating, advanced decay and dry remains). Analyses of walking tracks on a Kramer sphere inside a constant air stream revealed significantly higher mean walking speeds of beetles when odour plumes of the decomposition stages post-bloating, advanced decay or dry remains were applied in comparison to the solvent control, respectively.

Such an observed change in the searching behaviour of newly emerged *N. vespilloides* females could enhance their environmental exploration due to an increase in their travelled distance. Furthermore, in the advanced decay stage we registered a significantly higher preference of beetles for upwind directions to its specific odour plume when compared to the solvent control. Such a change in walking upwind behaviour could be a pre-condition for the detection of large cadavers in *N. vespilloides* burying beetles. Our findings could be of general importance for applied forensic entomology because newly emerged *N. vespilloides* females on large cadavers can and should be regarded as potential indicators of prolonged postmortem intervals.

☐35 Christin Wurmitzer A 702 / 14:30

Olfactory preferences in dung beetles (Scarabaeoidae: Geotrupidae & Scarabaeidae)

Authors: *Christin Wurmitzer*[1], *Belén Maldonado*[2], *Kai Dworschak*[3], *Federico Ocampo*[2], *Nico Blüthgen*[3], *Thomas Schmitt*[1]

Affiliations: [1]*Department of Evolutionary Biology and Animal Ecology, Faculty of Biology, Albert-Ludwigs-University Freiburg*; [2]*Instituto Argentino de Investigaciones de las Zonas Áridas, CCT-CONICET, Mendoza, Argentina*; [3]*Ecological Networks, Faculty of Biology, TU Darmstadt*

Adult dung beetles as well as their offspring feed on the excrement of vertebrates, a feeding habit which is defined as coprophagy. Feces are a rare and highly unpredictable resource which is available for short times only. Therefore a coprophagous insect's chance of encountering an adequate food source should be higher for polyphagous feeders than for specialists. Thus coprophagous Scarabaeidae are regarded as polyphagous. However, there is evidence for preferences for feces produced by vertebrates with certain dietary habits, e.g. herbivores, by some beetle species. Nevertheless these dung beetles are not specialized. To locate dung, adult beetles rely on olfactory cues. Earlier studies proved that excrements are chosen in response to their volatiles. Yet it remains undetermined which volatile substances from the headspace of dung act as attractants for coprophagous beetles and what the function of the volatiles for the beetles' preferences is. For my study, I chose four volatiles for which an attractive effect on dung beetles has been hypothesized. A comparison of the attractive effect on dung beetles was conducted using pitfall traps baited with different types of dung and different combinations of these four volatiles. Fieldwork took place in Argentina, Austria and Germany. We found that while single substances as well as mixtures do lure dung beetles, their level of attractivity varies. Furthermore, the level of specialization of species was compared by means of network analysis and a higher level of specialization was found for the Argentinian dung beetle fauna compared to the Austrian one.

☐36 Michael Heethoff A 702 / 14:45

Chemical Ecology of oribatid mites - The significance of oil-gland secretions for predator defense

Author: *Michael Heethoff*[1]
Affiliation: [1]*University Tübingen, Institute for Evolution and Ecology*

Oribatid mites are among the most diverse and abundant animals in forest soils, where they represent an important part of the decomposer system. While several studies have investigated bottom up energy flow, there is much less information on top-down control of these animals. Predation experiments resulted in the hypothesis that oribatid mites live in an 'enemy-free' space and this has been explained by their morphological protection (e.g. hardened cuticle, elongated setae, ptychoidy). In addition, most oribatid mites possess a pair of opisthosomal exocrine oil-glands. While the chemistry of oil-gland sectretions has been investigated for 20 years now, little is known about their biological functions. Here, I show that the oil-gland secretions provide a significant protection from predation and that this chemical protection is effective even when morphological protection is absent. Defensive secretions can be regenerated after depletion, but it takes some time to restore sufficient quantities for effective chemical defense.

☐37 Ann-Marie Rottler A 702 / 15:00

Wax scent and its communication function in bumblebee colonies

Authors: *Ann-Marie Rottler*[1], *Manfred Ayasse*[1]
Affiliation: [1]*Institute of Experimental Ecology, University of Ulm, Germany*

Social insects rely on a highly efficient information transfer between colony members. They are able to communicate and identify caste, sex, kin, nestmate and fertility by means of cuticular lipids. However, the signaling function of cuticular lipids is not limited to the recognition of individuals. These substances have been shown to provide information on colony identity in the nest environment of honeybees and paper wasps. In this study we examined communication functions of wax lipid patterns and their effect on nest recognition and social behavior in the bumblebee *Bombus terrestris*.

Our chemical analyses and bioassays showed that wax contained colony specific chemical patterns that allowed bumblebees to recognize wax from their own nest. However, not only colony identity but also colony age had a strong effect on wax profile variations. With increasing colony age, the same subset of substances changed in a similar manner in all colonies observed. Interestingly some of these substances are known to advertise fertility on the cuticle surface of female bumblebees. From behavioral assays we found, that these changes in colony scent influenced the decision of workers to reproduce. Worker groups started to compete for reproduction despite the presence of a queen when facing wax from a colony in a later stage of development.

As nest wax can provide a multitude of information and affects worker reproduction, we suggest that it plays a decisive role in the social communication of bumblebees.

This study was supported by the Carl Zeiss Foundation and the DFG (AY12/3-1).

☐38 Marko Rohlfs A 702 / 15:15

Insect-fungus interactions driven by sex and toxins

Authors: *Marko Rohlfs*[1], *Silvia Caballero Ortiz*[1], *Subhankar Chatterjee*[1], *Katharina Döll*[1], *Petr Karlovsky*[1], *Stefan Scheu*[1]

Affiliation: [1]*J.F. Blumenbach Institute of Zoology and Anthropology, Georg August University Göttingen, Germany*

Inducible defense strategies are well established for plants attacked by herbivorous insects. In contrast, fungi, despite their tremendous importance in the decomposer food web, have largely been neglected. Direct fungivore resistance is mediated by chemical properties of fungal tissue, e.g. production of toxic secondary metabolites (mycotoxins). However, whether fungi control the synthesis of toxic metabolites in response to insect fungivory and thereby affect insect behavior and fitness is unknown. We demonstrate that insect fungivory on *Aspergillus nidulans* induces a chemical phenotype that repels future fungivores and retards fungivore growth. We found a significant up-regulation of various SMs and key genes involved in SM synthesis in insect-challenged fungi, which coincided with the formation of sexual fruiting bodies that were better protected against fungivory than asexual structures. Our study thus demonstrates adaptive plasticity in the ability of fungi to resist fungivory, which can be expected to affect multitrophic interactions in fungivore communities.

Monday, September 24, 2012

Invited speaker 2: Chair – Ingo Hahn A 702 / 11:00

Stefan Lötters (Trier)

Ecological niches in Amazonian amphibians: linking macroecology to evolution

Author: *Stefan Lötters*[1]

Affiliation: [1]*Biogeography Department, Trier University*

Macroecology addresses the abundance, distribution and diversity of organisms at large spatial scales. In recent years, the ecological niche has received considerable attention in macroecological research by increased efforts in developing models of niche dimensions and, derived from that, species distributions models. Many of the studies focus on the development and performance of techniques. I am interested in the ecology and evolution of tropical biota, in particular Amazonian amphibians. In this presentation, I give examples how we apply niche and species distribution modeling to study (i) the Pleistocene biogeography of species which perform Müllerian mimicry, (ii) the spatial ecology and history of allopatric congeneric species, (iii) the Disturbance Vicariance hypothesis.

Chair: Stefan Lötters

☐39 Janos Hennicke A 702 / 16:00

Foraging strategy and plasticity of the Abbott's Booby: keys to a unique life history in an extreme environment?

Authors: *Janos Hennicke*[1], *Henri Weimerskirch*[1]
Affiliation: [1]*Marine Predator Group, CEBC - CNRS, Villiers-en-Bois, France*

Seabirds have evolved various life history traits and foraging strategies to successfully reproduce under the variable, heterogeneous and unpredictable conditions of their marine foraging habitat. Oceanic tropical waters are specifically low but relatively stable in prey availability. Thus, tropical pelagic seabirds should have evolved specific adaptations in reproductive and foraging behaviour but knowledge on this is sparse.

The Abbott's Booby *Papasula abbotti* is endemic to Christmas Island in the tropical Indian Ocean. It shows reproductive life-history traits (e.g. the longest breeding period of all seabirds) and a morphology that differ from all other Sulid species suggesting extreme adaptations to a highly oligotroph environment.

In a seven year study with contrasting oceanographic conditions, the foraging behaviour of Abbott's Boobies was investigated using GPS- and Depth-loggers to examine 1) if the species shows foraging strategies that lie at the origin of its unique reproductive life history traits and distinct morphology, and 2) how the birds adjust their foraging behaviour to interannually varying conditions in their generally stable marine environment.

Abbott's Boobies showed several unique foraging behaviours: Flight velocities were slower and diving activity lower than in other boobies. Foraging efficiency was enhanced by distinct temporal tuning of diving activity and trip timing. Bearings and sense of rotation of foraging trips suggested a strong reliance on wind for energy saving gliding.

Birds exhibited a restricted foraging flexibility: Trip duration, trip range and maximum dive depth increased and diet composition changed to buffer poor prey conditions, while parameters like diving activity and sinuosity did not change. Remarkably, the time spent on the water increased counteracting the increase in trip duration.

Despite the limited plasticity, Abbott's Boobies were able to keep their body condition stable and reproduce even under unfavourable conditions in contrast to other, sympatric booby species. However, while the long chick-rearing period reduces energetic demands per unit time, the buffering capacity of the restricted foraging plasticity may eventually reach its limits due to the length of the period. This trade-off might pose problems for the endangered species, if the expected changes in its marine habitat due to global warming eventuate.

☐40 Frauke Krüger A 702 / 16:15

Seasonal and geographical dietary variation in a typical European trawling bat, *Myotis dasycneme* Boie, 1825

Authors: *Frauke Krüger*[1], *Florian Gloza-Rausch*[2], *Martin Klempt*[3], *Silvia Kaschner*[3], *Robert Sommer*[1]

Affiliation: [1]*Department of Landscape Ecology, Institute for Natural Resource Conservation, Christian-Albrechts-University Kiel*; [2]*Noctalis –World of Bats GmbH, Bad Segeberg*; [3]*Max-Rubner-Institute, Kiel*

Many bat species depend on aquatic habitats as major food supply. Of the European Vespertilionidae at least five species can be found foraging along water bodies. The pond bat (*Myotis dasycneme Boie*, 1825) is probably the largest and most adapted European water foraging bat, strongly connected with aquatic ecosystems and predating mainly aquatic arthropod communities. To understand the trophic strategy of water hunting bats during reproduction, animals' diets were studied across the distribution range of *M. dasycneme* considering time related shifts. Our study presents a detailed dietary analysis of pond bats, representing a typical trawling Myotis species, showing a rather consistent feeding behaviour across its areal. Prey items found in the diet of the studied bat represent as well trawling behaviour as aerial hawking. Pond bats seem to feed mainly on Chironomidae adults and sub-adults, especially during lactation, but shift predation towards other prey items, e.g. Lepidoptera, around the time of weaning. Additionally they also seem to feed regularly on fish during gravity and lactation, only shown by molecular dietary analyses. Whether Pond bats are "scavengers" feeding opportunistically on everything available on water surfaces or if they select for certain prey groups is being discussed.

☐41 Tamara Pokorny A 702 / 16:30

Long distance dispersal of male orchid bees across the Yucatán peninsula

Authors: *Tamara Pokorny*[1], *Nils Blumreiter*[1], *Javier Quezada-Euan*[1], *Thomas Eltz*[1]

Affiliation: [1]*Ruhr-Universität Bochum, Department for Animal Ecology, Evolution, and Biodiversity*

A characteristic trait of male orchid bees (*Apidae, Euglossini*) is the collection of volatile chemicals (fragrances) from the environment, which are stored in specialized hind leg pockets for later exposure during pre-mating behavior. The search for volatiles may lead to large foraging ranges or even an entirely nomadic life style in males, and the very low population genetic structure observed in orchid bees is in agreement with either notion. Flight distances of a few kilometers have been demonstrated previously by classical mark-recapture and radiotelemetry. Here, we applied two novel mark-recapture techniques for assessing flight distances of male euglossines on the Yucatán peninsula, a large area of rather uniform vegetation and topography in southern Mexico. Bees were marked manually with lasting scratch patterns on the thorax cuticle, or marked themselves chemically by collecting from fragrance baits intermixed with distinct and not naturally occurring substances. Over the course of three weeks, bees were captured along transects across Yucatán and checked for scratch marks or marker substances (laboratory analyses using GC/MS).

Our results revealed that though some male bees remained in the same region over extended periods of time, a few covered extraordinary distances, extending the observed flight distances of male orchid bees by more than an order of magnitude.

☐42 Robert Sigl A 702 / 16:45

Plastic responses to food limitation in Acanthaster planci observed by in vivo magnetic resonance imaging (MRI) and subsequent 3D modeling

Authors: *Robert Sigl*[1], *Anastasia DeMotte*[1], *Christian Laforsch*[1]
Affiliation: [1]*Department Biology II, Ludwig-Maximilians-University of Munich*

Mass outbreaks of *Acanthaster planci* are known to threat coral reefs in the Indo-Pazific region and the Red Sea for several decades. Understanding the biology of this corallivore starfish might help to foster management strategies and to uncover the mechanisms underlying the outbreak phenomenon which still remains a subject of speculation. In our experiments we used magnetic resonance imaging (MRI) and subsequent 3D-reconstructions to follow size changes of pyloric caeca of *A. planci* in fed and starved individuals. Our results show that the pyloric caeca undergo enormous size changes, strongly suggesting that they act as an energy source under limited food conditions. In addition, digital image analysis revealed that the body wall seems to be used for the mobilization of energy reserves, as animals showed significant negative growth when starved. All of the morphometric changes are reversible and negative growth of certain body parts was strongly positive when animals were fed again. Our results show and quantify, for the first time in vivo, how strong structural reorganization is in Echinoderms that experience food limitation. Further, the results may explain why often masses of similar sized *A. planci* individuals appear on reefs at the beginning of an outbreak, when having in mind that the animals might have travelled long distances from exploited reefs. During their migration they do not have predictable food sources, therefore starve and might shrink to similar sizes.

☐43 Ingo Hahn A 702 / 17:00

2010 Chilean tsunami: impacts on soil, flora and fauna of the threatened ecosystem of Robinson Crusoe Island

Authors: *Ingo J Hahn*[1], *Pablo M Vergara*[2], *Gerardo E Soto*[2], *Julia Baumeister*[1]
Affiliations: [1]*Animal Work Group, Inst. Landscape Ecology, University of Muenster*;
[2]*Departamento de Ingeniería Geográfica, Universidad de Santiago de Chile, Santiago, Región Metropolitana, Chile*

Soil, flora and fauna of the threatened island ecosystem of Robinson Crusoe, especially in the littoral zone, are prone to changes through extreme maritime events. Tsunamis, like the 2010 tsunami in Chile, have severe impacts on the life in general along the coast side (Prasad et al. 2010). E.g., for 3 % of the human population of Robinson Crusoe Island this event was mortal. This Chilean island, although having only an area of 47 qkm, is also the prime conservation hot-spot within the country, e.g. hosting rare soil types and c. 20 % of the county's endemic bird species. Very little is known in general about the impacts of tsunamis on soils,

flora and fauna. However, the impact on mineral grain transport (and thus soils) was found to be extensive (Bahlburg & Spiske 2011, Bahlburg & Spiske 2011). On Robinson Crusoe the endemic hummingbird, the Juan Fernandez Firecrown (*Sephanoides fernandensis*), showed a total population size of about 1100 individuals. As a nectar feeder it highly depends on flowering plants, and has co-evaluated with the endemic Asteraceen species *Dendroseris litoralis* which is mainly found along the coast side (Hahn et al. 2010). In turn, these plants depend on intact soils and thus also need supply from nutritious and protective mould/humus layers. In this study we investigated how a tsunami critically endangers a soil-plant-bird system as an example for a natural catastrophe event.

Bahlburg, H. & M. Spiske (2011): Sedimentology of tsunami inflow and backflow deposits: key differences revealed in a modern example. Sedimentology 59(3): 1063–1086. Hahn I., P. Vergara & U. Römer (2010): Forest structures of the Juan Fernandez Islands, Chile: significance for bird community composition and conservation. Geo-Oeko 31:1–10. Prasad, P. R. C., K. S. Rajan, C. B. S. Dutt & P. S. Roy (2010): A conceptual framework to analyse the land-use/land-cover changes and its impact on phytodiversity. Biodivers Conserv 19: 3073–3087. Spiske, M. & H. Bahlburg (2011): A quasi-experimental setting of coarse clast transport by the 2010 Chile tsunami (Bucalemu, Central Chile). Marine Geology 289: 72–85.

☐44 Daniel Lewanzik A 702 / 17:15

Artificial light at night affects ecosystem services provided by bats

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Artificial light at night (LAN) has been shown to affect various organisms including plants as well as invertebrate and vertebrate animals. Obligate nocturnal animals such as bats can be expected to be particularly affected by LAN, since LAN is present in urban as well as in many rural habitats during their nocturnal activity period. Among bats, a large diversity of feeding habits can be found. Temperate species feed exclusively on insects, whereas in the tropics – besides several generalists - many bat species are specialized on other food items such as nectar and fruits. Consequently, bats offer a multitude of ecosystem services, of which many are invaluable for humans (Ghanem & Voigt 2012). For example, it was calculated that by controlling pest insects the monetary value of bats to the U.S. agricultural industry amounts to about 23 billion US$ per year (Boyles et al. 2011). Also, bats are important pollinators and dispersers of many tropical plant species. Short-tailed fruit bats (genus Carollia), for example, are specialized on fruits of the genus Piper and constitute the main disperser of many Piper species - important pioneer plants in the Neotropics that grow at forest edges or gaps and thus are key to forest regeneration. However, due to this habitat preference, Piper plants are predisposed to become affected by LAN, for example if street lights become installed along roads. We asked whether LAN is reducing the visitation rate, and thus the dispersal of seeds by Carollia when frugivorous bats avoid illuminated areas due to an improved visibility to predators. We captured individuals of Carollia sowelli in a Costa Rican rainforest and transferred them singly to a flight cage. After a short acclimatization period, bats could choose to harvest fruits in a dark compartment or in a compartment dimly illuminated by a street light. On average, C. sowelli chose the dark compartment for its first entry into the choice area more often than would be expected by chance. Also, they conducted more flights and, importantly, harvested more fruits in the dark than in the illuminated compartment. We conclude that LAN reduces the variety and quantity of ecosystem services that bats provide, i.e. specifically a reduction of seed dispersal and probably also of pollination. This might be particularly relevant in the tropics, where ecosystem services of bats are ecologically important for ecosystem functioning, and where at the same time the potential for light pollution to increase is very high.

JG Boyles, PM Cryan, GF McCracken, TH Kunz (2011) Economic importance of bats in agriculture. Science 332:41-42. SJ Ghanem, CC Voigt (2012) Increasing awareness of ecosystem services provided by bats. In: HJ Brockmann, TJ Roper, M Naguib, JC. Mitani LW Simmons (eds.) Advances in the study of behavior 44, Burlington Academic Press, pp. 279-302.

7. *Ecology POSTERS*

♦40 Isabelle Flaig

Recruitment behaviour and communication in *Partamona orizabaensis*

Authors: *Isabelle C. Flaig[1], Ingrid Aguilar[1], Thomas Schmitt[1], Stefan Jarau[1]*
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Social insects have evolved communication systems to recruit nest mates to food sources. Foragers of several stingless bees species deposit pheromone trails on solid substrates to guide nest mates to food sources. Over fifty years ago, Kerr (1969) stated that stingless bees of the genus Partamona create aerial odour trails to recruit workers to resources. He postulated that foragers release pheromones during flight and lead naïve bees in large groups to food sources. However, experimental proof is lacking. We studied recruitment behaviour and communication mechanisms in the species Partamona orizabaensis.

During field experiments, newly recruited bees had to choose between a recruitment feeder visited by experienced foragers and an unvisited control feeder. The recruits always preferred the recruitment feeder over the control, indicating that an efficient recruitment to the known feeding site took place. However, we never observed scent trail marking between the feeder and the nest.

Additionally, we recorded the bees' choice behaviour towards feeders baited with labial- and mandibular gland extracts, potential sources for recruitment pheromones. The bees did not prefer any of the gland extracts. Rather, mandibular gland compounds had a clear deterrent effect at feeders.

Chemical analyses revealed that labial gland secretions are predominately composed of alkenes, whereas mandibular gland secretions contain alcohols and esters. This is interesting because esters are known to serve as recruitment pheromones in trail laying species. Whether these compounds are released by Partamona foragers during flight in order to guide recruits to food sources needs to be clarified in future studies.

Kerr W. E. 1969. Evol. Biol. 3: 119-175

♦41 Faten Gabsi

A modeling approach to characterize population-level effects of sub-lethal exposure to toxicants in *Daphnia magna*

Authors: *Faten Gabsi*[1], *Thomas Preuss*[1]
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In this study, we aim to determine how sub-lethal effects measured on individuals affect population properties in *Daphnia magna*.

Toxicant-induced changes on individuals translate differently at the population level. For instance, population decline may arise from simple affected individual-level endpoints, whereas a significant influence on other endpoints might have negligible impact on population size and/or structure.

Population modeling has been used as a powerful tool to extrapolate measured effects on individuals to the population level. It allows including the variability between individuals in response to chemical's exposure and accounting for the different mechanisms of action of a toxicant.

In this work, we use an already developed and validated individual-based model for *D. magna* (IDamP, see Preuss et al, 2009) as a virtual laboratory in order to investigate the sub-lethal effects of a hypothetical toxicant on the population level, and to compare their relative magnitudes of effects.

Different simulation scenarios will be tested: Effects on reproductive performance might be exerted via various mechanisms like reduction in the filtration rate, delay in the time to first reproduction, etc. A slowed or inhibited growth induced by exposure to the toxicants will also be assessed solely or combined to reproductive effects.

Modeling these different responses will be addressed in combination to varying environmental factors like variable food levels.

Using such an approach allows us to explain the interactions between natural factors and toxicity at the level of individuals which ultimately emerge as effects on populations' properties.

♦42 Michael Gerth

Patterns of Wolbachia infections in bees (Anthophila)

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Endosymbiotic bacteria of the genus Wolbachia infect nematodes, arachnids, crustaceans and insects with a prevalence of up to 66%. The various ways Wolbachia alters the reproduction of its hosts and thereby promotes its own vertical transmission have received much attention. Recently, it has become clear that the high prevalence and worldwide spread of Wolbachia has happened through frequent lateral transfers of infections between even distantly related hosts. The mechanisms thereof are only partially understood.

In bees (Anthophila), Wolbachia infects about two thirds of all species. A previous study has suggested that many strains are transmitted horizontally among bees. The biology of bees is well studied and therefore they represent a good model for the investigation of horizontal transfer of Wolbachia.

In our study, we aim to contribute to the understanding of Wolbachia transfer. As a first step, using a MLST-approach we sequenced five bacterial housekeeping genes to classify strains that infect bees.

By phylogenetic analyses of Wolbachia strains we tried to distinguish between vertical and horizontal bacteria transfer. Moreover, by mapping ecological traits on our tree we tried to identify ecological prerequisites that make bees especially susceptible to infections. Factors included in our analyses comprise nesting biology (endogeic or epigeic nesting), lifestyle (solitary, social or kleptoparasitic), pollen source and also phylogenetic relatedness.

Our findings will help to comprehend the pathways of Wolbachia in general.

♦43 Holger Goerlitz

The sensory ecology of a predator-prey community: neural representation of bat predation risk in moths

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Predator cues are some of the most vital types of environmental information for animals. The threat posed by predators differs between sympatric predators within a community and also between predator communities. We hypothesized that prey sensory systems are adapted to the sympatric predator community, differ between areas with different predator communities and provide a constant representation of predator threat independent of predator species. The ears of Noctuid moths are an adaptation to detect the echolocation calls of predatory bats, consisting of two auditory receptors with frequency-dependent hearing thresholds. We determined auditory receptor thresholds of 15 moth species for pure tones to obtain audiograms and also for the echolocation calls of 13 sympatric bat species both in the lab and in the field, and compared them to potential information provided in the echolocation calls of bats. We show that bat call frequencies are tightly correlated with four bat characteristics related to predator threat (flight speed, call intensity, duration, and interval). The frequency-dependent hearing threshold of moths could potentially exploit this correlation to functionally link the predation threat posed by different bats to the elicited neural activity. We discuss different proxies of predation threat (bat distance, time to detection, and number of calls to detection) and how they are neurally represented across the whole bat-moth-community.

♦44 Monika Greschista

Oviposition is not necessary for long-term memory formation in the parasitoid wasp *Nasonia vitripennis* (Hymenoptera: Chalcidoidea: Pteromalidae)

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Learning and memory formation are essential to cope with changing environmental conditions, and therefore are common within the animal kingdom. In parasitoid wasps, olfactory learning is generally assumed to be important for host finding. In many of these wasp species, oviposition experience is required for protein synthesis-dependent long-term memory (LTM) formation. Here, we show that this is not true for the model organism Nasonia vitripennis WALKER, 1836. Female wasps were conditioned to cinnamon (conditioned stimulus) in the presence of two fly pupae (unconditioned stimulus). Six days after conditioning, the reaction of the wasps towards cinnamon was tested. Five different procedures were used for conditioning, revealing that LTM was formed after I) drilling plus host feeding, II) three drilling events (spaced conditioning), III) 1h-conditioning and IV) 24h-conditioning, but not after V) one single drilling event. Fly pupae used for conditioning of the wasps were afterwards collected and checked for emerging wasps. Interestingly, oviposition did only occur during 24h-conditioning. In many animal species, the transcription factor CREB (cAMP responsive element-binding protein) has been demonstrated to play a crucial role in LTM-formation. We knocked down CREB using RNAi, in order to show LTM-formation via 1h-conditioning (including drilling and host feeding). Wasps were injected with dsRNA of CREB (test group) or DsRed (control group) two days prior to conditioning and tested six days afterwards. The wasps of the test group did not show a significant preference for cinnamon while the control group did so. These results support the hypotheses that 1) LTM-formation in N. vitripennis does not depend on oviposition and 2) that CREB is involved in LTM formation in this species.

♦45 Axel Hochkirch

The combined effects of climate change and habitat fragmentation on the decline of a flightless wetland grasshopper

Authors: *Axel Hochkirch*[1]*, Jessica Weyer*[1]*, Katja Rohde*[1]*, Michael Veit*[1]
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Deterioration and fragmentation of wetlands is of major concern for nature conservation. Many biota are strongly dependent on wetlands, including a large number of invertebrates. We studied population trends, mobility and population genetics of an endangered grasshopper, *Chorthippus montanus*. Our results suggest that this species is strongly threatened by climate change as it has lost all populations < 400 m in Rhineland-Palatinate during the last 30 years. Furthermore, we found a very low mobility of this species on five study sites. However, mobility correlated positively with habitat size and negatively with vegetation density. We also performed mark-release experiments, which showed that mobility increased dramatically in unsuitable habitat (forest). In hybridization and mate choice experiments, we found out that *Ch. montanus* may hybridize rapidly with *Ch. parallelus*, particularly when heterospecific abundance is much higher than conspecific abundance. This might explain the records of intermediate morphotypes at localities where the *Ch. montanus* occurred before. Altogether, our results suggest that *Ch. montanus* is strongly threatened by climate change. Due to the strong fragmentation of the populations and its low dispersal abilities, it is not able to rapidly colonize suitable habitat. After periods of drought, it might be displaced by hybridization with *Ch. parallelus*.

♦46 Hannes Imhof

A new, highly efficient method for the quantification of Plastic Particles in sediments of aquatic ecosystems

Authors: *Hannes K. Imhof[1], Johannes Schmid, Reinhard Niessner, Natalia P. Ivleva, Christian Laforsch*
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Although plastic debris is constantly accumulating in aquatic environments, the impact on aquatic ecosystems is not yet fully understood. Once plastic litter enters natural environments, UV radiation, mechanical abrasion, biological degradation and disintegration cause the formation of tiny fragments. Those persist and are not completely degraded in any human scale of time. Harmful consequences of plastic debris for aquatic organisms have been already shown. Next to mechanical impairments of swallowed plastics mistaken as food, many plastic associated chemicals are proven to be carcinogenic, endocrine-disrupting or acutely toxic. Hence, it is indispensable to identify and quantify the types of plastic debris of different size classes in aquatic habitats for future risk assessment studies. A first important step in order to assess the consequences of plastic debris in aquatic ecosystems is a reliable, verified and standardized method to quantify the amount of plastic particles. Hence we developed an accurate method based on density separation in a ZnCl2 solution (at density 1.6 - 1.7kg/l), which allows for an extraction and quantification of plastic particles from sediments of aquatic environments. Furthermore, we constructed a Plastic Sediment Separator (PSS) which enables a reliable separation of different types and size classes (including S-MPP) of plastic particles from sediment samples. Our study is the first providing validated recovery rates of 100% for large micro-plastic particles (L-MPP, 1-5 mm) and 95.5% for small micro-plastic particles (S-MPP, <1 mm). Subsequent identification of the particles with spatial resolution down to 1 µm can be performed using Raman microspectroscopy. Our new method, therefore, can be used for a reliable separation, identification and quantification of plastic fragments ranging from meso-plastic particles (20-5 mm) to S-MPP (<1 mm) from samples of aquatic sediments and even plankton samples. This will help to foster studies quantifying the increasing contamination of aquatic environments with plastic particles, which is a crucial prerequisite for future risk assessment and management strategies.

♦48 Simon Korn

New pheromones from granary weevils *Sitophilus granarius*?

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Affiliation: [1]*Universität Hohenheim, Institut für Zoologie, Tierökologie 220c, Stuttgart*

The granary weevil *Sitophilus granarius* is one of the major pests of stored grains worldwide. Because the development of the larvae takes place inside the grain kernels, an infection with *S. granarius* leads to qualitative and quantitative losses in grain and causes enormous economical damage. Due to insecticide resistances and

healthcare issues, alternative control methods are more and more important. Sitophilate, the aggregation pheromone of *S. granarius* is not suitable as attractant for monitoring and/or mass trapping of the beetles. Therefore, we report on the development of new attractive lures. Bioassays in a static four-chamber olfactometer combined with the video tracking software BioMotionTrack D.S. revealed that larval faeces of *S. granarius* are attractive to both sexes of the weevil. In order to identify the attractive compounds, extracts of the larvae faeces were fractionated and attractive fractions analysed by GC-MS. The identification of attractive substances from the faeces might help to develop new lures to control these pest organisms.

♦49 Frauke Krüger

Eco-morphology of trawling Myotis'

Authors: *Frauke Krüger*[1]*, Stefan Greif, Sandor Zsebok, Robert Sommer, Björn Siemers*

Affiliation: [1]*Institute for Natural Resource Conservation*

Morphology is crucial for foraging performance in bats. Especially in trawling bats the ability to fly low over water, take and lift prey from or beneath the water surface and to feed on prey of different size is likely to be limited by morphological adaptations. Therefore we describe different morphological parameters, which are helpful in discussing ecological niches and foraging ecology of trawling bats. Wing measurements as well as bite force measurements were taken from live bats in the field in northern Germany. Measurements of lifting performance were taken from live bats under lab conditions. All results were correlated with dietary results for the species in the same region. Despite significant morphological differences both species showed high dietary overlap and similar niche breath. But differences regarding the prey types, referring to the terrestrial or aquatic life-cycle of prey groups, seem to support spatial segregation and different hunting preferences also indicated by different morphological adaptations. High resource abundance is also likely to allow the coexistence of both species´ within the same hunting habitat.

♦50 Jan-Jakob Laux

Can insect eggs learn to fly? - Dispersal ecology and population genetics of reed beetles (Genus: *Macroplea*)

Authors: *Jan-Jakob Laux*[1]*, Gregor Kölsch*

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Many freshwater invertebrates are - to lesser or greater extent - incapable to disperse themselves actively over longer distances and therefore have to rely on passive dispersal mechanisms.

Uniquely among the many species of leaf beetles, members of the genus *Macroplea* are adapted to a completely aquatic lifestyle. Living in brackish and freshwater habitats in inland lakes and the Baltic Sea, these beetles show strikingly little potential for active dispersal. They are flightless, their comparatively weak legs don't carry their weight out of water and they are even unable to swim actively.

Details of the life cycle of the beetles and population genetic structure hint at different mechanisms of passive dispersal for coastal and inland populations. While geneflow among populations in the Baltic Sea is probably mainly provided by drift with ocean currents, these species might also show adaptions for (endo-) zoochorous dispersal via water birds, enabling them to colonize otherwise inaccessible inland habitats.

The project focuses on population genetic analyses, GIS-based analysis of water bird movements and feeding trials to test for possible mechanisms of passive dispersal in the species *Macroplea mutica*.

♦51 Patrick Daniel Mack

A new pheromone compound in the sawtoothed grain beetle *Oryzaephilus surinamensis*

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The grain feeding beetle *Oryzaephilus surinamensis L.* (Silvanidae) causes major damages of stored grains worldwide. To develop control measures based on pheromone traps, we tested the biological activity of 5Z, 8Z, 12S)-5, 8-Tetradecadien-12-olid (?Cucujolide Va?) to male and female beetles in a four-chamber olfactormeter. This macrolide was isolated from feces of this beetle, but is not yet described as pheromone. Its molecular structure is similiar to the *O. surinamensis* aggregation pheromone Cucujolide V, which was described earlier. The study revealed sex-specific reactions to the R- and S-enantiomer: Whereas male beetles did not react to neither the R- nor to the S-enantiomere, female beetles were arrested by the R-macrolide, but not by the S-form. Interestingly, the R-macrolide is attractive when offered alone. This is in contrast to all other macrolides described as pheromones in *O. surinamensis*, which are reported to act only as mixtures. This might facilitate the use of these pheromones to control the beetles.

♦52 Lea Mauz

Monitoring of the rare click beetle species *Elater ferrugineus L.* in Baden-Württemberg using pheromone traps

Authors: *Lea Mauz[1], Sabrina Reimann[1], Till Tolasch[1], Johannes L.M. Steidle[1]*
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The click beetle, *Elater ferrugineus L.*, develops exclusively in tree hollows with wood mold, feeding on larvae of scarab beetles like *Osmoderma eremite SCOP*. As a result of massive habitat loss caused by modern forestry, *E. ferrugineus* is threatened throughout its entire distribution range and regarded as an indicator species for undamaged natural forests. However, monitoring of this species by standard collecting methods is difficult due to its hidden life style. Up to 2010, only seven specimen were recorded from Baden-Württemberg. Here we report on a new method for the monitoring of this species, based on the recently identified female sexual pheromone by our group (Tolasch et al. 2007) as well as the sexual pheromone of its preferred prey organism *O. Eremita*. The latter was supposed to be an attractant for both sexes of *E. ferrugineus* (Svensson et al. 2003).

Single pairs of test and control traps were placed in suitable habitats in the area of Stuttgart, Pforzheim, Heilbronn, Schwäbisch Hall, Ellwangen, Heidenheim, Geislingen, Tübingen and Calw. Thereby, beetles were trapped in 26 of 77 sites in quantities of up to 70 beetles per trap, raising the number of known sites with *E. ferrugineus*-occurrence in Baden-Württemberg to more than 30. Almost no beetles were found in traps baited with the pheromone of *O. eremita*. Thus, trapping with sexual pheromones proves to be an efficient method for the monitoring of *E. ferrugineus*. In contrast, the pheromone of *O. eremita* is probably not suitable for this purpose.

♦53 Anja Portsch

Trade-off between dispersal and reproduction in the pygmy grasshopper *Tetrix subulata* (Orthoptera: Tetrigidae)

Authors: *Anja Portsch[1], Arne W. Sehmann[1], Gerlind U.C. Lehmann[1]*
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Dimorphism in wing length is well known in many insect species. It is generally believed that a trade-off between dispersal and reproduction exists, with the long-winged (LW) morph being a better disperser due to flight capability. The short-winged (SW) morph is less mobile: so SW females are potentially able to invest more energy reserves into offspring production. We tested several assumptions of life-history trade-offs in the wing-dimorphic pygmy grasshopper *Tetrix subulata*. Morphological examination supports the occurrence of two clearly distinct wing morphs in both sexes. SW individuals were smaller and showed greater variability in body size than LW individuals, the differences being particularly pronounced in males. In accord with a reproductive compensation hypothesis, SW females produced larger eggs. We show experimentally that the wing morph form has a strong influence on male mating duration: LW males copulate for a shorter period. The mating time for females, however, is unrelated to whether they have long or short wings. Our results in the pygmy grasshopper are consistent with theory, predicting a trade-off between wing development and reproduction.

♦54 Monika Poxleitner

Can a hybrid outcompete its parental species? - a life-history experiment with a 'super clone' (*Daphnia galeata* × *longispina hybrid*)

Authors: *Monika Poxleitner[1], Johanna Griebel, Sabine Gießler, Justyna Wolinska*
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In general, hybrids show lower fitness than the parental species. However, recently collected field data from the *Daphnia longispina* complex indicates that there might be exceptions from that. In the Feldmochinger See, a quarry lake in Munich, there is an F1 hybrid clone (‘super clone’) of *D. longispina* and *D. galeata* that was able to outcompete parental species and, moreover, has dominated the entire population of hybrids in this lake. The analyses of genetic data revealed that taxa composition in this lake fluctuated greatly from year to year. Specifically, in 2008 the community was composed of F1 hybrids belonging to several clones. In 2009 only *D. galeata* was found. In 2010 and 2011 only one F1 hybrid clone was present (the same one which

was already detected in 2008). We conducted a fitness test comparing this 'super clone' with other F1 hybrids and clones of the parental species (13 *D. longispina*, 11 *D. galeata* and 6 of their hybrids) isolated from several quarry lakes around Munich. The results of this experiment will help to understand what fitness components let the 'super clone' outcompete other hybrids and parental species. As the studied quarry lakes were created and thus opened for colonization only about 20 years ago, we will be able to analyse how hybrid-specific traits may facilitate the colonization of novel habitats.

◆55 Wesam Salah El-Dien Ali Meshrif

Genetic variation among *Drosophila melanogaster* isofemale lines underlying cellular encapsulation of the parasitoid, *Asobara tabida*

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One of the most important factors affecting the outcome of host-parasite interactions is genetic variation especially of the host. In this study, genetic variation in *Drosophila melanogaster* population was tested to underlie encapsulation ability to the parasitoid, *Asobara tabida*. To explore to what extent genetic variation exists within a Drosophila population regarding cellular encapsulation phenotype, and does it affects the resistance to the parasitoid, 10 isofemale lines, represent different levels of encapsulation ability were used. I scanned encapsulation ability and related characters such as infestation, avoidance, parasitism and superparasitism rates 8-days following oviposition. Thereafter, the same parameters plus mortality rate were observed in narrow range of lines after emergence. Weight of larvae, protein contents and phenoloxidase in extremes and intermediate lines, were investigated. Results extracted from encapsulation experiment, indicated that genetic difference among lines influences encapsulation and avoidance, parasitism and superparasitism rates. In emergence experiment, the difference among lines seems also to have a role in infestation rate of the parasitoid and mortality rate of the flies. Infestation rate with the parasitoid was statistically proven to reduce the weight of larvae and their protein contents. The variation among isofemale lines in encapsulation ability could be interpreted by phenoloxidase activation obviously in the lines with extreme encapsulation rates. These findings could help to design successful biological control programs and to interpret the outcomes. Otherwise, this study pays attention to the use of Drosophila-parasite system as a model to understand similar phenomena in other organisms.

◆56 Gabi Schmid

The smell of death: Attractive carcass odours for the parasitic wasp *Nasonia vitripennis*

Authors: *Gabi Schmid*[1]*, Pawel Malec*[1]*, Till Tolasch*[1]*, Joachim Ruther*[1]*, Johannes L.M. Steidle*[1]
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Since parasitoids cannot reproduce without suitable hosts, successful host finding is crucial for individual fitness of female parasitoids. Thereby, specific odour blends are often used to find the respective host. The wasp *Nasonia vitripennis* WALKER 1836 (Hymenoptera: Pteromalidae), a parasitoid of fly pupae, uses odours of carcasses and bird nests for host location. Earlier studies point to the existence of different host races in *N. vitripennis*, specialized on one of the two habitats, carcasses or bird nests. Here, we report on the identification of carcass odour compounds attractive for N. vitripennis females. Extracts and fractions of odour bouquets released from mouse carcasses in different stages of decomposition (1 week, 2 weeks and 4 weeks old) were produced and tested in a four chamber olfactometer.
Tested wasps originate from specimen emerging from fly puparia, which were found either next to carcasses or in birds nest.

♦57 Johannes Steidle

Phenology of *Nasonia vitripennis*, a parasitoid of fly pupae

Authors: *Johannes L. M. Steidle*[1]*, Maik Henrich*[1]*, Pawel Malec*[1]
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To investigate the possible basal position within the Annelida of Oweniidae and Magelonidae, we conducted ML- and Bayesian-based analyses using traditional Sanger ESTs and next generation sequencing. With extended taxon sampling we recovered a well-supported phylogeny with strong support for two major splits (Errantia and Sedentaria) including the biggest fraction of annelid diversity, indicating that life-history characters are phylogenetically informative. We found additional support for the backbone of the annelid tree comprising Chaetopterids, myzostomids, sipunculids grouping together with oweniids and magelonids outside the core Annelida and are not part of the Pleistoannelida.

♦58 Julian Torres-Dowdall

Ecological and Evolutionary trade-offs as the cause of stable distribution limits.

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Determining why organisms have restricted geographic distributions has been challenging because organisms interact in complex way their environment, but biologists agree that abiotic factors, biotic factors and/or their interaction affect species distribution. However, what is still unclear is why species do not evolve to overcome these ecological limitations and expand their distributions. Here, we explored the ecological factors and evolutionary forces driving the stable parapatric distribution of two Poeciliid fishes along a salinity gradient on the island of Trinidad. *Poecilia reticulata* is widely distributed across freshwater habitats, but abruptly drops at the brackish-freshwater interface. *Poecilia picta* occupy lowland brackish and freshwater habitats, but disappears further upstream. We found that *P. picta* is more tolerant to salinity than *P. reticulata*, but *P. reticulata* consistently outcompetes *P. picta* when they are force to interact. This suggest an ecological trade-off, with biotic interactions limiting the competitively subordinate, but more tolerant *P. picta* to the harshest end of the gradient, and abiotic conditions limiting the better competitor, P. reticulata, to the mildest end of the gradient. Interestingly, this trade-off was also observed at the family level in *P. reticulata*. Families more tolerant to salinity are worst competitors than less tolerant ones. Thus, selection to increase stress tolerance in this species will come at the expense of a reduction on competitive ability. We conclude that the downstream limit to the distribution of *P. reticulata* is driven by salinity, and is evolutionarily stable; and that the upstream limit to the distribution of *P. picta* is driven by competitive exclusion, and is potentially non-stable.

♦59 Monika Trienens

Chemical defense and reciprocal benefits mediate trophic interactions of *Drosophila melanogaster* with microfungi

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Development of *Drosophila melanogaster* is linked to decaying fruit. Here, microfungi transmitted by adults to breeding sites crucially affect larval development as dietary mutualists (e.g., yeasts) and antagonists (e.g, moulds). The mechanisms underlying these contrasting patterns of insect-microfungal interactions are poorly understood. Despite strong feeding pressure on yeast, *Saccharomyces cerevisiae*, larval foraging activity provided, in an insect density-dependent manner, a net benefit to the growth of yeast cell populations. In contrast, the toxin-producing filamentous fungus, *Aspergillus nidulans*, did not support larval development; yet, a chemical deficient A. nidulans mutant turned out to serve as a suitable, but rapidly diminishing dietary resource for *D. melanogaster* larvae. In addition to its dietary function for *D. melanogaster* larvae, we found yeast to suppress mould growth by means of volatile emission. Moreover, *D. melanogaster* females prefer to lay eggs on yeast-infested patches but avoid the ones heavily infested with moulds. While the combined positive effects of *D. melanogaster* egg-laying and larval foraging behaviour on yeast population growth support the idea of an insect-fungus mutualism, chemical defence, filamentous growth, and antagonism with Drosophila-transmitted yeasts represent a critical combination of mould properties that foster evolution of insect-fungus antagonisms.

♦60 Martina Weiss

Population structure of *Gammarus fossarum* in a central German low mountain range (Hochsauerland)

Authors: *Martina Weiss*[1], *Marcus Liebert*[1], *Jan Macher*[1], *Ralph Tollrian*[1], *Florian Leese*[1]
Affiliation: [1]*Department of Animal Ecology, Evolution and Biodiversity: Ruhr University Bochum*

Gene flow between populations of freshwater organisms is affected by extrinsic and intrinsic factors. The former encompass geographical distance, geological relief and hydrological barriers, whereas intrinsic factors include the ability to disperse actively.

Besides active movement of specimens, gene flow patterns can be affected by passive drift and transportation e.g. by animal vectors. As a consequence, the realized connectivity between populations in a landscape is difficult to predict based on a species? life cycle and the observed mobility only. In this study, we analysed the genetic connectivity between 26 populations of the hololimnic species *Gammarus fossarum* (Crustacea; Amphipoda) in the headwaters of several adjacent catchments in a German low mountain range (Hochsauerland). Using a 658 bp fragment of the variable mitochondrial CO1 gene, we tested whether the genetic distance between the populations is primarily correlated with the stream distance (isolation by stream distance scenario) or whether *Gammarus fossarum* is also dispersing by other means across catchment boundaries. Our results suggest that whereas gene flow is generally very limited, occasional transport even across catchment boundaries is possible.

8. Evolutionary Biology TALKS

Saturday, September 22, 2012

Invited speaker 1: Chair – Thomas Schmitt A 703 / 12:00

Anna Lindholm (Zürich)

Selfish genes in house mice

Author: *Anna Lindholm*[1]
Affiliation: [1]*Institute of Evolutionary Biology and Environmental Studies, University of Zurich*

Mendelian inheritance is the norm - when we reproduce, each of our alleles has a 50% chance to be passed to our offspring. What happens when this is not the case? The *t* haplotype provides a fascinating example. The *t* haplotype is a linked set of genes in wild house mice that shows drive: more than 50% (usually 90%) of offspring inherit the *t* when the sire is a carrier. The underlying mechanism is a poison-antidote system active in the testes of carrier males, resulting in damage to the developing wild-type sperm. There is a disadvantage to carriers, as there are fitness costs associated with the *t*, reducing the average fitness of *+/t* individuals compared to +/+. The *t* is therefore called a selfish genetic element, since it acts to bias its own transmission to the next generation, despite costs to the whole organism. Here I present recent theoretical and empirical research in our lab on the evolution of this selfish genetic element.

Chair: Sandra Steiger

☐45 Ilka Kureck A 702 / 14:00

Increased sexual investment in a highly inbred ant

Authors: *Ilka Maria Kureck*[1], *Evelien Jongepier*[1], *Susanne Foitzik*[1]
Affiliation: *[1]Universität Mainz*

Inbreeding can lead to the expression of deleterious recessive alleles and to a subsequent fitness reduction. In Hymenoptera, deleterious alleles are purged in haploid males moderating inbreeding costs. However, in these haplo-diploid species, inbreeding can result in the production of sterile diploid males. We investigated the effects of inbreeding on the individual and colony level in field colonies of the highly inbred ant Hypoponera opacior. In this species, outbreeding winged sexuals and nest-mating wingless sexuals mate during two separate reproductive periods. We show that regular sib-matings lead to high levels of homozygosity and the occasional production of diploid males, which sporadically sire triploid offspring. On the individual level, inbreeding was associated with an increased body size in workers and winged queens. On the colony level, we found no evidence for inbreeding depression as productivity was unaffected by the level of homozygosity. Instead, inbred colonies altered their allocation strategies by investing more resources into sexuals than into workers. This shift towards sexual production was due to an increased investment in both males and queens, which was particularly pronounced in the dispersive generation. The absence of inbreeding depression combined with increased reproductive investment, especially in outbreeding sexuals, suggest that these ants have evolved active strategies to regulate the extent and effects of frequent inbreeding.

☐46 Michael Weber A 702 / 14:15

Hierarchies, courtship and paternity: swordtail interactions in a natural-like setting

Authors: *Michael* Weber[1], Julia *Jones*[1], *Frederico Henning*[1], *Manfred Schartl*[2], *Axel Meyer*[1]
Affiliations: *[1]Lehrstuhl für Zoologie und Evolutionsbiologie, Department of Biology, University of Konstanz; [2]Physiological Chemistry I, Biozentrum, University of Würzburg; Zukunftskolleg, University of Konstanz*

Sexual selection is known to act via female preference for exceptional traits. Female association with preferred males is commonly inferred as a signature of sexual selection. To date, however, there is little evidence that such preferences translate into mating success for preferred males. To address this question we used the green swordtail, *Xiphophorus hellerii*, whose elongated colourful caudal fin (or sword) is a textbook example of female association preferences. We implemented a mesocosm setting where females were able to interact with males in a normal community environment. In each replicate experiment females had the opportunity to freely interact with long and short sworded males. Male sword length was artificially manipulated in accord with natural variation observed in the wild, and males were matched closely for all other traits. We recorded the behaviour of males and females

and genotyped all resulting offspring, embryos and any stored sperm using microsatellite markers. Contrary to previously documented female preference for longer swords via association tests, this preference does not always translate into greater paternity for those males in our set-up.

☐47 Alexandra Schrempf A 702 / 14:30

The consequences of double mating in Cardiocondyla obscurior

Authors: *Alexandra Schrempf*[1]*, Astrid Moser, Juergen Heinze*
Affiliation: [1]*University of Regensburg*

In social hymenoptera, young queens mate only during a short time span early in life, and afterwards store the sperm, with which they fertilize all eggs throughout their entire life, in their spermatheca. We could recently show that single mating increases the lifespan and fertility of female sexuals in the ant species Cardiocondyla obscurior. This is is in agreement with the assumption that - in case of such a lifelong pair bonding- both partners should aim to maximize their joint reproductive success. However, females of several ant species mate with more than one male, and competition between males can be strong. Accordingly, males have been shown to manipulate females e.g. by the transfer of mating plugs to prevent mating with a second male, or by biasing the sperm use of the female after copulation. In this study, we show, that also females of *Cardiocondyla obscurior* mate with more than one male, and investigate whether and how male-male competition causes manipulations and influences sperm use and female fitness in comparison to single mating.

☐48 Michaela Thoß A 702 / 14:45

Parent-offspring correlations in heterozygosity enhanced by non-random mating and allelic frequencies

Authors: *Michaela Thoß*[1]*, Petteri Ilmonen*[2]*, Kerstin Musolf*[3]*, Felix Knauer*[4]*, Dustin Penn*[1]
Affiliations: [1]*Konrad Lorenz Institute of Ethology, Department of Integrative Biology and Evolution, University of Veterinary Medicine Vienna;* [2] *Division of Genetics and Physiology, Department of Biology, University of Turku;* [3]*Institute of Evolutionary Biology and Environmental Studies, University of Zurich;* [4]*Institute for Wildlife Ecology, Department of Integrative Biology and Evolution, University of Veterinary Medicine Vienna*

It has been suggested that mating with heterozygous individuals can enhance offspring heterozygosity, though this idea is controversial because it is generally assumed that heterozygosity is not heritable. Here, we investigated this question in populations of wild-derived house mice (M. musculus musculus) in semi-natural population enclosures and a captive breeding colony. In the enclosures, we found a significant correlation between parent and offspring heterozygosity and allelic diversity within litters. A random mating simulation did not produce such a correlation, and therefore, we investigated how sexual selection could explain our findings. We found no significant evidence that heterozygous parents were more likely to avoid inbreeding or mate disassortatively than homozygous ones. Yet, we found a positive correlation between the overall heterozygosity of dams versus sires and assortative mating for heterozygosity significantly increased offspring heterozygosity. We found more heterozygous parents carried more rare alleles ? and they conferred more rare alleles to their offspring ? than other parents, which provides an additional mechanism to explain the heritability of heterozygosity. In mice arbitrarily bred in our colony, we also found correlations in parent-offspring heterozygosity and offspring genetic diversity, though much weaker than in enclosures. In summary, we found more heterozygous individuals produced more heterozygous and genetically diverse offspring than homozygous ones, and these correlations were more pronounced under conditions in which individuals mate assortatively for heterozygosity and heterozygotes carry more rare alleles than homozygotes.

☐49 Dieter Thomas Tietze A 702 / 15:00

Evolution of traits in the song of leaf-warblers (Aves: Phylloscopidae)

Authors: *Dieter Thomas Tietze*[1/2], *Balduin Fischer*[1], *Jochen Martens*[3], *Martin Päckert*[2]
Affiliations: [1]*Institut für Ökologie, Evolution und Diversität, Goethe-Universität Frankfurt am Main*; [2]*Senckenberg Naturhistorische Sammlungen Dresden, Museum für Tierkunde*; [3]*Institut für Zoologie, Johannes-Gutenberg-Universität Mainz*

A comparative phylogenetic approach is applied to identify mechanisms shaping the evolution of bird song in 80 taxa of leaf-warblers (Phylloscopidae). The effects of body size, horizontal and elevational distribution, habitat and migratory behavior on 20 song parameters were tested via simple and multiple regressions. A multi-locus phylogeny was compiled to assess the phylogenetic signal in song features and to account for the confounding effect of phylogenetic history on the regression analyses. High levels of evolutionary lability were corroborated for most song features, while element time parameters were found to be rather neutrally evolved. This pattern is attributed to the impact of adaptations: Most song features were driven by various selective forces leading to fast and irregular trait evolution across the tree. Conversely, high levels of genetic inheritance (proven by previous isolation experiments) and its role in species-specific recognition may have contributed to a slow evolutionary rate in element time parameters in leaf-warblers. In accordance with previous studies, body size had a large effect on overall frequency parameters, being higher pitched in smaller birds due to morphological constraints of the vocal apparatus. Surprisingly, no adaptations to the acoustic properties of the habitat were detected. Similarly, effects of migratory behavior were small. In contrast, numerous relationships with measures of horizontal and vertical distribution were indicated many of which remain difficult to link to a specific underlying causation. Overall, the results suggest that the evolution of song features in leaf-warblers is shaped by a complex network of environmental effects and morphological constraints as well as history.

☐50 Jannis Liedtke A 702 / 15:15

When should cuckolded males care for extra-pair offspring?

Authors: *Jannis Liedtke*[1], *Lutz Fromhage*[1]
Affiliations: [1]*University of Hamburg*

In socially monogamous species with bi-parental care, males suffer reduced reproductive success if their mate engages in extra-pair copulations (EPCs). One might therefore expect that males should refuse to care for a brood if they can detect that an EPC has occurred. Here, we use a game-theory model to study male brood care in the face of EPCs in a cooperatively breeding species in which offspring help to raise their (half-) siblings in their parents? next breeding attempt. We show that under certain conditions males are selected to care even for broods completely unrelated to themselves. This counterintuitive result arises through a form of pseudo-reciprocity, whereby surviving extra-pair offspring, when helping to rear their younger half-siblings, can more than compensate for the cost incurred by the male that raised them. We argue that similar effects may not be limited to cooperative breeders, but may arise in various contexts in which cooperation between (half-) siblings occurs.

Chair: Thomas Hoffmeister

☐51 Enrico König A 702 / 16:00

More than microbes: a new perspective about the evolution of antimicrobial peptides in the defensive skin secretion of anuran amphibians

Authors: *Enrico König*[1], *Olaf R. P. Bininda-Emond*[1], *Chris Shaw*[1]
Affiliation: [1]*Carl von Ossietzky Universität Oldenburg*

Amphibians exhibit characteristic adaptations as a consequence of their ‘incomplete’ shift from the aquatic to terrestrial habitats. For example, cutaneous mucous glands produce moist secretions to prevent potential desiccation, whereas the syncytial granular glands have been adopted for the biosynthesis of a wide range of defensive molecules. Here, we initially provide an overview of the chemical weaponry of Anura (frogs and toads) present in their skin secretions. We place special emphasis on peptides, which can be grouped into numerous families with homologues in mammalian tissues (e.g. central and peripheral nervous system or gastrointestinal tract) that act as hormones, neurotransmitters and neuromodulators. This overview permits a new perspective into the evolution and function of anuran antimicrobial peptides (AMPs), the most diverse frog skin peptide family. Traditionally, these peptides are viewed as being part of the innate immune system, protecting the skin against a broad range of microorganisms through a cytolytic mechanism due to their cationic, amphipathic and ?-helical character. However, these peptides are distributed sporadically (i.e., non-universally) across Anura with each species presenting a unique, complex cocktail of host-defensive peptides that is largely independent from its phylogenetic relationship to other species. Together with the intriguing observation that all anuran species known to produce neuropeptides also co-secrete cytolytic peptides in their granular glands, the traditional role for AMPs

cannot bear up under evolutionary aspects and requires a revised scenario that we illustrate here.

☐52 Miriam Stock A 702 / 16:15

Adaptation of a fungal pathogen to individual versus social immunity in ants

Authors: *Miriam Stock*[1], *Anna V. Grasse*[1], *Sylvia Cremer*[1]
Affiliation: [1]*Institute of Science and Technology Austria*

The armsrace between hosts and pathogens is characterized by continuous adaptations of both opponents in a co-evolving system. In social insects, these adaptions do not only include the hygiene behaviour and physiological immune system of the individual group members, but also their collectively performed, social disease defences ranging from sanitary behaviours, use of antimicrobials and organisational adaptations. We used the Argentine Ant, Linepithema humile, and the general insect pathogenic fungus Metarhizium to perform a selection experiment employing different selection pressures on the pathogen caused by the different levels of the colony immune system. We exposed worker ants to a mix of natural isolates of the obligate killer Metarhizium and reared the ants either in isolation or in contact with unexposed nestmates. We then determined pathogen adaptation to the selection pressure under individual host defences (isolation treatment) or individual plus social immunity (group treatment), respectively. First analyses reveal that both rearing conditions led to increased killing rates over time. Interestingly, the dynamics of pathogen adaptation and fungal strain composition between the isolated versus group treatment showed differences suggesting that the additional group level defences in insect societies add new selection pressures for their coevolving pathogens with measurable effects on disease dynamics.

☐53 Phillip Gienapp A 702 / 16:30

Predicting demographically sustainable rates of adaptation: can great tit breeding time keep pace with climate change?

Authors: *Phillip Gienapp*[1], *Marjolein Lof*[1], *Tom Reed*[1], *John McNamara*[2], *Simon Verhulst*[3], *Marcel Visser*[1]
Affiliations: [1]*Netherlands Institute of Ecology;* [2]*University of Bristol;* [3]*University of Groningen*

Human activities have already affected the biotic and abiotic environment of many species. Populations can cope with such environmental changes by evading to unaffected areas or adapting in situ by phenotypic plasticity or micro-evolution but in the long-term adaptation through micro-evolutionary change will be necessary. A key question is how the maximal possible micro-evolutionary change compares to the predicted rate of environmental change given that there is a 'critical rate of environmental change' beyond which increased maladaptation leads to population extinction. Here we parameterise the theoretical model by Bürger & Lynch (1995) to predict this critical rate using data from a long-term study of great tits (Parus major). We used stochastic dynamic programming to predict changes in optimal breeding time under three different climate scenarios. We accounted for phenotypically plastic changes of breeding time in response to warmer temperatures in our model. Our results indicated that even under 'mild' rates of climate change the predicted change in optimal breeding time would be close to the critical rate with which the great tits could cope by evolutionary change. For scenarios close to the upper limit of IPCC climate projections the calculated critical rate would however be clearly exceeded with possible negative consequences for population persistence. We therefore tentatively conclude that 'evolutionary rescue' in this population would only be possible for mild rates of climate change, although the model makes necessarily many simplifying assumptions which effects remain to be evaluated.

☐54 Sebastian Klaus A 702 / 16:45

Rapid adaptation to cave life: The freshwater crabs of Bohol, Philippines

Author: *Sebastian Klaus*[1]
Affiliation: [1]*Carl von Ossietzky University Oldenburg*

Within brachyuran crabs morphological adaptation to darkness is known from several groups, especially from primary freshwater crabs. Despite the remarkable hypogean diversity of brachyurans detailed phylogenetic or morphometric studies of cave adaptation in any of these groups, are still lacking.

Here the phylogenetic relationship, timing of cave colonisation and morphological adaptation to cave life within freshwater crabs of the genus Sundathelphusa (family Gecarcinucidae) is described. With more than 1400 registered caves, the small island of Bohol was already considered an ‘island of caves’.The caves from Bohol are inhabited by a species-rich cave fauna, including the freshwater crabs. These show different levels of troglomorphy within a small area of less than 40×40km, that led to the recognition of five species. Adaptation to cave life occured several times independently during the Pleistocene. Cave populations of the surface species already show signs of troglomorphism.

☐55 Lukasz Mitko A 702 / 17:00

Olfactory specialization in orchid bees and its role in speciation

Authors: *Lukasz Mitko*[1], *Thomas Eltz*[1]
Affiliation: [1]*Lehrstuhl für Evolutionsökologie und Biodiversität der Tiere, Ruhr-Universität Bochum*

Male neotropical orchid bees (Euglossini) collect volatile substances from orchids and other sources and store them in tibial pouches, accumulating complex and species-specific bouquets. These fragrances are later exposed at display sites, presumably to attract females. Former analysis of tibial fragrances of sympatric species revealed substantial chemical disparity among all lineages with an outstanding divergence between closely related species. We hypothesized that the outstanding divergence of the fragrance bouquets between closely related species is mediated by underlying species-specific, sensory adaptations which may be the product of reproductive character displacement on a sensory level, a possible driving force of speciation. Within the scope of this study we conducted electroantennographic measurements with 20 sympatric Panamanian species in the genius Euglossa with the aim of showing species-specific sensory tuning in favor of certain compounds. Our results have shown that the peripheral fragrance perception is species-specific even though there was no significant difference between closely related, sympatric species. However, strong antennal responses to some single fragrance compounds such as HNDB, ipsdienol, anisylacetate and hexahydrofarnesyl acetone indicate the existence of possible key compounds which could have an important influence in the process of speciation.

☐56 Alexander Kupfer A 702 / 17:15

Sperm storage in caecilian amphibians

Authors: *Alexander Kupfer*[1], *Susanne Kuehnel*[1]

Affiliation: [1]*Institut für Biochemie und Biologie, Universität Potsdam*

Female sperm storage has evolved independently multiple times among vertebrates to control reproduction in response to the environment. In internally fertilising amphibians, female salamanders store sperm in cloacal spermathecae, whereas among anurans sperm storage in oviducts is known only in tailed frogs. Facilitated through extensive field sampling we tested for sperm storing structures in the female urogenital tract of fossorial, tropical caecilian amphibians for the first time. In the oviparous *Ichthyophis cf. kohtaoensis*, aggregated sperm were present in a distinct region of the posterior oviduct in females prior to oviposition. Amounts of sperm were related to the reproductive status of females and sperm were absent in females past oviposition. Our findings indicate short-term oviductal sperm storage in the oviparous *Ichthyophis cf. kohtaoensis*. We assume that in female caecilians exhibiting high levels of parental investment sperm storage has evolved in order to optimally coordinate reproductive events and to increase fitness. Sperm competition likely applies.

Kuehnel S. and Kupfer A. (2012) Frontiers in Zoology 9:12

Sunday, September 23, 2012

Invited speaker 2: Chair – Gregor Kölsch A 703 / 11:30

Joseph Hoffman (Bielefeld)

Heterozygosity and fitness in seals

Author: *Joseph Hoffman*[1]

Affiliation: [1]*University of Bielefeld*

Many important fitness traits including parasite resistance, survivorship and reproductive success often correlate with heterozygosity in natural populations. However, because most studies use only around ten randomly selected microsatellite markers, we do not yet know which of two possible mechanisms, inbreeding depression or associative overdominance, is most important. I will outline the state of the art in this field in relation to an ecologically compelling group of marine mammals, the Pinnipedia (seals and sea lions). In particular I will draw upon novel insights from an exceptionally detailed long-term study of a breeding colony of Antarctic fur seals (*Arctocephalus gazella*) at South Georgia in the Southern Atlantic.

Chair: Alexander Kupfer

☐57 Adina Renz M 627 / 14:00

The mosaic evolution of the Dlx4 gene in the sauropsid lineage: Phylogenetic and expression analysis

Authors: *Adina J. Renz*[1]*, Axel Meyer*[1]*, Shigehiro Kuraku*[2]
Affiliations: [1]*LS Zoology & Evolutionary Biology, University of Konstanz;* [2]*Genome Resource and Analysis Unit, Center for Developmental Biology (CDB), Kobe, Japan*

Most derived vertebrates appear to possess six paralogs of the homeobox-containing distal-less (dll) gene, the Dlx genes. Commonly, these transcription factors are found as three convergently transcribed pairs in the genomes of most model vertebrates. Previous studies have reported conserved non-coding elements inside these clusters, suggesting their contribution to the maintenance of syntenic relationships. However, the intactness of the Dlx3-Dlx4 cluster has not been shown continuously in the genomes of all vertebrates. Generally, this cluster is known to be more derived functionally and phylogenetically. Inside the Dlx3-Dlx4 cluster, Dlx4 shows a higher rate of evolutionary change than Dlx3. One previous study reported that the chicken Dlx4 gene is a pseudogene, lacking a start codon, and so far, no intact cluster structure could be demonstrated for chicken. In this study we report the occurrence of Dlx4 orthologs, proven by maximum-likelihood phylogenetic analyses, and the existence of the intact Dlx3-Dlx4 cluster, employing already published sequence data of sauropsid species. Additional sequencing was performed for Dlx4 in Anolis carolinensis, the turtle species Pelodiscus sinensis and Emydura subglobosa, as well as the gecko Paroedura picta. We also investigated the expression patterns of Dlx4 during chick development, and we compared this Dlx4 expression to previously described expression data of Dlx3 and Dlx5. The in situ hybridization analysis of chick embryos at stage 23 show an expression of Dlx4 in the branchial arches 1 and 2, whereas an expression in the nasal pits and the apical ectodermal ridge was not detected in comparison to Dlx3 and Dlx5.

☐58 Oscar Brusa M 627/ 14:15

Divergent evolution in the polymorphic granular poison-dart frog, Oophaga granulifera: genetics, colouration, advertisement calls and morphology.

Authors: *Oscar Brusa*[1]*, Adriana Bellati*[1]*, Ivonne Meuche*[1]*, Nicholas Mundy*[1]*, Heike Pröhl*[1]
Affiliation: [1]*Institute of Zoology, University of Veterinary Medicine, Hannover*

Intraspecific geographical variation in colouration is a common phenomenon in animal species. Among those, aposematic animals represent a peculiar case because such a variation is expected to be highly constrained. Characterising geographical patterns of phenotypic and genetic divergence is important to understand the processes responsible for the evolution of colour diversity in aposematic species. We investigated the phylogeographic structure of the poison-dart frog *Oophaga granulifera* in Costa Rica, analysing mtDNA and microsatellite loci, and contrasted the observed divergence to the variation in colouration, advertisement call and morphology. We found two clearly divergent southern and northern lineages, the former phenotypically red and the latter including red, green and an array of intermediate variants. The reflectance spectra analysis showed gradual variation in a colour transition area between the red and green morphs. Those extreme morphs diverged in advertisement call and morphology revealing potential for assortative mating. The lack of a clear genetic differentiation among morphs suggests a recent origin of colour divergence in *O. granulifera*.

☐59 J. Susanne Hauswaldt M 627 / 14:30

Comparison of phylogeographies and transcriptome data of Rana temporaria and R. dalmatina, two co-distributed species of Western Palearctic brown frogs

Authors: *J. Susanne Hauswaldt*[1]*, Sebastian Steinfartz*[1]*, Pablo Orozco-ter Wengel*[1]*, David R. Vieites*[1]*, Miguel Vences*[1]
Affiliation: [1]*TU Braunschweig*

We have reconstructed range-wide phylogeographies of two widespread species of brown frogs with largely overlapping ranges, the common frog (*Rana temporaria*) and the agile frog (*R. dalmatina*). We sampled 27 populations of *R. temporaria* and 21 of *R. dalmatina* and analyzed mitochondrial (cyt-b), and nuclear gene (RAG-1) sequences, eight microsatellite loci, and SNPs (single nucleotide polymorphisms) of the transcriptome of both species. While in *R. temporaria* we found substantial population genetic structure and genetic diversity at the individual level across the different marker systems used, in *R. dalmatina* we found a single most common haplotype across Europe both in cyt-b and RAG-1, with only one genetically divergent population in southern Italy. *R. dalmatina* also showed significantly less diversity in the microsatellites and in the number of SNPs per 100 bp compared with *R. temporaria*. Our overall observed genetic patterns are in agreement with paleoclimatic models, such as a refugium for *R. dalmatina* in southern Italy and highly fragmented smaller populations during the last glacial maximum (LGM). In *R. temporaria* we found basal lineages in Spain and indication of wider and continuous distribution during the LGM. Higher genetic diversity in *R. temporaria* may explain higher morphological diversity and wider habitat-breadth found in this species

compared with *R. dalmatina*. We are currently conducting statistical phylogeography analyses to test for various demographic models and expansion patterns.

☐60 Claudia Laurenzano M 627 / 14:45

South American homogeneity versus Caribbean heterogeneity: population genetic structure of the western Atlantic fiddler crab Uca rapax (Brachyura, Ocypodidae)

Authors: *Claudia Laurenzano, Christoph Schubart*
Affiliation: [1]*University of Regensburg*

Fiddler crabs are a well-studied genus in terms of their sexual selection, visual and acoustic display, combat and foraging behaviour, and male asymmetry. However, only little research has been undertaken on intraspecific differentiation potential and population genetics within this genus. Here we examine the population genetic structure of *Uca rapax* (Smith, 1870) along the tropical western Atlantic, comparing populations from different Caribbean islands to mainland populations as far south as São Paulo State, Brazil. Due to a rather extended planktonic larval development, a high level of gene flow and consequently a low degree of differentiation among populations would be expected. Nevertheless, big rivers such as the Amazon or Orinoco have been postulated to form biogeographic barriers to invertebrate dispersal and thus to promote genetic structuring. Could these or other oceanographic features impair genetic exchange between geographic regions? Specimens of six populations from Cuba, Jamaica, the Dominican Republic, St. Martin (Dutch Antilles), Suriname, Pará State, and São Paulo State (both Brazil) were collected by us or obtained from museum specimens. DNA sequence data were obtained from the cytochrome c oxidase subunit 1 (Cox1) mitochondrial gene (880 basepairs). Analyses of molecular variance (AMOVA) were carried out and a haplotype network was constructed. Our results give evidence for significant geographic population structure at different levels. Differentiation among Caribbean populations is significant, but lower than between Caribbean and mainland populations. No significant restriction was observed among South American mainland populations. Restricted gene flow between geographically close islands suggests larval retention or lack of connectivity promoted by ocean currents.

☐61 Jana Dömel M 627 / 15:00

Phylogeographic structure and genetic diversity in the circumpolar Southern Ocean sea spider *Austropallene cornigera*

Authors: *Jana Sophie Dömel*[1]*, Ralph Tollrian*[1]*, Florian Leese*[1]
Affiliation: [1]*Lehrstuhl für Evolutionsökologie und Biodiversität der Tiere, Ruhr-Universität Bochum*

The marine Antarctic benthos has received considerable attention in the last decade in particular due to its high number of newly discovered cryptic species. Molecular studies have played a central role in discovering these species and the results of these have questioned the traditional concept of circumpolar distribution of benthic taxa. At the same time the finding of several independent cryptic species with allopatric or parapatric distribution ranges has stimulated a discussion about the

possibility of shelf refugia during the past glaciations. Although sea spiders (Pycnogonida) are a particular species-rich and endemic taxon in the Southern Ocean it has received comparatively little attention. The pycnogonid with the broadest reported distribution range in the Southern Ocean is Austropallene cornigera. In the present study we analysed 7 populations of *A. cornigera* from three different shelf regions around the Antarctic continent as well as from sub-Antarctic islands for their variation in the mitochondrial COI and the nuclear 18S and 28S genes. Genetic differentiation patterns between continental shelf and island populations indicate that gene flow was and to a certain extent is limited in this benthic brooder. Our results suggest that *A. cornigera* may have survived the last glacial periods inside the Antarctic separated from sub-Antarctic populations.

☐62 Danilo Harms M 627 / 15:15

Vicariance and the origins of diversity in pseudoscorpions (Arachnida: Pseudoscorpiones)

Author: *Danilo Harms*
Affiliation: [1]*The University of Western Australia*

Globally distributed lineages may show one of two patterns of relatedness: relationships strictly follow vicariance predicted by continental drift or, dispersal following drift generates unpredictable patterns of relatedness. Pseudoscorpions are globally distributed and allow tests of the relative importance of these two biogeographic models. I analysed relationships in the family Pseudotyrannochthoniidae using five genes - a total of 7000 base pairs. Bayesian, likelihood and parsimony approaches were used to infer phylogenetic trees and the age of divergence dates was estimated using BEAST. Northern and southern hemisphere faunas form two independent monophyletic lineages consistent with the break-up of Pangaea into northern (Laurasia) and southern (Gondwana) landmasses some 180 mya. Eastern Palaearctic and western North America faunas show strong phylogenetic affinities, highlighting an ancient trans-Beringian distribution predating the Paleogene. The Southern hemisphere has 1) an eastern-Gondwanan clade comprising species from Madagascar, eastern South Africa and Sri Lanka, and 2) a southern Gondwanan clade comprising species from Australia, Chile and the Cape Provinces in South Africa. The fauna of Australia is paraphyletic with respect to Chile and this pattern is ancient, reflecting a former connection via Antarctica. The South African fauna is polyphyletic and includes lineages from both eastern and southern Gondwana.

Several landmasses have seen extensive in-situ speciation events, resulting in high numbers of endemic species and highly interesting intra-continental distribution patterns reflecting vicariance since the mid-Tertiary. These patterns are highlighted by the Australian fauna, a continent with recent dramatic climatic change, resulting in aridification and contraction of its original mesic biomes.

Monday, September 24, 2012

Chair: Phillip Gienapp

☐63 Frederico Henning A 703 / 14:00

Genetics of polychromatism in the Midas cichlid

Authors: *Frederico Henning[1], Shoji Fukamachi[2], Julia Jones[1], Paolo Franchini[1], Axel Meyer[1]*

Affiliations: *[1]University of Konstanz; [2]Japan Woman's University*

Theoretical advances in speciation research have come a long way since the dawn of the new synthesis. The genetic architectures and ecological factors that are more conducive to speciation, with or without geographic isolation, have been identified. Testing these theoretical predictions requires knowledge of the genetics of traits underlying reproductive isolation in addition to the ecological parameters that result in selection. Such information is not easy to obtain in non-model organisms, and empirical data is still lacking. The Midas cichlids of Nicaragua are an excellent study system for conducting such an investigation. In these fish a color polymorphism exists in many different populations. The majority of each population has normal greyish coloration and a proportion of the population undergoes melanophore cell death, resulting in an amelanic morph that is gold colored. The onset of morphological color is variable. Several studies have reported that mating is assortative with regard to color, and interestingly,, incipient speciation based on this trait has been proposed. The results of genetic mapping, candidate-gene, genotype-phenotype association and analysis of differential expression have led to a much more comprehensive view of the genetic basis of this phenotype. We show that the gold phenotype is dominant and coded by a single mendelian locus, termed gold. In addition, we describe codominant inheritance of pleiotropic traits of ecological significance. Melanophore cell death occurs as early as 6-7 months of age and there is evidence that some genetically gold fish remain untransformed throughout their lives. Transcriptomic analysis of the downstream effects of gold revealed the upregulation of chemokines, early immediate response genes and surprisingly, anti-apoptotic regulators during color change. As expected, genes within the melanin biosynthesis pathway were all down regulated after color change. Genes down regulated in gold fish included novel candidate color-genes but also several well-known color genes that are responsible for convergent phenotypes in many taxonomic levels, from zebrafish to man.

☐64 Gonzalo Machado Schiaffino A 703 / 14:15

Phylogeography and colonization events of Ugandan crater lake cichlid fish

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Ugandan crater lakes located in the South West of Uganda represent an ideal model to test if independent parallel diversification patterns can be observed that follow independent colonization events. This almost unexplored area consists of more than 50 crater lakes that originated through volcanic activity in the East African Great Rift Valley approximately 50,000 years ago. Each Ugandan crater Lake is likely to harbor different endemic haplochromine species, which makes these lakes an excellent system to study the relative speed and strength by which geographical isolation and natural selection promote phenotypic diversification and speciation. We investigated these crater lake haplochromine cichlid radiations and their presumed ancestral populations (Kazinga Chanel and the older Lake Kivu) genetically using mitochondrial and microsatellite markers.
At least 13 different genetic clusters were identified. As expected, only low levels of gene flow were detected between the source lakes (Edward-Kazinga-George) and moderate levels of genetic differentiation were found between Lake Kivu and Edward-Kazinga-George, providing evidence that these lakes were connected in the past. Divergence times between the ‘source’ and the crater lakes were estimated to be between 40-60 thousands years. That period of time corresponds to one of the most geologically active periods reported for that area. Divergence times among the source lakes (Edward-Kazinga-George) was estimated to being around three to seven thousands years, reflecting the actual connection extisting among them that allow gene flow among these haplochromine populations. Most of the endemic haplochromine cichlids of the Ugandan crater lakes showed strong genetic (highly significant Fst for both mtDNA and microsatellite markers) and morphological differentiation from the populations of the large ‘source’ lakes but also with some of the others crater lakes, highlighting the effects of crater lakes in triggering differentiation and as potential cradles for speciation events.

☐65 Ji Kang A 703 / 14:30

Comprehensive phylogenetic analyses of the swordtails and platyfish (genus Xiphophorus) reveals that Xiphophorus monticolus is a hybrid species

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Males in some species of swordtails (genus Xiphophorus), small freshwater fishes from Meso-America, have an extended caudal fin, or sword ? hence their common name. Males with longer swords are preferred by females from both sworded and ? surprisingly also, non-sworded (platyfish) species that belong to the same genus. Swordtails have therefore been studied widely as models for sexual selection, and specifically, they are seen as one of the few examples for the pre-existing bias hypothesis. Many of the phylogenetic relationships within this genus still remain unresolved hindering progress in the interpretation of, for example, behavioral work. We constructed a comprehensive molecular phylogeny of all 26 known Xiphophorus species, including the four recently described species (X. kallmani, X. mayae, X. mixei and X. monticolus). Different phylogenies based on maternally inherited mitochondrial DNA and nuclear DNA markers strongly suggest that one of the newly described swordtail species, Xiphophorus monticolus, is likely to have arisen through hybridization. Xiphophorus monticolus is placed with the southern platyfish in the mitochondrial phylogeny, but with the southern swordtails in the nuclear phylogeny. By using likelihood approaches we find that possessing the sexually selected sword trait is the ancestral state for the genus Xiphophorus, and that therefore, the sword has been lost repeated during the evolution of this genus. The phylogenetic relationships among the species within the previously unresolved northern swordtails supports the hypothesis that their current geographical distribution was shaped by an original dispersal pattern from the South to North.

☐66 Eugenia Zarza A 703 / 14:45

Prior information as a tool for biogeographical and paleoclimatic hypothesis comparison in a Bayesian framework

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Inferring the impact of biogeographical and paleoclimatic events on diversification has been a central question in evolutionary biology. Here we offer a Bayesian approach for hypothesis comparison that takes advantage of prior information and that serves as an alternative to the traditional null-hypothesis testing method. The main aim of this study is to explore if assigning constrained-age priors to nodes of interest in a time-calibrated phylogeny would serve as a means for hypothesis comparison. These priors would be equivalent to scenarios for lineage origin under different hypotheses. From comparing the likelihood values of the competing hypotheses, modeled under different priors, we would be able to select the hypothesis that explains best the data and thus assign a level of confidence to evolutionary inferences. A simulation approach was taken to evaluate the performance of the proposed method and the power of indices for hypothesis selection (e.g. Bayes Factors, Akaike Information Criterion). With our approach the correct hypothesis is selected at least 85% times. For a best performance, data sets with 3500-10000 bp sequences are required. The method is most reliable when competing hypothesis are not temporally too close. Indices for hypothesis comparison have similar performance.

☐67 Martin Plath A 703 / 15:00

Gradient evolution of body coloration in surface- and cave-dwelling Poecilia mexicana and the role of phenotype-assortative female mate choice

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Ecological speciation assumes reproductive isolation to be the product of ecologically based divergent selection. Beside natural selection (e.g., via H2S-toxicity, darkness or predation), female mate choice in favour of males from their own, locally adapted population (phenotype-assortative mating) is thought to play a key role in promoting reproductive isolation among populations from ecologically different habitat types. Using the neotropical fish Poecilia mexicana from a system that has been described to undergo incipient ecological speciation in adjacent, but ecologically starkly divergent habitats characterized by the presence or absence of two environmental stressors (toxic H2S and darkness in cave habitats), we show (1) a gradual change in male and female body coloration along the ecological gradient of light/ darkness, including a reduction of male ornaments that are under both inter- and intra-sexual selection in surface populations. (2) In dichotomous choice tests using video-animated stimuli we found surface females to have a strong preference for males from their own population over the cave phenotype. (3) In another experiment we asked whether morphological and/or behavioural differences between surface and cave ecotypes translate into female mate choice for the resident male phenotype in cave females, too. When investigating the choices of female cave fish on site (i.e. in darkness, using infrared observation techniques), however, females preferred to associate with surface males rather than size-matched cave fish males, likely reflecting the female predilection for better-nourished (in this case: surface) males described beforehand. Hence, divergent selection of body coloration indeed translates into phenotype-assortative mating in the surface ecotype, thereby promoting reproductive isolation by selecting against potential migrant males. Female cave fish, by contrast, do not have such a preference, identifying natural selection against migrants imposed by the cave environment as the major driver of the observed divergence.

☐68 Anne Weeda A 703 / 15:15

Diploid males - the unknown sex: A study on mating behaviour and fertility of diploid Bracon brevicornis males

Authors: *Anne C. Weeda*[1], *Andra Thiel*[1], *Thomas S. Hoffmeister*[1]
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While females in the Hymenoptera (ants, bees and wasps) develop from diploid fertilized eggs, males normally derive from unfertilized eggs and are thus haploid. Diploid males however, may arise whenever a female mates with a male who carries a sex allele matching one of her own. What are the consequences of diploid males within a population? Given they cannot sire offspring, they pose a twofold load: first, their production is a waste of resources, since they represent zero fitness individuals; second, they constrain the females they mate with to produce only sons and thus bias the population sex-ratio. Especially small isolated populations are predicted to go extinct under these conditions. However, in some species, males have been found to sire offspring that may be triploid. We studied the parasitic wasp Bracon brevicornis laying clutches of eggs on their lepidopteran host larvae and thus having a large potential for diploid male production through sib-mating. We analysed diploid male production, diploid male fertility and diploid male recognition by females and found that diploid males are not fully sterile but that some of them produced triploid daughters. Although most of these triploid females were sterile some succeeded in producing either a son or a daughter.

9. Evolutionary Biology POSTERS

♦61 Bianca Aichinger

Do closely related marine coastal crab species hybridize? A case example with European representatives of the genus Pilumnus (Brachyura: Pilumnidae)

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Bristle crabs of the genus *Pilumnus* are commonly found in shallow waters along the European coast. They are easily identifiable as a genus, but intrageneric classification is quite complex (based on the presence of pereiopodal spines and/or the shape of characteristic bristles). Overall, there is no general agreement on the number and nomenclature of species that should be recognized from European waters. Therefore, this genus is well-suited for comparative molecular taxonomic studies. Specimens of the presumed species *Pilumnus hirtellus* (Linnaeus, 1761), P. *villosissimus* (Rafinesque, 1814), P. *spinifer* (H. Milne Edwards, 1834), P. *aestuarii* (Nardo, 1869), and *Pilumnus* sp. 1 (d'Udekem d'Acoz, 1994) were gathered from as many localities as possible ranging from the Black Sea to Atlantic islands. DNA sequence data were obtained from different mitochondrial genes and used for reconstruction of phylogenetic trees and haplotype networks. We tested for hybridization with large sample size mtDNA sequencing of a population with mixed morphological characters and with AFLP analyses. Our results give evidence for five mitochondrial haplogroups within the species complex that correspond to the above mentioned species. There is little geographic variation, suggesting high levels of gene flow within the presumed species. AFLP data are currently being analyzed. The European crabs of the *Pilumnus hirtellus* complex represent a good case study to define evolutionary units. If they will be confirmed as good species, they must be relatively young, and we may possibly witness ongoing processes of morphological, genetic, and ecological differentiation. The mechanisms and origin of the postulated recent genetic isolation remain to be investigated.

◆62 Lutz Bachmann

Mitogenomics of the historic Spitsbergen Stock of Bowhead Whales (Balaena mysticetus)

Authors: *Lutz Bachmann*[1], *Joost Grond*[1], *Charlotte Lindqvist*[1], *Øystein Wiig*[1]
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Arctic marine mammals are among the most iconic species of the marine ecosystem, and are frequently referred to in discussions on the effects of climate change. The Spitsbergen Stock of bowhead whales was once the largest stock but has been heavily depleted by whaling. The stock is currently considered 'critically endangered' by the IUCN. Up to ca 50,000 years old whale bones with excellent DNA survival have been collected at Svalbard. By means of conventional PCR targeting five short overlapping fragments, nucleotide sequences of the mitochondrial CR could be obtained with a 96% success rate. Using a simple and straightforward PCR-based screening assay the most suitable samples for next-generation sequencing were identified. Multiplexed HiSeq 2000 runs delivered complete mitochondrial genomes for several bowhead whale individuals. We will present a summary of the approach for obtaining mitochondrial genomes for the historic Spitsbergen stock of bowhead whales as well as analyses of the mitochondrial genomes with respect to genetic diversity and structure of the stock.

◆63 Stephanie Bauerfeind

The effects of temperature and photoperiod on stress resistance traits in Drosophila melanogaster

Authors: *Stephanie Bauerfeind*[1], *Vanessa Kellermann*[1], *Neda Moghadam*[1], *Volker Loeschcke*[1], *Klaus Fischer*[1]
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The long-term survival of species and populations depends on their ability to adjust phenotypic values to environmental conditions. In particular, the capability to deal with environmental stressors in order to buffer detrimental effects on fitness is considered to be of pivotal importance. The resistance to stressors such as thermal extremes and a lack of resources (desiccation, starvation) is affected by a wide range of environmental factors. We here use *Drosophila melanogaster* lines from a laboratory experimental evolution experiment, in which lines were exposed to two constant and two fluctuating thermal regimes, in order to investigate plastic responses to temperature and photoperiod regimes in stress resistance traits. Our results revealed that stress resistance traits (cold, heat, starvation, and desiccation resistance) were predominantly and according to expectations affected by temperature and sex: the lower temperature enhanced cold tolerance, while the higher temperature enhanced heat tolerance; moreover, lower rearing temperatures increased desiccation and starvation resistance. Except for heat tolerance, females were more stress-tolerant than males (i.e. they were more cold-, desiccation-, and starvation-resistant). While photoperiodic effects on resistance traits have usually been attributed to the concomitant induction of a resting phase we here demonstrate photoperiod effects in directly developing flies. These effects were less pronounced than the effects of temperature: the longer photoperiod increased cold

and desiccation resistance, while heat and starvation resistance remained unaffected by photoperiod.

♦64 Patrick Beckers

Nemertean nervous system: Structure and phylogenetic evaluation

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In recent years, neuroanatomical studies by immunohistochemistry have yielded promising data to contribute to unraveling the phylogeny of the invertebrate metazoans. For Nemertea, however, only one species has been investigated, which most likely shows derived characters. Nemerteans are unsegmented, vermiform spiralians that are doubtlessly monophyletic. In the classical view nemerteans fell into three higher taxa: Palaeo-, Hetero- and Hoplonemertea. This classification is among others based on the anatomy of the nervous system. Ingroup relationships within Nemertea are still unclear, but there is some consensus that Hetero- and Hoplonemertea are monophyletic and form an evolutionary lineage called Neonemertea (Tholleson & Norenburg 2003). Palaeonemerteans form a basal, probably paraphyletic group and are accordingly most informative for comparisons with other invertebrate groups. In this study we describe the structure of the nervous system of members of different nemertean taxa order to create a data matrix based on the morphological elements present in nemertean nervous system. Classical Azan staining was chosen to get an entire view of the elements present in the nervous system and to be able to infer the position of the central nervous system in relation to the body wall layers. Immunochemistry was chosen to reveal the fine structure of the elements of the nervous system. A number of 61 characters concerning the morphological elements of the nervous system arose of this investigation. The analysis resulted in one most parsimonious tree. Hoplonemerteans and heteronemerteans are monophyletic and form a monophyletic taxon called Neonemertea. Palaeonemerteans are paraphyletic. Compared to other recently published results the nervous system, although being just one organ system turned out to be a reliable morphological system to infer nemertean phylogeny.

♦65 Gerhild Bornemann

Trade offs and operational sex ratio affect reproductive success in a scorpionfly mating system

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Two test populations of the scorpionfly species *Panorpa alpina* that differed in the daily amount of food provided per individual were observed until 90% of the individuals had died. A comparison of population means revealed that especially males do not differ in several traits linked to reproductive success but clearly differ in survival. This pattern can be interpreted as the result of a tradeoff between investment in reproduction and investment in survival, i.e. males from the population receiving less food per individual invested approximately the same amount of energy in reproduction as males from the better fed population, thus having less energy left for survival. Another trade off exists between the time males spend on calling and the time they need to find food. In the population, in which individuals got less food, males spent more time on foraging and less time on calling. But despite of their lower investment in calling and, additionally, their shorter life spans, the mating success of the badly fed males was nearly as high as that of the well fed males. Here, the operational sex ratio, which differed between the two test populations, affects reproductive success through varying levels of intrasexual competition.

♦66 Christiane Bramer

Evolution of cardenolide sequestration and resistance in lygaeid bugs

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Conspicuous black and red aposematism is a pervasive feature of the hemipteran subfamily Lygaeinae distinguishing them from other members of the mostly dull colored family Lygaeidae. Indeed, the warning coloration is associated with chemical defense which is often relying on sequestered host plant toxins. The best investigated species, the large milkweed bug Oncopeltus fasciatus, obtains cardenolides from Asclepias seeds and displays intricate adaptations to these toxins. However, usage of cardenolides seems to be widespread within the Lygaeinae. Cardenolides are powerful toxins which specifically inhibit the ubiquitous animal enzyme Na+K+-ATPase. In O. fasciatus cardenolide resistance is mediated by a Na+K+-ATPase possessing reduced sensitivity to cardenolides (target site insensitivity). To reconstruct the evolution of cardenolide sequestration and metabolism as well as target site insensitivity we established a molecular phylogeny comprising 18 lygaeine species and 4 outgroups (CO I/II; 28S rRNA). Cardenolide sequestration and metabolism were assessed by feeding studies with radioactive tracers in 7 species. Target site insensitivity was evaluated by in vitro assays of Na+K+-ATPase and sequence analysis. We found that sequestration of cardenolides and also target site insensitivity are probably synapomorphic characters of the lygaeine subfamily. Our data suggest that European members of the genus Arocatus lost black and red aposematism as well as the ability to sequester cardenolides. Nevertheless target site insensitivity, was retained although these species are no longer exposed to dietary cardenolides. The extensive association of Lygaeines with apocynaceous plants and the basal origin of adaptations to cardenolides suggest that this host plant relationship is the original one yet dependence on cardenolides led the bugs on to plants from many other families (Ranunculaceae, Plantaginaceae, Brassicaceae, Asparagaceae) featuring these compounds.

♦67 Danon Clemes Cardoso

Terrestrial gene flow along the southern Brazilian coast: Phylogeopgraphy and genetic diversity of the endemic sand dune ant Mycetophylax simplex

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The Brazilian Atlantic Forest (Mata Atlântica) presents a wide range of vegetation types with conspicuous changes across landscapes that include open habitats covered predominantly by herbaceous and shrubby plants which develop on marine deposits, so called Restinga. Even with an increasing number of phylogeographic studies in the past few years, very little is known about the evolutionary history of the Atlantic Forest. Many species associated with wet forest environments have been used to infer the evolutionary process that occurred during the last glacial maximum (LGM) in the Atlantic Forest, but little work focused on organisms associated with dry environments. *Mycetophylax simplex* is a small 'basal' Attini ant (Formicidae: Myrmicinae) endemic to sand dunes environment along the Brazilian coast occurring from southern São Paulo State to Rio Grande do Sul. This species has never been found living outside of these dry sand dunes, making it a good model organism to test different scenarios from those of associated wet species. By means of mitochondrial COI analyses of 96 specimens we compared the genetic divergence between populations that comprise the whole known range of this ant. Our results show some shallow phylogeographical structure along the populations analyzed with an isolation by distance effect. However, the data do not allow recognizing old or recent phylogeographic barriers with an abrupt change of genotypes. Open shrubland, grasslands and sandy environments are the dominant coastal environments in southern Brazil and our results suggest that *M. simplex* was not affected during the LGM and does not show any split distribution.

♦68 Safaa Dalla

How insects achieve resistance to dietary toxins: in vitro tests of amino acid substitutions in their Na,K-ATPase

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The Na, K-ATPase is a ubiquitous protein which catalyses 1 molecule of ATP to exchange 3 Na+ ions for 2 K+ ions across the cell membrane. This important transmembrane carrier is specifically inhibited by cardenolides (cardiac glycosides) such as ouabain that bind to a well described binding pocket on the extracellular side of the enzyme. Nevertheless, some insect species that feed on cardenolide-containing plants have a high tolerance to cardenolides. Genetic analysis of the Na,K-ATPase revealed that amino acid substitutions in the cardenolide binding pocket may play a role in making the enzyme insensitive to cardenolides. We genetically engineered the *D. melanogaster* Na,K-ATPase ? subunit to incorporate amino acid

substitutions that we observed in adapted insects and transfected the constructs into Hela cells. Immunofluorescence confirmed the heterologous expression of *D. melanogaster* Na,K-ATPase ? subunits in the cell membrane. To test whether the introduced substitutions confer reduced sensitivity to cardenolides, we monitored the survival and growth of cells transfected with each construct under a 0.1 µM and 0.5 µM ouabain selection regime. These assays indicate that several of the substitutions observed in insects on cardenolide plants significantly decrease the sensitivity of their Na,K-ATPase for cardenolides. Similar to the situation in mammals combined substitutions of two residues in the first extracellular loop of the enzyme, Gln111 and Asn122, confer the greatest resistance.

♦70 Temim Deli

Population genetic structure of the common littoral prawn Palaemon elegans (Crustacea: Caridea: Palaemonidae) in the southern Mediterranean Sea

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The common littoral prawn *Palaemon elegans Rathke*, 1837 has a great ecological plasticity: it can cope with different types of habitats, being found from hypersaline lagoons, tidal rock pools, shallow rocky subtidal, Zostera, Posidonia and Cymodocea sea grass meadows, to partly brackish estuaries. *P. elegans* is widespread within the northeastern Atlantic Ocean (from Scotland and Norway to Mauritania including the Azores, Madeira and Canary Islands) and the entire Mediterranean Sea and Black Sea. Despite its high dispersal capacities with a complete larval development of 6 to 9 zoeal stages, which potentially results in high rates of gene flow and panmictic population structure, several population genetic investigations showed significant genetic heterogeneity in the Atlantic Ocean (Berglund & Lagercrantz, 1983) and high genetic variability within the Mediterranean Sea (Fortunato & Sbordoni, 1998). The recent study by Reuschel et al. (2010) revealed surprisingly complex population structure with the existence of three main haplogroups along a wide geographical spectrum and the probable occurrence of cryptic species. The current investigation aims at expanding our knowledge of the population structure of *P. elegans* to the southern and eastern Mediterranean coasts. Mitochondrial sequences of the COI gene (up to 900 base pairs) were obtained from specimens of *P. elegans* from Greece, Syria, and Tunisia and compared with available sequences from European populations. The results of this study are discussed in relation to understanding ecological and historical components that can shape the population structure of this wide-spread prawn species.

♦71 Lars Dietz

New insights into the evolutionary history and the present distribution of the common Southern Ocean pycnogonid Colossendeis megalonyx

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Colossendeis megalonyx, one of the most widespread Southern Ocean sea spiders, has long been considered a species with typical circumpolar distribution. However, it was recently found that *C. megalonyx* consists of several clearly distinct mitochondrial lineages with a narrower distribution. Here we present further mitochondrial data from specimens representing a broader geographical sampling area, showing that several clades occur in both West and East Antarctica, and that a clade from the South American Coast is nested inside the Antarctic clades. This suggests that circumpolar distribution of the different *C. megalonyx* clades is common. In addition, we present evidence from morphology and nuclear genes corroborating that the currently distinguished clades represent overlooked species and showing that the North Pacific species C. *tenera* is not part of the *C. megalonyx* species complex. Analysis of reduced representation libraries of representatives of different clades generated using next-generation sequencing techniques are used to obtain further insights into both inter- and intra-clade relationships within the *C. megalonyx* complex. This allows drawing conclusions on its phylogeographic history, including influence of Pleistocene glacial expansions and possible expansion from refugia both within Antarctica and in the Subantarctic. The results contribute to our understanding of the history of the Antarctic benthos in general.

♦72 Vasco Elbrecht

Connectivity and dispersal potential of Dinocras cephalotes populations (Plecoptera): A population genetic case study in the Sauerland region.

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The distribution range of a species and the connectivity among its populations can be modelled using geo-referenced presence/absence data in a GIS framework. In freshwater ecosystems, information about the connectivity and diversity is essential for understanding the impact of human alterations, for panning and management purposes. Genetic methods can greatly improve the accuracy of presence/absence based models. By using molecular data, morphospecies can be validated and gene flow between populations estimated with greater precision. In this project, we focus on the population connectivity and genetic diversity of the stonefly *Dinocras cephalotes* (Plecoptera) in the Sauerland region. We analysed over 300 samples from 29 populations for the mitochondrial marker Cytochrome c Oxidase 1 (CO1) and the nuclear “Wingless” gene. In addition, microsatellites have been developed de novo, which will provide additional information regarding the dispersal potential of Dinocras cephalotes. A central aim of the project is to compare the results obtained from the genetic data with the results obtained from GIS models."

♦73 Manuela Ferrari

Cooperation versus exploitation: communal nursing in house mice (*Mus domesticus*)

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To understand the evolution and maintenance of cooperative behaviour requires testing the opportunity of exploitation. Female house mice (*Mus domesticus*) show optional communal nursing, where two (rarely more) females raise their litters together, and do not discriminate between own and alien young during nursing. In situations where one female has a smaller litter than her partner, she thus might be exploited. Both females will invest the same amount of energy (milk) and time into the communal litter, but the pay-off - the number of weaned pups - will differ for both partners. Under laboratory conditions, we compared the behaviour and reproductive output of communally nursing females (direct descendants of wild caught house mice) that differed in litter size with females that had similarly sized litters at birth. We manipulated litter sizes of familiar full-sisters with a genotype dependent mating design based on the t haplotype, a selfish genetic element in house mice. Mated with a t heterozygote male, a t heterozygote female will suffer a loss in litter size by 40% in utero, whereas her wildtype sister will give birth to a 'normal' sized litter. As a control, we mated two sisters differing at the t haplotype with a wildtype male. Such experimental manipulation allowed to test whether cooperative behaviour is modified in an enhanced conflict situation. Our study revealed that females, indeed, invested according to the total number of young in the communal nest. To minimize the risk of being exploited, females generally reduced the litter size of the other female when still being pregnant (first born litters in a communal nest had a lower survival probability). Furthermore, females showed a reduced propensity to cooperate in communal nursing in the enhanced conflict situation.

♦74 Carmelo Fruciano

Absence of cryptic diversity in *Archocentrus centrarchus*, a cichlid living in sympatry with the Midas cichlid complex in the crater lakes of Nicaragua

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The Midas cichlid (*Amphilophus citrinellus*) species complex in Nicaraguan crater lakes is a well-known model system in evolutionary biology. Several crater lakes house a small set of endemic species that arose in sympatry in those lakes. The same great lakes and crater lakes of Nicaragua, where the Midas species have speciated quickly to form about a dozen described species so far, also harbor multiple other cichlid species. So far, for none of these other lineages of cichlids, besides the Midas cichlids species complex, have any new species been recognized taxonomically. There is, however, also a lack of intra-specific studies on non-Midas cichlids - so, it is simply not known yet how many heretofore unrecognized species there are. We sampled *Archocentrus centrarchus* ? the phylogenetically closest relative of Midas cichlids in the Nicaraguan crater lake Xiloa and the big source lake Managua from which the populations that now live in Xiloa are derived. Based on mitochondrial control region sequences and geometric morphometric data for both body shape and pharyngeal jaws, we tested for variation between lakes and explored the possible presence of intra-specific clusters. The results of the morphometric analyses do not show any intra-specific clustering and the haplogroups identified through a network representation of mtDNA haplotype relationships do not differ in morphology. Therefore, both molecular and morphometric data suggest the absence of cryptic species in this lineage. These data confirm that *A. centrarchus* did not speciate, highlighting the uniqueness of the Midas cichlid group.

♦75 Sonja Grath

Influence of degree and conservation of male-biased transcription on the rate of amino acid substitution in Drosophila

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Sex-biased gene expression (i.e., the differential expression of genes between males and females) is common among sexually reproducing species. However, genes often differ in their sex-bias classification or degree of sex bias between species. There is also an unequal distribution of sex-biased genes (especially male-biased genes) between the X chromosome and the autosomes. Previous studies suggested differences in evolutionary rates of male-biased genes between different Drosophila lineages. However, these studies might be influenced by different experimental design or different gene selections. We used whole-genome expression data and evolutionary rate estimates for two different Drosophilid lineages, melanogaster and obscura, spanning an evolutionary time scale of around 50 Myr to investigate the influence of sex-biased gene expression and chromosomal location on the rate of molecular evolution. In both lineages, the rate of protein evolution correlated positively with the male/female expression ratio. Genes with highly male-biased expression, genes expressed specifically in male reproductive tissues, and genes with conserved male-biased expression over long evolutionary time scales showed the fastest rates of evolution. An analysis of sex-biased gene evolution in both lineages revealed evidence for a fast-X" effect in which the rate of evolution was greater for X-linked than for autosomal genes. This pattern was particularly pronounced for male-biased genes. Genes located on the obscura "neo-X" chromosome, which originated from a recent X-autosome fusion, showed rates of evolution that were intermediate between genes located on the ancestral X-chromosome and the autosomes. This suggests that the shift to X-linkage led to an increase in the rate of molecular evolution."

♦76 Meike Hiermes

The dynamics of UV-signals in the three-spined stickleback (*Gasterosteus aculeatus L.*)

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Ultraviolet (UV) signals are widespread throughout the animal kingdom and have been shown to be of importance in various contexts in numerous species. However, there are hardly any studies dealing with the dynamics of these UV-signals. For the three-spined stickleback (*Gasterosteus aculeatus L.*), which is able to transmit and perceive in the UV wave range, there exist several studies on the dynamics of signals in the visible wave range, indicating temporal changes in the red mosaic signal as well as a change in the sensitivity for red coloration with changing reproductive status.
To test for changes in UV-signaling during the reproductive cycle, the F1-generation of wild-caught sticklebacks from an anadromous population from Texel, the Netherlands, was raised under full-spectrum conditions until they reached the reproductive stage. Reproductively active males and females were then housed individually and the UV-reflection was recorded regularly using spectrophotometry. For females the change in UV-signals after stripping them from eggs until becoming ripe again was recorded, while for males a change in UV-signals, beginning with the nestbuilding period, continuing through the courtship period and ending after the completion of the broodcaring period with the hatching of the fry, was recorded. Furthermore, males' and females' change in UV-reflection was recorded before and after animation with a reproductively active male, to investigate if UV-reflections can be actively increased or diminished. The results are discussed in the context of possible functions as well as costs and benefits of UV-signaling.

♦77 Cornelia Hinz

Influence of kinship and MHC class II genotype on visual traits in zebrafish larvae (*Danio rerio*)

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The evolution of altruistic behaviour requires mechanisms to avoid cheating. This favours the recognition of kin and the differential behaviour towards related and unrelated individuals. Recent studies showed that polymorphic genes of the major histocompatibility complex (MHC), code for chemical recognition signals.
In zebrafish, the capability to differentiate between kin and non-kin is based on a non-self referent phenotype-matching process. At day 6 post fertilization larval zebrafish experience a sensitive period of 24 hrs during which they learn the olfactory template of their kin. Later they can use this template to identify even unfamiliar kin. Imprinting does not occur when larvae experience olfactory or visual cues of non-kin, suggesting a genetic predisposition for both cues. While we had shown in a recent study that olfactory imprinting is based on MHC class II allele similarity between related individuals, the underlying mechanism for the visual imprinting remained unclear.

Here we show that family specific differences in morphometry and pigmentation pattern in six days old zebrafish larvae exist. While rump, tail and body pigmentation were dependent on relatedness per se, iris pigmentation and morphometry was influenced by their MHC class II genotype. Our study revealed that the MHC not only influences the chemical signature of individuals but also their visual appearance.

♦78 Thomas Hoffmeister

Decision making in *Nasonia vitripennis*: influence of experience vs. internal state

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Optimal foraging theory assumes a forager's behaviour to be adapted to the environment. If the latter varies over time, information processing may allow optimizing resource exploitation according to the current environmental state. To achieve this, experienced resource density and quality may be used as proxies for the overall quality of the habitat. Yet, also the physiological state of a forager may influence foraging decisions. To unravel the importance of environmental information vs. physiological state on the decision making process, we studied clutch size decisions in the parasitic wasp *Nasonia vitripennis*. We manipulated host quality and density and analyzed the effect of egg load and environmental information on the clutch size. The study identified egg load as the major factor influencing clutch size as well as the time spent with the host. Despite the strong impact of this internal cue, our experiments revealed that also the time between two oviposition opportunities triggers changes in foraging behavior. Surprisingly, the quality of a host encountered did not influence subsequent resource exploitation. We discuss these findings considering varying scenarios of time and egg limitation.

♦79 Martin Husemann

Population and species divergence in Lake Malawi rock-dwelling cichlids

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Understanding the divergence of populations provides insight into the creation of species. Here, we examine this phenomenon in one of the world's most diverse vertebrate radiations: the cichlid fishes of Lake Malawi, East Africa. Previous studies have shown that populations of these species are easily isolated by environmental barriers and little gene flow connects geographically proximate populations. Such conditions suggest that these populations may rapidly diverge. In this study, we used population genomics, a coloration phenotype and geometric morphometrics to study genetic and phenotypic differentiation of populations of rock-dwelling cichlids in order to detect signals of selection and drift.

♦80 Regina Jäckel

Metapopulation structure in a leaf beetle driven by a reproductive parasite

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Wolbachia bacteria often affect reproduction as well as mtDNA population structure of their hosts. We recently showed that the leaf beetle species Altica lythri is infected with three different Wolbachia strains. The species shows a sex ratio distortion resulting in a distinctive female excess and linkage disequilibrium between three Wolbachia strains and three mtDNA haplotypes indicating that the population structure of mtDNA has been shaped by genetic hitchhiking.

To correlate mtDNA diversity with gender, sex ratio and Wolbachia, we analysed mtDNA type and Wolbachia infection of 542 specimen collected from 15 populations across Germany. We detected a total of 11 haplotypes and three Wolbachia strains (wA1, wA2, wB). Five haplotypes (HT1, HT1*, HT2, HT2*, HT3) were widely distributed and mostly occurred sympatrically. Sex and haplotype, and haplotype and Wolbachia infection were strongly correlated. Individuals carrying HT1 were female, mostly infected and if so bore wA1. Individuals bearing HT1* were female and almost exclusively uninfected. HT2-and HT2*-individuals could be both genders and were mostly infected and if so bore wA2. HT3-individuals were either male or female and mostly bore wB. Since HT1 was usually the most frequent haplotype, a distinctive female excess follows inevitably. All-female HT1-individuals and the association with wA1 strongly support that this Wolbachia-strain is a sex ratio distorter and responsible for the lack of males. Since females need to copulate to produce offspring, populations with a pervasive wA1 infection should be at a high risk of local extinction. This may explain the highly unusual sympatric occurrence of several disjunct Wolbachia and mtDNA haplotypes in a single species.

♦81 Nathalie Kaffenberger

The phylogenetics behind community assembly: phylogenetic structure of lowland rainforest anuran communities in Central Guyana

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Evolutionary biology and ecology have diverged into largely separate disciplines in the past, but with the advancement of analytical and computational procedures and because of an exponential increase in available phylogenetic data both disciplines seem to merge again. Approaches focussing on community assembly processes are ideal to combine both fields of investigation. In general, several processes are inferred to influence community assembly and structure: 1. niche-related processes, 2. neutral processes and 3. historical processes. Phylogenetic community ecology can help to clarify which of these tree processes is the driving force in a certain community.

In an interdisciplinary project that combines ecological field data collected on lowland rainforest frog assemblages of Guyana with results of phylogenetic analyses based on mitochondrial and nuclear marker genes we aim at identifying drivers of

biological community assembly. We specifically ask whether frog communities are phylogenetically clustered or overdispersed to reveal whether neutral or niche related and/or historical processes are the main driving forces behind community assembly. In a second step we will test for structure in species traits across phylogenies to elucidate whether clustering or overdispersion is reflected at the trait level. In combination with the analyses of species abundance patterns and species-habitat relations these results will ultimately contribute to a more refined picture of community assembly and the evolution of species-trait-habitat associations.
Here we introduce our community phylogeny approach, present first results and give a short prospect on further aims of our interdisciplinary investigation.

◆82 Dorothea Kimpel

Population differentiation in *Synchaeta pectinata* (Rotifera): Is 'everything everywhere' or is 'nothing nowhere'?

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The 'Everything is Everywhere' hypothesis (EisE) holds that individual species of microorganisms have an extended, if not worldwide distribution, appearing wherever a suitable niche is to be found. Many species of rotifer, a clade of microscopic, aquatic animal, are widely considered to have a cosmopolitan distribution in line with the EisE hypothesis. However, it is still unclear how and to what extent gene flow occurs between apparently isolated populations over large distances. For example, preliminary findings from the monogonont rotifer *Keratella quadrata* do support the EisE hypothesis, with populations from Alberta, Canada and Oldenburg, Germany showing restricted COI sequence divergence. To get an estimate of the degree of genetic population differentiation (with respect to allele frequency changes and gene flow), we employed a denser sampling scheme over different geographical ranges for the monogonont rotifer Synchaeta pectinata using COI and 18S rDNA as genetic markers. We discuss our finding in the context of the EisE hypothesis and relate them specifically to relevant and distinguishing characteristics of these organisms. Of particular interest here is the facultative asexual reproductive system of monogononts, where extended asexual reproduction alternates with the production of sexual resting eggs, which play a key role in dispersal. Future research revolves around establishing a set of microsatellites for the genus, which will enable even greater precision regarding the population genetics and phylogeography of this group of organisms.

◆83 Ulrich Knief

QTL mapping of beak morphology in the zebra finch

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The intra- and interspecific diversity of avian beak morphologies is one of the most compelling examples for the power of natural selection acting on a morphological trait. The development and diversification of the beak has also become a textbook example for evolutionary developmental biology, and variation in expression levels of several genes are known to causally affect beak shape. However, until now no genomic polymorphisms have been identified that are related to beak morphology in birds. Here we estimate heritability and genetic correlations for beak length, depth and width and perform a QTL linkage analysis for these traits based on 1,404 informative single nucleotide polymorphisms genotyped in a four generation pedigree of 992 captive zebra finches (Taeniopygia guttata). Beak size, relative to body size, was sexually dimorphic (larger in males). Heritability estimates ranged from 0.47 for beak length to 0.74 for beak width and genetic correlations were high (ranging from 0.46 between length and width to 0.65 between depth and width). QTL mapping revealed four to five regions of significant or suggestive genome-wide linkage for each of the three beak dimensions (nine different regions in total). All beak dimensions had at least one exclusive QTL linkage peak which demonstrates that there is additive genetic variance for each of the dimensions independent from the other dimensions. Eight out of eleven genes known to influence beak morphology are located in the nine peak regions. Five QTL do not cover known candidates demonstrating that yet unknown genes or regulatory elements may influence beak morphology in the zebra finch.

◆84 Nina Kniel

Mate-choice copying in female zebra finches Taeniopygia guttata castanotis - Tests of alternatives

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Animals use public information in a number of contexts, such as food acquisition, shoaling and mate choice. Individuals copy the mate-choice of their conspecifics by observing them during sexual interactions. It occurs in many species and research in this field has become quite common. Are there any alternative explanations to mate-choice copying? We investigated this question in female zebra finches. First, a female was given the choice between two males (one adorned with the red feather on the forehead, one an unadorned wild-type). Then, she could observe new males, a single wild-type male and an adorned male with his mate. Finally she could again choose between two new males. If the adorned male and his mate were separated by a clear glass screen, females showed mate-choice copying. If they were separated by an

opaque screen, females showed no mate-choice copying. In experiments testing alternative explanations, females did not change mate choice when only males or only females of both phenotypes were presented in experiments. Our experiments showed that a certain amount of interaction (acoustic and visual) between the adorned male and the female is necessary for observing females to change mate choice. A physical interaction or even copulation are not necessary. We also ruled out that the presence of and the physical interaction between two birds of the same sex did affect females´ mate choices. Thus, our results showed that so far alternative mechanisms cannot explain mate-choice copying in female zebra finches.

♦85 Gregor Kölsch

Where do you come from? ? Sagrinae and Donaciinae (Coleoptera, Chrysomelidae) harbor similar bacterial endosymbionts

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Many insects live in symbiosis with bacteria. The origin of such mutualistic associations often remains unclear. In order to shed light on the evolution of the symbiosis between reed beetles (Coleoptera, Chrysomelidae, Donaciinae) and intracellular symbionts belonging to the Enterobacteriaceae, we searched for similar bacteria in other beetle groups. Three criteria directed our search: phylogenetic proximity of the host, similarity of the mycetomes containing the bacteria, and cocoon formation of the beetle larvae (in Donaciinae the bacteria provide the cocoon material). We analyzed the partial sequence of the 16S rRNA of bacteria we found in other beetle groups (Cerambycidae, Anobiidae, other Chrysomelidae). We discuss the ecology of each association in the context of the phylogenetic analysis. The bacteria in *Sagra femorata* (Chrysomelidae, Sagrinae) are very closely related to those in the Donaciinae and are located in similar mycetomes. The Sagrinae build a cocoon for pupation like the Donaciinae, in which the bacteria produce the material required for the cocoon. These aspects support the close relationship between Sagrinae and Donaciinae. This is in line with earlier studies and makes a common ancestry of the symbioses likely. Using PCR primers specific for fungi, we found Candida sp. in the mycetomes of a cerambycid beetle along with the bacteria.

♦87 Hyuk Lee

Handed foraging behavior in scale-eating cichlid fish: does head asymmetry predict feeding direction?

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The scale-eating cichlid fish, Perissodus microlepis, from Lake Tanganyika is a textbook example for the extreme degree of morphological and ecological specialization that can be found in the adaptive radiations of cichlid fish. The ?left (L)? morph opens its mouth towards the left and a ?right (R)? morph towards the right. These fish display handed (lateralized) foraging behavior, where the L morph preferentially feeds on the scales of the right side of its victim fish and the R morph bites the scales of the left side. We studied the degree of handedness and individual variation of laterality of foraging behavior in relationship to morphological mouth laterality in P. microlepis. In wild-caught adult fish mouth laterality is, as expected, a very strong predictor of preferred attack orientation. Also laboratory-reared juveniles exhibited a strong laterality in behavioral preference when feeding on scales, even at an early age, although the initial level of mouth asymmetry appeared to be small. This suggests that pronounced mouth asymmetry is not a prerequisite for handed behavior in juvenile scale-eating cichlid fish and might suggest that behavioral preference to attack a particular side of the prey might play a role in facilitating morphological asymmetry.

♦88 Gerlind U.C. Lehmann

Manipulating experiments on the role of internal genitalia in a bushcricket (Orthoptera: Tettigoniidae): anchors or stimulatory devices?

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Among most species male genitalia as well as secondary sexual organs are more diverging compared to other body parts; hence they are one of the key properties in species identification. In contrast to the broad knowledge about their morphological form, the evolutionary selection forces affecting the shape and often even the function of certain structures, which seem not to be directly involved in sperm transfer, remains unclear.

In Tettigoniidae males of certain taxa possess sclerotisized internal genital structures, called titillators. These titillators consist of paired structures that are covered inside the male. During copulation, they are inserted rhythmically into the female?s genital chamber. Their function for spermatophore transfer is unknown. Based on comparative data (Vahed et al. 2011) it has been suggested, that they may act either as anchors or stimulatory devices for female acceptance of the courtship and/or the male's spermatophore. In this study, we tried to elucidate the function of the titillators in Metrioptera roeselii. Therefore, two series of experiments were carried out: (i) We removed the titillators in one group of males. During copulation we counted the rhythmical titillator movement between unmanipulated males and those with titillators cut off. Manipulated males showed a significant decrease of rhythmical movements. Furthermore, males without titillators had a significant number of failed spermatophore transfers, underlining the importance of the titillators for the male reproductive success.

(ii) We deep froze couples in liquid nitrogen during copulation to examine the positioning of the titillators inserted into the female?s genital chamber. The involved anatomical structures of mating pairs were analyzed by high-resolution X-ray CT. Visualizing the contact sides of the male titillators inside the female revealed no anatomical counter structures in the females.

Based on these new findings, we assume a function of the titillators in stimulation during copulation and discuss cryptic female choice as possible evolutionary selection force involved.

Vahed, K., Lehmann, A. W., Gilbert, J.D.J., Lehmann, G.U.C. (2011): J. of Evol. Biol. (24): 1960-68.

♦89 Marion Mehlis

The relationship between breeding coloration, sperm morphology and sperm motility in three-spined sticklebacks (*Gasterosteus aculeatus*)

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Recent studies have shown that sexually selected traits signal sperm quality and hence male fertilization success. The expression of male sexual ornamentation and associated sperm characteristics often depend on an individual's ability to cope with oxidative stress. In many species, the development of breeding coloration is based on carotenoid pigments, which have to be obtained from the diet. When carotenoid availability is limited, these pigments are traded off between fitness components such as sexual ornamentation and immunoresponsive capacities.

The three-spined stickleback (*Gasterosteus aculeatus*) is a well-studied model species subject to sperm competition, in which males develop a conspicuous carotenoid-based coloration in the cheek region during the breeding season. The relationship between sexual ornamentation and sperm characteristics was studied in wild-caught and laboratory-bred stickleback males from the same population. Well-established methods for the quantification of sperm motility, sperm morphology and breeding coloration variables were used under standardized laboratory conditions. Data of the current study revealed that breeding coloration (e.g. carotenoid chroma) is significantly positively correlated with sperm motility indicating the honesty of the carotenoid-based breeding coloration in three-spined stickleback males. Moreover, the results showed that some sperm morphology traits such as head to tail length ratio are good proxies for sperm motility.

♦90 Michael Mende

Natural History Collections as a window to the past - Historic-DNA phylogeography of the Spurge Hawkmoth (Lepidoptera, Sphingidae) in the Central Mediterranean

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The Hyles euphorbiae species comprises six distinct mitochondrial lineages in the Mediterranean area, based on about 2300bp of the COI/II genes. These show a phylogeographic structure reflecting the refuges during the ice ages and subsequent postglacial range expansions. Today all of Southern Italy is exclusively inhabited by a lineage, provisionally titled "italica", which is nearly solely confined to this area. Northeast of the Northern Apennines it is replaced by the two European mainland lineages, euphorbiae and "enigmatica", most probably colonizers from two Eastern European glacial refuges. Paradoxically, the Maltese population is composed of three lineages: euphorbiae, the endemic lineage “melitensis” and migrants of the North African tithymali. By contrast, no “italica” could be found on Malta. We hypothesize that the euphorbiae lineage must have arrived on Malta via Italy but might have vanished in Southern Italy possibly as recently as the end of the 20th century, concurrently with climate warming. Thus, euphorbiae could have been outcompeted in Italy by “italica” which - as typical for more southern populations - potentially tends to generate more generations per year, while it could have been maintained by isolation and genetic drift on the island of Malta. We scanned 27 Natural History collections (mostly Italian and German museums) for relevant individuals from Italy and Malta and were able to obtain tissue samples from more than 200 moths that were caught as far back as 1884. For genetic analyses we sequenced three short fragments of about 800bp in total of the COI/II genes with which the main lineages are still distinguishable. We found substantial variation in the distribution and frequency of the lineages through the decades, demonstrating the occurrence of the European mainland lineages euphorbiae and “enigmatica” in Southern Italy and Sicily before 1970. Hence, the dominance of “italica” in Southern Italy has not always been as strong as inferred from the recent sampling.

♦91 Barbara Milutinovic

The Red Flour Beetle as a Model for Bacterial Oral Infections and Host-Parasite Coevolution

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Host-parasite interactions are ideal systems for studying fast co-evolutionary processes of adaptation and counter-adaptation. Laboratory infection systems that make use of natural ways of infection enable experimental studies of such host-parasite co-evolutionary processes. We established an oral infection protocol for the red flour beetle *Tribolium castaneum* and its coleopteran-specific microparasite *Bacillus thuringiensis var. tenebrionis* (Btt). We found that the infection success depends on the dietary spore concentration and the exposure time, as well as on the host genetic background since *T. castaneum* populations varied in their susceptibility in the laboratory. The concentration of spores isolated from single, experimentally infected cadavers was sufficient for reinfection of further larvae. However, the spore number and growth capabilities of individual isolates varied strongly among beetle cadavers, which may indicate variability in the strength of host counter-measures against this micro-parasite.

◆92 Sabine Nöbel

Public information influences sperm transfer to females in sailfin molly males

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The social environment can serve as a public information network in which individuals can gather public information about the quality of potential mates by observing conspecifics during sexual interactions. The observing individual itself is also a part of this information network. When recognized by the observed conspecifics as an audience, his/her presence could influence the sexual interaction between those individuals because the observer might be considered as a potential mate or competitor. One of the most challenging questions in sexual selection to date is how the use of public information in the context of mate choice is linked to the fitness of individuals. Here, we could show that public information influences mate choice behaviour in sailfin molly males, Poecilia latipinna, and the amount of sperm males transferred to a female partner. In the presence of another audience male, males spent less time with the previously preferred larger of two females and significantly more time with the previously non-preferred smaller female. In another experiment, males could physically interact with a female and were faced with an audience male, three audience females or no audience. Males transferred more sperm to a female partner in the presence of an audience male than without audience or with female audience and spent less time courting his female partner. Males transferred significantly more sperm to his female partner in the presence of an audience male. Males did not transfer less sperm to their partner in the presence of audience females than without audience. This is the first study showing that public information use turns into fitness investment, which is the crucial factor to understand the role of public information in the dynamic processes in sexual selection.

◆93 Maykon Passos Cristiano

Phylogeography of the leafcutting ant Acromyrmex striatus: reconstruction of the demographic history of an open-environment associated species

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The Pleistocene refugia model is the most invoked hypothesis to explain origin and diversity of tropical forests, but it is mainly applied to fauna associated with wet and shaded habitats. Paleo-modeling studies predict large and stable forests in north and eastern Brazil during the last glacial maximum, but fail to predict possible stable areas in south Brazil. Moreover, some studies did not support the Pleistocene refugia hypothesis, and alternative models, e.g. the possible role of marine incursion and Tertiary orogeny promoting diversification, may need to be further investigated. Acromyrmex striatus is a leafcutter ant associated to open and arid environments distributed throughout Southern Brazil (Santa Catarina and Rio Grande do Sul states), Argentina, Uruguay and Paraguay. In Santa Catarina State, A. striatus occurs only along the coast, whereas in Rio Grande do Sul state this species occurs additionally in inland areas (pampas). Thus, our goal is to investigate the phylogeography of Acromyrmex striatus by means of the distribution and diversity of mtDNA haplotypes. We sampled colonies covering the entire distribution of the species in Brazil and some sites in Argentina. A 922-basepair fraction of Cox1 gene from at least five colonies per sample point were sequenced. The analysis of sequences of 156 specimens shows a high heterogeneity in the geographical distribution of the genetic polymorphism, with a pattern of isolation by distance from the north to the south of the distribution. The current patchy geographical distribution in A. striatus is apparently closely linked to past events which occurred mainly during the Late Quaternary, when the distribution of dry vegetation and pampas expanded and was constrained during glacial and interglacial events.

♦94 Markus Pfenninger

From the niche to the gene - genomic basis of niche segregation among two cryptic sister spieces of non-biting midges

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If the niche is rather a trai of the respective species, its evolution must have left its traces in the genome. Sister species comparisons are therefore particularly informative to track the genomic basis of niche evolution, because all observed niche differences must have evolved during or after their speciation. Using field data, population genetics, ecological experiments and evolutionary genomics, I report here how differentially selected candidate genes and transcriptional stress response strategies have shaped the observed niche differences among the cryptic sister species pair *Chironomus riparius* and *C. piger* (Diptera, Chironomidae).

♦95 Maria Rusche

Investigating age effects on blue tit Cyanistes caeruleus sperm morphology

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Age effects on fertilisation success have been studied in different species and social groups. In socially monogamous passerines where extrapair copulations frequently occur, gaining extrapair paternities as well as securing withinpair paternities play an important role to increase overall male fertilisation performance. For several species, including the blue tit *Cyanistes caeruleus*, it has been shown that older males are more successful in gaining extrapair mating success while keeping extrapair young in their own brood to a minimum. Yet causes explaining the increasing fertilisation success with age are largely unknown. One possible yet unexplored explanation might be that age affects sperm morphology, favouring older individuals in sperm competition, which presupposes individual phenotypic plasticity in sperm morphological traits.

Here we analyse natural variation in sperm traits in a wild blue tit *Cyanistes caeruleus* population, a socially monogamous passerine with extrapair mating behaviour. We investigate if sperm morphology varies with age in a cross-sectional as well as in a longitudinal analysis. Identifying sperm morphological traits that can explain extrapair and overall fertilisation success would help to understand the evolution of sperm design and function.

♦96 Joachim Ruther

Pheromone evolution: how a protective wax layer becomes a sexual signal

Author: *Joachim Ruther*[1]
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The cuticle of virtually any insect is covered by a complex mixture of cuticular hydrocarbons (CHCs) functioning as a water barrier. In many insects, CHCs are also used as contact sex pheromones, but the selective forces driving the evolution of this function as well as the mechanisms involved are only poorly investigated. I will outline a scenario of sex pheromone evolution in the pteromalid wasp Lariophagus distinguendus. Males of this pupal parasitoid of stored product infesting beetles use CHCs and other cuticular lipids to find and recognize mating partners. I argue that CHCs have initially evolved as a protective layer. The structural diversity of CHCs implies potential information which is used by L. distinguendus males as a pheromonal cue for the early detection of potential mates. Consequently, they are arrested on hosts containing conspecifics about to emerge. However, males are unable to discriminate the sexes at this stage and show courtship behaviour (wing fanning) towards newly emerged conspecifics of either sex. Subsequently, however, pheromonal activity develops differentially in males and females because newly emerged males smelling like females are less successful in mating contests due to regular courtship attempts by other males. Therefore, males (but not females) deactivate the pheromone within the first days after emergence. This pheromone deactivation is an active process requiring males to be alive. The chemical changes in the CHC profile of ageing males enabled us to decipher the chemical basis of pheromone deactivation in L. distinguendus males: The selective removal of a single component (3-MeC27) from the CHC profile rendered them biologically inactive. Hence simple chemical modifications of CHC profiles may translate species-specific into gender-specific information, thus increasing the reliability of sexual communication.

♦97 Tim Schmoll

Climate change and timing of reproduction in pied flycatchers: Evolution not needed?

Authors: *Tim Schmoll*[1]*, Wolfgang Winkel*[1]*, Loeske Kruuk*[1]
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Climate change affects the phenology of life cycle events in a variety of taxa, and many bird species of temperate regions have responded to increasing spring temperatures by shifting their timing of reproduction towards earlier breeding over the last decades. However, the relative contributions of phenotypic plasticity, microevolutionary responses and changing demography to the widely observed trends on the phenotypic level remain unclear. Disentangling these fundamental biological mechanisms and quantifying their relative contribution is of crucial importance for predicting how populations will respond to future climate change and for informing managing decisions.

Here we analyse a data set of more than 3000 breeding events from a German pied flycatcher Ficedula hypoleuca population which is characterised by a substantial forward shift in reproductive phenology over the last 37 years. Multiple observations of known-age individuals in different environments (i.e. spring temperatures) allow quantifying the role of individual phenotypic plasticity and demography for the observed changes in the timing of reproduction. Variation in the timing of reproduction has a heritable component in the study population and quantitative genetic analysis will reveal to what degree microevolutionary shifts also have contributed to the observed trends in the phenotype over time.

Using a random regression approach, we finally test for individual and additive genetic variation in reaction norm slopes to explore whether phenotypic plasticity itself has the potential to evolve, or has evolved during the study period, in this population.

♦98 Karin Schneeberger

Eco-Immunology of Mammals

Authors: *Karin Schneeberger[1], Gábor Czirják[1], Christian Voigt[1]*
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Ecological and social factors are central in the emergence and transmission of infectious diseases, thus bearing the potential for shaping a species? immune competence. Previous studies demonstrated a link between social factors such as promiscuity and the cellular immune system in captive mammals. However, it is yet poorly understood how ecological factors correlate with both cellular and humoral immune parameters. In addition, comprehensive studies on wild mammals are still lacking. Here, we tested if the cellular and soluble mediated constitutive immune system of free ranging bats is influenced by two ecological factors: diet and shelter choice. We found that total and differential white blood cell counts (WBC) of 24 co-existing Neotropical bat species varied with the species-specific diet and body mass. Bats that included at least partially vertebrates in their diet exhibited the highest WBC, followed by phytophagous and insectivorous species, which is consistent with the prediction that the immune system is linked to the pathogen transmission risk of a trophic level. Roost choice did not influence the cellular immune system, nor was the soluble mediated constitutive immune response, assessed by an in vitro bacterial killing assay, influenced by the ecological factors assessed. Our results suggest that the ecology of mammals is an important factor in the evolution of the immune system.

♦99 Maximilian Schweinsberg

Intracolonial genetic variability in the scleractinian coral Acropora hyacinthus

Authors: *Maximilian Schweinsberg[1], Raul Gonzales-Pech[1], Kathrin P. Lampert[1], Ralph Tollrian[1]*

Affiliation: [1]*Lehrstuhl für Evolutionsökologie und Biodiversität der Tiere, Ruhr Universität Bochum*

Coral reef degradation is a major economical and ecological concern. Consequently, coral reef conservation is a main goal of environmental protection. To protect reefs effectively, information about the genetic diversity of populations and the gene flow between sites are necessary. Population genetic data on coral species are therefore of prime scientific interest.

In addition, in recent years, the new phenomenon of intracolonial genetic variability within a single coral colony has been described. This connotes that coral colonies do not necessarily consist of only a single genotype, but contain several distinct genotypes. Harboring more than one genotype might allow for fast adaptation under rapidly changing environmental conditions. However, so far it remained unclear if the intracolonial genetic variability is transferred into the next generation or only exists within the adult colony.

We investigated the occurrence of intracolonial genetic variability using eight microsatellite loci in 15 adult colonies of the hermatypic coral *Acropora hyacinthus*. We analyzed eight tissue samples and the respective eight egg/sperm bundles per colony to determine whether different genotypes are present and passed onto the next generation. Our results indicate that several different genotypes can occur within the parent colony, and in the egg/sperm bundles.

Our results show that during reproduction of the coral *Acropora hyacinthus* more than one genotype per coral colony is transferred into the next generation potentially ensuring the colony's survival as well as reproductive success. Understanding the transfer of genotypes between generations will help us to better understand coral reef genetic diversity and site connectivity.

♦100 Martin Schwentner

Cyclestheria hislopi (Crustacea: Branchiopoda): a group of morphologically cryptic species with origins in the Cretaceous

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Affiliation: [1]*Universität Rostock, Allgemeine und Spezielle Zoologie, Institut für Biowissenschaften*

Cyclestheria hislopi is thought to be the only extant species of the Cyclestherida. It represents the sister taxon of all Cladocera, featuring morphological characteristics intermediate of Spinicaudata and Cladocera. Employing one mitochondrial (COI) and two nuclear (EF1? and 28S rRNA) markers we tested the hypothesis that *C. hislopi* represents a single circumtropic species. We included South American (French Guiana), Asian (India, Singapore) and several Australian populations. Phylogenetic and genetic distance analyses revealed remarkable intercontinental genetic differentiation (uncorrected p-distances COI > 13 %, EF1? > 3 % and 28S > 4 %). Each continent featured at least one distinct Cyclestheria species, with Australia revealing four distinct genetic lineages which may be attributed to two to three species. The divergence of these species (corresponding to crown-group Cyclestherida) was dated to the Cretaceous based on phylogenetic analyses of COI and EF1? combined with molecular clock estimates employing several fossil branchiopod calibration points or a substitution rate of 1.4 % per million years for COI. At that time the South American lineage split form the Asian-Australian lineage, with the latter diverging further in the Paleogene. Today's circumtropic distribution of Cyclestheria may be best explained by a combination of Gondwana vicariance and later dispersal among Asia and Australia when the tectonic plates of Australia and Asia drew closer in the early Miocene. The lack of morphological differentiation over such long evolutionary times contrasts with the great differentiation and diversification observed in its sister taxon the Cladocera. Further insights into the evolution of Cyclestheria may help to understand the evolutionary success of the Cladocera.

♦101 Sandra Steiger

No sex during biparental care: males adjust mating rate to female reproductive condition

Authors: *Sandra Steiger*[1], *Katharina Engel*[1], *Anne-Katrin Eggert*[1], *Christian von Hoermann*[1], *Josef Müller*[1]
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In many animal species, males exhibit plastic mating tactics by adjusting copulation frequency, mating duration, or number of sperm transferred on female mating status or the presence of rivals. Because copulations may entail costs that limit male reproductive capacity, males that strategically increase investment in reproduction only when it yields reproductive benefits will have a fitness advantage. Here we show for the first time that male insects can flexibly adjust mating rate during the period of parental care. Extensive video observation throughout the period of parental care in the biparental burying beetle Nicrophorus vespilloides revealed that males mated repeatedly in the beginning of the reproductive bout, but copulation rate dropped shortly before larvae hatched. During the period of larval feeding, when females do not normally oviposit, males did not engage in copulations. When larvae are withheld from their parents, female burying beetles are known to resume egg laying.We found that in this situation, males did not cease to mate, but continued to engage in frequent copulations with their partner. Moreover, further experiments demonstrated that males do not use the presence or absence of larvae as a cue to adjust copulation rate, but instead use female-specific cues to determine female reproductive state and adjust mating rate accordingly. Therefore, our study reveals that female beetles express cues that display their reproductive condition and males have evolved the ability to detect these cues and respond with prudent allocation of sperm.

◆102 Christian Sturmbauer

Genetic differentiation in relation to body shape change in sympatric and non-sympatric Tropheus populations of Lake Tanganyika

Authors: *Christian Sturmbauer[1], Michaela Kerschbaumer[1], Philipp Mitteröcker[1], Nina Znidaric[1], Christine Börger[1], Immanuel Karner[1]*
Affiliation: [1]*Department of Zoology, University of Graz, Austria*

Allopatric speciation often yields ecologically equivalent sister species, so that secondary admixis of such species pairs must enforce competition and possibly character displacement. This scenario is difficult to study in complex species communities. The rocky shores of Lake Tanganyika are populated by about 120 distinct populations of the cichlid fish genus Tropheus, some of which live in sympatry. We utilized the partial natural co-occurrence of *Tropheus moorii 'Kaiser'* and 'Kirschfleck' with *Tropheus polli* at the central eastern coast. When alone Tropheus occupies a relatively broad depth zone but in sympatry fish segregate by water depth. In a previous study we demonstrated via standardized pond breeding experiments that the observed diffenences between sym- and non-sympatrically living Tropheus 'Kaiser' have a genetic basis despite large-scale phenotypic plasticity. Using geometric morphometrics and neutral genetic markers, we investigated whether the sympatric populations differ consistently in body shape from their non-sympatric allies and if differences are likely to result from adaptation. We found significant differences in mean shape between non-sympatric and sympatric populations, whereas all sympatric populations of both color morphs clustered together in shape space. Sympatric populations had a relatively smaller head, smaller eyes, and a more anterior insertion of the pectoral fin than non-sympatric populations. Genetically, however, non-sympatric and sympatric 'Kaiser' populations clustered together to the exclusion of T. 'Kirschfleck'. Genetic distances, but not morphological distances, were correlated with geographic distances. Within- and between-population covariance matrices for *Tropheus moorii* populations clearly deviated from proportionality. It is thus likely that divergent natural selection on body shape acts on both phenotypic plasticity and genetically-based traits. The pattern observed in five sympatric populations is consistent with character displacement.

◆103 Meike Teschke

An evolutionary perspective on MHC sequence diversity

Authors: *Meike Teschke[1], Inka Montero[1]*
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The Major Histocompatibility Complex, a genomic region harboring genes with key roles in the immune system of all jawed vertebrates, is known for its extraordinary polymorphism and heterozygosity. Despite decades of intense empirical and theoretical research, the evolutionary mechanisms of the origin and the long preservation of polymorphism are not fully understood. Several authors suggest the solution in a combination of different selective forces like balancing selection, heterozygote advantage and frequency dependent selection. However, the majority of empirical studies harbor caveats in either sample and/or locus selection or in data

acquisition. We collected an outstanding comprehensive data set on sequence diversity in various natural populations of wild house mice covering numerous MHC class I and class II genes. A highly cost effective labeling procedure allowed us to sequence 13 functional exons in 75 individuals representing five populations using next generation sequencing technology. Comparing ancestral with derived lineages and comparing different subspecies of house mice should help to identify the degree of natural polymorphism in different populations and the influence of population history. Inferences on the role of MHC genes on local adaptations against pathogens as well as differences in the molecular evolution of class I and class II genes will be possible based on such data.

♦104 Anne Thielsch

Evolutionary history and current environmental changes explain contrasting population genetic structures in large-lake Daphnia species

Authors: *Anne Thielsch[1], Robert Kraus[2], Klaus Schwenk[1]*
Affiliation: *[1]University of Koblenz-Landau; [2] Senckenberg Research Institute and Natural History Museum Frankfurt*

Cyclic parthenogens, such as many zooplankton organisms, display an alternation of asexual and sexual reproduction. During favourable conditions amictic individuals reproduce asexually, while deteriorating environmental cues induce sexual reproduction which results in dormant stages that enable dispersal through time and space. Although many zooplankton species are good dispersers through their sexually produced dormant stages, the influence of gene flow is assumed to be negligible, as the local populations successfully monopolize the available resources, preventing immigration of new genotypes. To evaluate the importance of the different factors influencing population genetic structure, we studied European populations of two widely distributed and ecologically plastic species of the genus Daphnia, *D. galeata* and *D. longispina*, using microsatellite and mitochondrial DNA markers. Although both taxa co-occur and inhabit similar ecological niches, they show contrasting population genetic structures. While *D. longispina* populations are highly differentiated at both studied DNA markers, *D. galeata* populations are genetically quite homogenous. This indicates historical diversification in *D. longispina* resulting in the development of mature populations with restricted gene flow probably due to monopolization of respective resources. In contrast, *D. galeata* expanded probably very recently and populations may still be connected through gene flow. The population genetic structure of both taxa was probably influenced by different historical events. *D. longispina* may have expanded its range after the last ice age and population differentiation would have been established by founder and priority effects leading to strong local adaptation. Recent expansion of *D. galeata* might be facilitated by current anthropogenic alteration of freshwater habitats (eutrophication) which enabled multiple successful invasions by this taxon.

◆105 Nicolas Thiercelin

Different gene flow and phylogeographic differentiation along the tropical American coastlines in the crab genera Aratus and Pachygrapsus

Authors: *Nicolas Thiercelin[1], Christoph Schubart[1]*
Affiliation: *[1]Universität Regensburg*

Physical oceanic barriers are considered to be a major limiting component for the connectivity among marine populations, and may lead to allopatric speciation. These barriers can be identified by the presence of genetic breaks among populations. Thoracotreme littoral crabs show marked differences in their ecological characteristics (e.g. habitat or dispersal abilities) and are common along tropical coastlines, where they often occupy patchy habitats like mangroves.

In this study, we used mtDNA sequences of the mitochondrial gene COI to identify and understand possible genetic differentiation along the distribution range of species inhabiting different coastal habitats. Populations of Aratus pisonii and Pachygrapsus tranvsersus were sampled and analyzed from their entire distribution range along the American continent (Florida to southern Brazil in the western Atlantic, Baja California to Ecuador in the eastern Pacific), and the transisthmian divergence used as relative time scale.

In the mangrove-dependent species Aratus pisonii, heterogeneity in the genetic structure along both tropical coastlines is observed. In contrast, the rocky shore species Pachygrapsus transversus and P. socius show a more homogeneous genetic structure. In addition, the degree of genetic differentiation could be related to the time of larval planktonic development.

The established gene flow barriers are not easy to be interpreted and partly differ from the postulated ones (e.g. Amazon Delta). Isolation by distance also fails as the only explanation, so that a mixed scenario of gene flow considering geographic distance, currents, habitat, and time of larval development needs to be elaborated.

◆106 Timo Thünken

Kin competition: small, hungry juvenile *P. taeniatus* avoid shoaling with kin

Authors: *Timo Thünken[1], Saskia Hesse[1], Denis Meuthen[1], Rebecca Kulbida[1], J. Alexander Müller[1], Theo C. M. Bakker[1]*
Affiliation: *[1]University of Bonn*

Inclusive fitness theory (kin selection theory) predicts benefits from grouping with kin. Indeed, laboratory and field studies in different animal taxa including fishes revealed that groups are often kin-structured and that preferences exist to group with kin. However, as theory also predicts grouping with kin can result in competition between kin which can negate the benefits of kin-biased behaviour. The cost/benefit ratio of kin-biased behaviour is assumed to depend on ecological parameters. Here, we investigated the influence of predation risk and of hunger on kin shoaling preference in the cichlid fish *Pelvicachromis taeniatus*, which lives in shoals as juvenile. Hungry and saturated juveniles were given the choice between a shoal consisting of unrelated individuals and a shoal consisting of related individuals with or without predation risk. Predation risk was simulated by adding conspecific alarm cues. Results showed that kin-shoaling preferences were not significantly influenced by predation risk. However, hunger level affected kin preferences depending on the body size of the test fish. Small, hungry juveniles avoided to shoal with kin whereas small, saturated juveniles as well as larger juveniles in general tended to preferentially shoal with kin. We discuss the results in the context of size-related energetic demands.

♦107 Arndt Wellbrock

To bleed or not to bleed? - Validation of buccal swabs compared to blood as DNA source for molecular sexing of birds

Author: *Arndt Wellbrock*[1]*, Christina Bauch*[1]*, Jan Rozman*[1]*, Klaudia Witte*[1]
Affiliation: [1]*Research Group on Ecology and Behavioral Biology, Section of Biology and Didactics, Department of Chemistry - Biology, University of Siegen*

Buccal swabbing is an easy, non-invasive and alternative method to blood sampling to get DNA for sexing birds. However, little is known about the reliability of this sampling method. Here, we investigated the reliability of buccal swabs for molecular sex determination in very young nestlings (0 to 14 days old) and adults of the Common Swift (Apus apus) by comparing sex determination based on buccal swabs and based on blood samples of the same individuals. Thereby, buccal swabbing was tested for sexing a small non-passerine bird for the first time. We found that buccal swabs are a reliable non-invasive source of DNA for sex determination in both adult and very young swifts. In 47 out of 53 (89%) nestlings and 10 out of 11 (91%) adults, we received enough DNA via buccal swabs for a successfull PCR. Sex determination based on DNA from buccal swabs matched the result of sex determination based on blood samples in 46 of the 47 nestlings (98%) and in all 10 cases in adults (100% matching). Since PCR amplification was performed only once per individual, we consider this success rate - and hence the reliability of buccal swabs as DNA source - as very high. Therefore, we recommend buccal swabs as a feasible non-invasive method in future genetic studies in birds, especially for small nestlings and in species which are sensitive to stress.

♦108 Mareike Wurdack

Consequences of an arms race between a host and its three brood parasites

Authors: *M. Wurdack*[1]*, J. Kroiss*[1]*, E. Strohm*[1]*, O. Niehuis*[1]*, T. Schmitt*[1]
Affiliation: [1]*Universität Freiburg*

Parasites and hosts have conflicting interests ? to either exploit or defend. This sets the board for an evolutionary arms race. The species pair follows a trajectory through repeated cycles of fine tuning of the parasite?s attack strategies and evasive actions of the host. Brood parasites in particular need to avoid detection by the host. Insect brood parasites may avoid olfactory detection by mimicking the host?s cuticular hydrocarbon (CHC) profile. The arms race would then lead to optimized chemical mimicry in the parasite. The host could e.g. escape a mimetic match by changing its CHC composition.

Ordinary parasitic associations consist of one enemy (the parasite) and one target (the host). But more complex variations are possible, too. In this study, a solitary host

(Hymenoptera: Eumenidae) and its three host-specific brood parasites (Hymenoptera: Chrysididae) serve as a model of a multi enemy / single target system. We compare the CHC profiles and predict that a brood parasite whose intrusion is detectable by the host should develop chemical mimicry. The host in return should establish counterstrategies. Competition between parasites may fuel the perfection of mimicry or the development of completely new intrusion strategies.
We find two chemotypes of the host that differ greatly in their CHC composition. The split could allow part of a population to escape one parasite?s mimicry. But two parasite species have evolved a close match in CHC composition ? one for each chemotype. The third parasite produces its very own CHC profile ? it has developed a new strategy for invading host nests and can no longer be fended off by the host.

♦109 Dietmar Zinner

Pleistocene mosaic of savannah refugia in East Africa: insights from baboon mtDNA

Authors: *Dietmar Zinner*[1], *Christina Keller*[1], *Christian Roos*[1]
Affiliation: [1]*German Primate Center*

Genetic studies of African savannah ungulates as well as palynological, palaeovegetation and fossil studies have suggested the presence a Pleistocene savannah mosaic of refugia in East Africa. Beside ungulates, a few primate taxa are primarily savannah species, including humans and baboons (Papio spp.). We therefore expected to find a similar genetic signature in baboons supporting the savannah mosaic of refugia hypothesis. Baboons occur in large parts of sub-Saharan Africa and our previous molecular studies using mitochondrial DNA sequence data indicated two major phylogeographic lineages - a southern and a northern, which diverged around 2 mya. In addition several local lineages had been detected in East Africa. To further investigate the phylogeography of these lineages, we collected faecal samples at more than 50 sites from Kenya to Malawi with special focus on Tanzania. We used complete cytochrome b and 'Brown region' sequences to further elucidate the phylogeography of baboons in East Africa. We estimated fossil calibrated divergence times by applying Bayesian coalescent-based methods. Preliminary results suggest the occurrence of at least 7 phylogeographic baboon lineages which split from each other during the Pleistocene. Our data is consistent with the hypothesis of Pleistocene mosaic refugia in East Africa.

♦110 Antje Engelhardt

Towards a theoretical framework for understanding the variation in female sexual traits among anthropoid primates

Authors: *Antje Engelhardt*[1], *James P. Higham*[1], *Constance Dubuc*[1]
Affiliation: [1]*German Primate Center*

Female sexually selected traits usually evolve to attract mates in species with sex-role reversal. In many anthropoid primates females exhibit sexually selected traits, mostly signals, without any sex role reversal. The functions of these traits thus seem to deviate from those of other taxa. Primate female sexual signals occur more commonly in polygynandrous species, but with marked variation in prevalence, form, information content and function. Here, we review what is known about these signals, and attempt to explain the observed variation. We suggest that anthropoid typical non-procreative mating has created the opportunity for females to manipulate male sexual behaviour through the development of sexual signals, with the range and function of signals adjusted to species-specific ecology. Based on the premise that the degree of breeding seasonality (i.e. temporal distribution of fertile females) determines the mode of male-male competition (direct versus indirect), we postulate that seasonality also shapes the evolution of female signals. We suggest that whereas female signals of non-seasonal species (direct male-male competition leading to high-quality dominant males), help to solve the female dilemma (the need to confuse paternity through promiscuity while preferring high-ranking males as sires), in non-seasonal species (indirect male-male competition with potential low-quality dominant males) female signals function to increase opportunities for female mate choice or sperm competition/female cryptic choice, and may play a role in female-female competition for mates.

10. Morphology TALKS

Saturday, September 22, 2012

Chair: Georg Mayer

☐69 Markus Lambertz A 703 / 14:00

Contributions to an understanding of pulmonary and associated structures in cryptodiran turtles

Authors: *Markus Lambertz*[1], *Steven F. Perry*[1]
Affiliation: [1]*Institut für Zoologie, Rheinische Friedrich-Wilhelms-Universität Bonn*

In turtles, as in all amniotes, the lungs are the primary organ for satisfying oxygen demand and all amniotes are true aspiration breathers. The unique, shelled bauplan of turtles consequently required the evolution of a highly specialized muscular mechanism to achieve a proper ventilation of the respiratory surfaces. The principal structure of the gas exchanger, however, is a relatively simple, multichambered lung, which is probably very similar to that suggested to be the plesiomorphic condition for amniotes. Nevertheless, among the various turtle clades there is a conspicuous diversity of pulmonary structure evident. Detailed study of this diversity serves two purposes: it sheds some light on the evolution of this organ system within the taxon and may help our understanding of lung evolution in amniotes as a whole.
After a brief introduction into the unique chelonian breathing mechanics and its muscular basis, we focus on other structural aspects of the respiratory apparatus. These include the morphological diversity of the extrapulmonary airways and the lungs themselves, as well as the coelomic integration of these elements. We have

examined specimens from most major cryptodiran taxa. Based on this comparison we provide some insights into a possible evolution of the cryptodiran respiratory apparatus and also discuss its value in systematics.

☐70 Falk Esser A 703 / 14:15

Characterization of waterextraction from moist soil by moisture harvesting lizards

Author(s): *Falk Esser*[1]*, Philipp Comanns*[1]*, Werner Baumgartner*[1]
Affiliation: [1]*RWTH Aachen Biologie II, Zelluläre Neurobionik*

A theory how *Moloch horridus* and *Phrynosoma cornutum* tackle their daily water demand is introduced. It is shown that *Moloch horridus* and *Phrynosoma cornutum* are able to perform moisture harvesting by microornamentation on the Oberhäutchen and capillary channels formed by scale hinges. Sherbrooke (1993) observed that Moloch showed a certain behavior in the early morning hours by pouring moist soil on to its back and rubbing its chest into the ground (Comanns et al. 2011, Sherbrooke 1993, Withers 1993). Imitating this early morning this behavior, the specimen´s integument was replicated with epoxy resin, with which experiments were conducted to test whether the specimen are able to extract water from moist soil. In the experiments the capillary forces of sand and the integument were measured and compared, moist sand was applied on the replicas and the behavior of applied water droplets was recorded. The experimental parameters where adapted so that they imitated the early morning behavior, shown by *Moloch horridus*. The experiments provide good evidence that under certain circumstances the specimen are able to extract enough water from the moist sand with their sand angel perfomance to cover their daily water demand.

☐71 Nina Furchheim A 703 / 14:30

Size matters when living in an intertidal washing machine: the smallest known brachiopod *Gwynia capsula*

Authors: *Nina Furchheim*[1]*, Anne Kaulfuss*[1]*, Carsten Lüter*[1]
Affiliation: [1]*Museum für Naturkunde, Berlin*

Gwynia capsula (Terebratulida, Gwynioidea) is one of the most unusual brachiopod species described so far. It is the smallest of all known living brachiopods (<1mm) and one of the few that inhabit waters as shallow as the lower littoral zone. In the past 150 years since its first description, few studies on *G. capsula* have been conducted focusing mainly on the shell morphology to discuss its unresolved relationship within Terebratulida. Aside from its trocholophous lophophore and limited brooding capacity of two larvae, nothing is reported on the inner anatomy and life habits of adult *G. capsula*. Here we present the preliminary results of the first histological, ultrastructural, and immunohistochemical investigation of the internal morphology of *G. capsula*. Specimens of *G. capsula* were collected during the lowest spring tide from shell gravel around Church Island in the Menai Strait, North Wales, where they live interstitially attached to empty serpulid worm tubes which are subject to relatively strong currents and exposure from the water during low tides. Living specimens were successfully transferred to salt water tanks at the Museum für Naturkunde in Berlin.

Semi- and ultra-thin sections and antibody staining of several specimens reveal detailed images of the internal anatomy. Only two ova ripen to maturity at the same time. Relative to the adult shell length of 0.5-1.0 mm the egg size of ~180 µm of *G. capsula* is the largest recorded in any brachiopod. Additionally, we detected early juvenile specimens inside previously uninhabited serpulid tubes which we placed in the same tank with the adults before lowering the temperature to mimic the beginning of winter. This is the first record of 'naturally' induced spawning of brachiopods in captivity.

☐72 Ronald Seidel A 703 / 14:45

3D reconstruction of brachiopod shells using non-invasive x-ray computed tomography (µCT)

Authors: *Ronald Seidel*[1], *Carsten Lüter*[1]
Affiliation: [1]*Museum für Naturkunde, Berlin*

The calcareous shells of Brachiopods offer a wealth of informative characters for taxonomic and phylogenetic investigations. Particularly scanning electron microscopy (SEM) is used to visualise internal structures of the shell, especially the complicated morphology of the lophophore skeleton, the brachidium.

However, to produce informative SEM data brachiopod shells after chemically dissolving the soft tissue need to be opened. This preparation occasionally leads to damage of the shell. Additionally, skeletal elements of taxonomic/systematic interest such as calcareous spicules which are loosely embedded in the lophophore and mantle tissue become disintegrated altogether during the preparation process.

Using a non-invasive µCT approach, we were able to document the internal shell anatomy including soft tissue (the latter with lower resolution though) and to visualise the shells of recent brachiopods in interactive 3D reconstructions. Furthermore, we accomplished to add structural and positional data on tissue-bound skeletal elements (e.g. spicules) to existing descriptions of brachiopod shell anatomy, thereby enhancing the quality and quantity of informative characters needed for both, taxonomic and phylogenetic studies.

We scanned representatives of 16 brachiopod genera for morphological analysis covering all recent articulate subgroups. All specimens were picked from either the historical wet collection of the Museum für Naturkunde, Berlin or from recently collected samples. Reconstruction and subsequent Visualisation in 3D movies was performed using VG Studio Max and AMIRA software.

☐73 Jörg U. Hammel A 703 / 15:00

A modeling approach to understanding fluid dynamics and flow in leuconoid sponge canal systems

Authors: *Jörg U. Hammel*[1], *Henry Jahn*[1], *Florian Wolf*[1], *Felix Beckmann*[1], *Jaap Kaandorp*[1], *Michael Nickel*[1]
Affiliation: [1]*Friedrich-Schiller-Universtität Jena, Institut für Spezielle Zoologie und Evolutionsbiologie*

As sessile filter feeding animals sponges (*Porifera*) rely on highly efficient fluid transport systems. Due to the high complexity of the 3D network of incurrent and excurrent canals in the leucon-type aquiferous system only limited data on flow velocities and transport rates are available to date and are mainly based on theoretical assumptions. This is mainly due to the limited availability of morphometric and quantitative data on canal system architecture. In our study we used the fresh water sponge *Spongilla lacustris* which is an ideal model system to study flow in sponge. Due to its transparency flow velocities can be determined experimentally inside canals near the surface and at the osculum. The limited architectural complexity and small body size enables the extraction of a 3D canal system model from a single specimen. Reconstructions were based on SR-µCT data. Flow through the canal system was studied using a finite element modeling approach. In order to verify the results of our modeling approach we conducted flow velocity measurements by particle tracking velocimetry at the osculum. Outflow velocities were between 0.6 ? 07 mm/s in our experiments and simulations. By quantitative morphometrics we determined the size and number of choanocyte chambers from a single specimen. We determined the pump rate of choanocyte chambers in *S. lacustris* to be 1200 µl3/s. Observed flow velocities in canal segments of different hierarchical orders were lower in our simulations than predicted based on calculations from the current model of flow for sponges.

☐74 ConradHelm A 703 / 15:15

The body musculature of polychaetes and allies: Implications for muscular ground patterns within Annelida

Authors: *Conrad Helm*[1], *Christoph Bleidorn*[1]
Affiliation: [1]*Molecular Evolution & Systematics of Animals, Institute of Biology, University of Leipzig, Germany*

Developmental modes and body plan diversification within annelids and related taxa are as diverse as the habitat types these lophotrochozoans are distributed in. Thus, it is necessary to investigate a huge variety of taxa sampled across the annelid tree of life to understand character evolution for several organ systems. One such prominent character complex is the muscular system. Although representing a distinct and consistent character complex, our knowledge concerning ground patterns and variability of character manifestation within annelids and related taxa is still sparse. A body wall musculature formed by an outer circular layer and longitudinal muscles situated beneath is considered to represent the plesiomorphic condition of annelids. Nevertheless, recent investigations on muscularly systems of several members of Annelida present a different point of view. Many species investigated so far are lacking circular muscle fibers, even though the discussion if absence of this character to be either primary or secondary is still unresolved. Regardless if errant or sedentary, macro- or meiobenthic, all annelid taxa investigated so far include several taxa which are lacking circular muscle fibers. Presence, general occurrence and characteristics of additional muscle complexes, e.g., bracing muscles or the parapodial muscle complex, are still investigated incompletely and discussed controversially.

So far, the interpretation of muscle patterns and their observation considering any direction of evolutionary change observed within this organ system was highly speculative, as a reliable annelid phylogeny was lacking. Recent phylogenomic investigations now present a solid background of annelid phylogeny.

In order to extend our knowledge concerning the variability of muscular patterns within Annelida, and to reconstruct a hypothetical muscular ground pattern valid for annelids and allies, we analyzed the distribution of f-actin, a widespread element of muscle fibers, within different annelid taxa using phalloidin labeling in conjunction with confocal laser scanning microscopy (clsm). Our investigations broaden the knowledge concerning the evolution of muscular characters in lophotrochozoans and provide implications for the evolution of muscular patterns in polychaetes and allies.

Sunday, September 23, 2012

Chair: Steffen Harzsch

☐74a Paavo Bergmann A 703 / 12:00

Automictic parthenogenesis in the oribatid mite, *Archegozetes longisetosus*

Authors: *Paavo Bergmann*[1], *Michael Laumann*[1], *Michael Heethoff*[1]

Affiliation: [1]*Institut für Evolution und Ökologie, Eberhard-Karls Universität Tübingen.*

Archegozetes longisetosus is a parthenogenetic, diplo-diploid model oribatid mite species. We examined oogenesis, meiosis, vitellogenesis, cleavage and early embryonic development by means of synchrotron X-ray microtomography, light- and electron microscopy. The ovary forms in the deutonymphal stage, oocytes enter meiosis I in tritonymphs. The occurence of meiosis is supported by the observation of a synaptonemal complex, which is the first ultrastructural direct evidence for automictic parthenogenesis in these animals. Oocytes remain arrested in prohase I until the adult stage, where they enter vitellogenesis during their course from the ovary towards the oviducts. Solidification of the egg shell occurs instantaneously at the transition point from the ovary to the oviducts, accomplished by a specialized wall epithelium, the oviductal bulb. At this point any chemical communication between mother and offspring ends, rendering the oviducts functional brood chambers. Cleavage is holoblastic and total, eggs in various developmental stages accumulate in the oviducts until oviposition.

☐74b Temim Deli A 703 / 12:15

Comparative phylogeography of two coastal crab species along the African Mediterranean coast: Carcinus aestuarii (Carcinidae) versus Pachygrapsus marmoratus (Grapsidae)

Authors: *Temim Deli*[1/2]*, Noureddine Chatti*[1]*, Khaled Said*[1]*, Christoph D. Schubart*[2]
Affiliations: [1]*Laboratoire de Recherche, Génétique, Biodiversité et Valorisation des Bioressources, Institut Supérieur de Biotechnologie de Monastir, Tunisia;*
[2]*Biologie I: Zoologie, Universität Regensburg*

Carcinus aestuarii (Nardo, 1847) and *Pachygrapsus marmoratus* (Fabricius, 1787) are two of the most common crab species from the Mediterranean coastline and play an important role in structuring the marine intertidal community. These two species occur in habitats with different wave exposure, have different dispersal strategies, and can cope with different environmental conditions. Recent investigations separately carried out on these species along the European coasts showed different population genetic structure and demographic histories. However, to this point, no attempt has been undertaken to compare phylogeographic population structure of these species, when collected from the same localities and at the same time. Furthermore, for both species population data are missing from the North African coast. The current investigation aims at shedding more light on the population genetic structure of these two sympatric species along the African Mediterranean coasts and to unveil the impact of the dispersal capacity (depending on length of larval development, retention mechanisms etc.) on shaping population structure in marine populations. Two highly variable and independent marker systems, the mitochondrial COI gene and a set of nuclear microsatellites loci, were used and analyzed in up to eleven populations from the Mediterranean coast of North Africa and compared to European populations. The results of this study show clearly different patterns in genetic diversity and phylogeographic structure between both species along this geographical spectrum and require discerning among possible biotic and abiotic factors that can be responsible for such diverging patterns of regional diversification.

Chair: Sabrina Kaul-Strehlow

☐75 Alexander Bär A 703 / 14:00

Comparative anatomical study reveals differences in the composition of slime glands in Onychophora (velvet worms)

Authors: *Alexander Bär*[1]*, Georg Mayer*[1]
Affiliation: [1]*Animal Evolution & Development, Institute of Biology, University of Leipzig*

Velvet worms use a unique hunting and defence strategy, which involves the ejection of an adhesive slime secretion produced by a pair of specialised glands. So far, a comparative study on the anatomy of these glands has not been carried out among different onychophoran species. Hence, we have analysed the anatomical features associated with slime glands in representatives of the two major onychophoran subgroups, Peripatopsidae and Peripatidae, from different parts of the world. Our data show that the musculature of the reservoir is conserved whereas the composition of the secretory duct displays taxon-specific variation. Major differences concern the arrangement of glandular endpieces, which are distributed along the duct in Peripatopsidae but condensed in numerous repeated rosettes in Peripatidae. In addition, there are differences in the attachment pattern of slime glands to the inner surface of the body wall and to the outer surface of the gut. A tube-like structure with a putative valve-like function is found at the transition of the secretory duct and the reservoir in the five Peripatopsidae species whereas it is absent in the two representatives of Peripatidae studied. Our findings suggest that the arrangement of musculature in the reservoir of the slime gland has remained unchanged since the divergence of Peripatidae and Peripatopsidae, while the composition of the secretory duct has been altered in one of these groups. However, the direction of evolutionary changes in duct composition cannot be determined unambiguously due to current uncertainty regarding the phylogenetic relationships of the onychophoran subgroups.

☐76 Ivo de Sena Oliveira A 703 / 14:15

Unexplored morphological character diversity in *Onychophora* (velvet worms)

Authors: *Ivo de Sena Oliveira*[1]*, Georg Mayer*[1]
Affiliation: [1]*Animal Evolution & Development, Institute of Biology, University of Leipzig*

Putative low character diversity among the nearly 200 described velvet worm species has been an obstacle for taxonomic and phylogenetic studies of *Onychophora*. To find additional characters, we analysed a high number of specimens (n>1000) of two closely related onychophoran species from the neotropics and a distantly related species from South-East Asia. Our screening approach using scanning electron microscopy on moulted skins, embryos, and specimens of different ages revealed novel characters and character states, which are potentially informative at different taxonomic levels. These include, for example, the distribution of different receptor types along the antennae, a specific pattern of head papillae, the arrangement of crater-shaped papillae along the body, the presence and shape of novel ‘interpedal organs’ on the ventral body surface, the structure of bean-shaped papillae on legs, the arrangement of mouth lips, the number, position and shape of crural tubercles and anal gland openings, and the presence and structure of embryonic foot projections. Our findings suggest a high number of unexplored characters in *onychophorans*, which should be considered when additional species are studied.

☐77 Sebastian Schmelzle A 703 / 14:30

The ptychoid defensive mechanism in Mesoplophoridae (Acari, Oribatida)

Authors: *Sebastian Schmelzle*[1]*, Michael Heethoff*[1]*, Roy A. Norton*[1]
Affiliation: [1]*Universität Tübingen*

Ptychoidy is the most complex morphological defensive mechanism in oribatid mites. Here, the animals can retract their legs and coxisternum into the idiosoma and seal themselves off with the prodorsum. In this encapsulated state no soft membranes are exposed, leading to a presumably effective protection against predators. This defensive mechanism has probably evolved three times independently within the Oribatida: in the *Ptyctima*, the *Protoplophoridae* and the *Mesoplophoridae*. It has been well study for the Ptyctima, but so far no studies are available concerning the functional morphology of ptychoidy in *Protoplophoridae* and *Mesoplophoridae*. By using synchrotron X-ray microtomography we studied the exoskeletal and muscular features of ptychoidy in mesoplophorid mites and compare them to the *Ptyctima*. The most important functional problem of ptychoidy - regulation of high differences in hydrostatic pressure - is solved differently in all so-far investigated groups.

☐78 Esther Appel A 703 / 14:45

Resilin in the dragonfly wing veins

Authors: *Esther Appel*[1], *Chung-Ping Lin*[2], *Stanislav Gorb*[1]
Affiliation: [1]*Department of Functional Morphology and Biomechanics, Zoological Institute, Christian-Albrechts-University of Kiel, Germany*; [2]*Department of Life Science, Tunghai University, No. 181, Section 3, Taichung, Taiwan*

Resilin, a rubber-like protein, has already been reported to play a key role in various arthropod locomotor systems. In insect flight systems, it was suggested to provide additional flexibility and adjustment to external loads, as well as energy storage. The discovery of resilin-bearing vein joints in damselfly wings led to the suggestion that resilin may contribute to the wings´ flexibility and elasticity, thereby influencing the ability of odonatan wings to generate passive wing deformations adapted to the momentary aerodynamic situation during flight [1]. In the present work, we report on the presence of resilin not only in wing vein joints, but in internal layers of each wing vein in wings of *Sympetrum vulgatum* (Anisoptera, Libellulidae) and *Matrona basilaris basilaris* (Zygoptera, Calopterigidae). In order to elucidate the structure and material composition of wing veins, we combined the application of bright-field light microscopy (LM), fluorescence microscopy (FLM), confocal scanning microscopy (CLSM), scanning electron microscopy (SEM), and transmission electron microscopy (TEM). Results suggest that dragonfly and damselfly wing veins consist of up to six different cuticle layers with the endocuticle being dominated by resilin. The asymmetrical construction arising from a stiff, tanned, and dehydrated exocuticle and a soft, compliant inner layer (endocuticle) was previously assumed to allow larger deformation before failure, to lead to increased elastic energy storage, and to prevent fracture formation [2]. This is especially important for longitudinal veins which do not have the possibility to yield to bending loads and torsional deformations with the aid of flexible, resilin-bearing joints.

[1] S.N. Gorb, Naturwissenschaften, Vol. 86 (1999), pp. 552-555. [2] J.F.V. Vincent, U.G.K. Wegst, Arthropod Structure & Development, Vol. 33 (2004), pp. 187-199.

☐79 Julius Braun A 703 / 15:00

Morphological and chemical analyses of adhesive tarsus structures in insects

Author: *Julius Braun*[1]
Affiliation: [1]*Universität Tübingen*

Insects are able to adhere to even smooth surfaces during locomotion. The adhesive performance is provided by morphological features of the tarsal surface as well as the chemical properties of adhesive liquids. We conducted both morphological examinations of the tarsus structure and chemical analyses of tarsal liquids in several beetle species. We also measured the adhesive performance as a function of surface energy and roughness. To examine the chemical composition of the tarsal fluid we directly collected samples from the tarsal surfaces via both solid-phase micro-extraction and solvent extraction. Subsequent analyses of the secretion were conducted by means of hyphenation of gas-chromatography to mass-spectrometry (GC-MS). According to its high sensitivity in the microgram range, this method is well-suited to characterize small sample amounts of the tarsal liquids.

☐80 Ute Eulitz A 703 / 15:15

Coleoptera remains from a neolithic well 7200 years old

Authors: *Ute Eulitz*[1]*, Klaus-Dieter Klass*[1]
Affiliation: [1]*Senckenberg Naturhistorische Sammlungen Dresden, Museum für Tierkunde*

Wells from the Neolithic period of Central Europe (Linear Pottery Culture) are valuable archives for archaeological investigations and allow for a new perspective on this culture. Wood, ceramics, bones, pollen and insect remains have been conserved in sediments still humid today. Six neolithic wells (5500 - 5000 BC) were found in Saxony; that of Brodau near Leipzig (ca. 5200 BC; discovered in 2005) was investigated in this study. A total of 80 samples yielded 2387 arthropod fragments, mostly from *Coleoptera* (besides few others from Hymenoptera, Diptera and Araneae).

Coleoptera remains are mostly isolated elytra, pronota and head capsules; legs, mouthparts or sternites are sparse. Conventional identification keys are not applicable to the fragments because they require consideration of several body parts. The fragments are usually well preserved including cuticular surface structures and occasionally colouration or hairs. We based species identification on (1) examination of fragments including details of the cuticular surface and (2) comparison with identified specimens in the institute's *Coleoptera* collection, using SEM and light microscopy. This revealed many previously unknown species-distinguishing characters, mainly on elytra. Yet, identification remains ambiguous in taxa including several very similar species. The beetle fragments were assigned to 20 families, 36 genera and 27 species. More than 60 % are *Aphodiinae* (Scarabaeidae) especially *Aphodius varians*, *A. granarius* and *Pleurophorus caesus*. Four synanthropic species were detected: *Tenebrio obscurus*, *Oryzaephilus surinamensis* (oldest records for both), *Sitophilus granarius* and *Tenebroides mauretanicus*, probably all pests on cereals. *Carabidae* (ca. eight species), *Ceutorhynchus* (Curculionidae) and *Platystethus* (Staphylinidae) were also well represented.

Monday, September 24, 2012

Invited speaker 1: Chair – Michael Heethoff A 703 / 11:30

Hendrik Müller (Jena)

Evolution of reproductive strategies and skeletal development in amphibians

Author: *Hendrik Müller*[1]
Affiliation: [1]*Institut für Spezielle Zoologie und Evolutionsbiologie, Friedrich-Schiller-Universität Jena*

Modern Amphibia - Anura, Caudata and Gymnophiona - display a broad range of different life styles and corresponding morphologies and this diversity is mirror in reproduction and development. Many amphibian taxa have departed from the ancestral mode of reproduction, with aquatic eggs and larvae, and exhibit a vast array of different reproductive strategies. In Anura alone, 39 different developmental modes have been defined, differing in egg deposition site, larval life style, parental behaviour and other parameters. Several of these different reproductive modes evolved repeatedly and independently within Anura and Gymnophiona and, to a lesser extent, Caudata. At the level of development, the majority of exotrophic, biphasic developing amphibians show a similar pattern of skeletal formation. Development in taxa with derived reproductive modes (direct development, viviparity, non-feeding terrestrial tadpoles etc.) shows numerous deviations that are interpreted as being either functional or the result of a loss of larval structures. The repeated independent evolution of derived reproductive strategies provides an opportunity to study common patterns in skeletal development.

Invited speaker 2: Chair – Peter Michalik A 704 / 12:00

Ellen Schulz (Hamburg)

Chewing mechanics in mammals: 3D morphology of enamel wear

Author: *Ellen Schulz*[1]
Affiliation: [1]*Biozentrum Grindel und Zoologisches Museum, University of Hamburg*

Mammals inhabit all types of environments and have evolved chewing systems capable of processing a huge variety of structurally diverse food components. Mammalian dental tissues have undergone evolutionary optimization in terms of fracture and wear resistance. Based on the high degree of correspondence between industrial machined and the tooth enamel surfaces, surface textures of cheek teeth should reflect the mechanisms of wear as well as functional traits. A new approach is developed using 3D topographic models of dental wear facets acquired with a high resolution confocal disc-scanning surface measuring system (µsurf Custom, NanoFocus AG Oberhausen, Germany). Forty-six industrial 3D surface texture parameters are applied after ISO/FDIS 25178-2, ISO 12781, motif, furrow, direction, and isotropy and flatness analysis to quantify wear using the µsoft analysis premium software (DigitalSurf Besançon, France). Cheek dentitions of extant and extinct grazing, browsing, and fruit feeding primates and ungulates were evaluated. These species represent a large magnitude of dietary traits which also are reflected in the dental structures. In order to calibrate wear signatures for the impact of intrinsic and exogenous abrasives feeding experiments on captive rabbits are conducted controlling the abrasiveness of animal feeds and testing for patterns in the surface texture signal. The hypotheses tested relates to the geometry and dynamics of chewing movements as well as biomechanical properties of food items comminuted. It is found that dental wear systems are controlled by chewing dynamics of fluids and solids indicating mixed friction in the highly dynamic interdental space. Surface textures reflect the geometry of particles dispersed in the fluid phase as well as their biomechanical properties of the antagonistic solid hard components as food inclusions and dental tissues.

Chair: Andy Sombke

☐81 Martin Fritsch A 702 / 14:00

Insights in the evolution of larval development in Branchiopoda (Crustacea) using an Event-Pairing approach: First indications of the evolutionary transformation towards Cladocera

Authors: *Martin Fritsch*[1]*, Stefan Richter*[1]
Affiliation: [1]*University of Rostock, Department of Zoology*

Cladocera, also known as water-fleas, are the ecologically most important group within the Branchiopoda (*Crustacea*). They are unquestionably branchiopods but their evolutionary origin remains unclear. One favored explanation of their origin is that they evolved from a reproductive larva of a ‘clam shrimp-like’ ancestor. In order to reveal a transformation and to identify (potential) changes in chronology (heterochrony), we investigated and compared the development of representatives of all six recent branchiopod taxa. One of the Anostraca, (*Branchinella sp.*), one of the Notostraca (*Triops cancriformis*), one of the three clam shrimp taxa: Laevicaudata (*Lynceus biformis*), Spinicaudata (*Leptestheria dahalacensis*) and Cyclestherida (*Cyclestheria hislopi*); and one of the Cladocera (*Penilia avirostris*). All six taxa develop indirectly, although the exact modes of the development are quite different, especially those of the Cyclestherida and Cladocera in comparison to all the others. The development of the nervous system, labeled and analyzed using immunohistochemical techniques was investigated with a confocal microscope. That of the external morphology was scanned either with an electron microscope or the autofluorescence of the external cuticle was detected with a confocal microscope. *Branchinella sp., T. cancriformis, L. biformis* and *L. dahalacensis* hatch as a free-swimming nauplius and the nervous system and external morphology develops gradually. In *C. hislopi* and *P. avirotris*, on the other hand, several internal and external structures develop prior to the hatching of non-swimming embryo-like larva which is still carried in a dorsal brood pouch. The development in *Branchinella sp., T. cancriformis, L. biformis* and *L. dahalacensis* is directed from anterior to posterior, whereas in *C. hislopi* and *P. avirotris* a more synchronous anterior and posterior differentiation is present.

A comparative analysis of all the developmental sequences using an Even-Pairing approach gives us the first indications of the evolutionary transformation which the Cladocera may have undergone from a clam shrimp-like ancestor.

☐82 Julia Huber A 702 / 14:15

Structure, mineral distribution and mechanical properties of the Pars incisica cuticule in the mandibles of Porcellio scaber Latreille, 1804.

Authors: *Julia Huber*[1], *Helge-Otto Fabritius, Andreas Ziegler*
Affiliations: [1]*Central Facility for Electron Microscopy, University of Ulm*, *Max Planck Institute for Iron Research Düsseldorf*

The isopod cuticle forms skeletal elements, which properties are adapted to their function and specific eco-physiological strains. As the main contact surface when grinding food items the cuticle of the Pars incisiva has to withstand strong abrasive forces. Using scanning-, transmission- and low-voltage scanning-transmission-electron microscopy, elemental analysis and nanoindentation we studied its structure, composition and mechanical properties. The unmineralized epicuticle of the tip is unusual thick (50 µm) in comparison to the epicuticle of tergites (200nm). Towards the middle and the base, the epicuticle narrows from about 5 µm to 3 µm. It consists of 2-4 layers varying in height and structure. In general, the exo- and endocuticle of Isopoda consists of chitin-protein fibres organized in a twisted plywood arrangement and mineralized mainly by calcium carbonate (Hild et al. 2008, Journal of Structural Biology 163, 100-108). In the middle region of the pars incisiva, however, the chitin-protein fibers within the exocuticle and distal endocuticle are parallel oriented, pointing with their long axes towards the cutting-edge. This may provide higher stability in the direction of maximum load (Nikolov et al. 2010, Advanced Materials 22, 519-526). In addition, exo- and endocuticle of the middle region contain phosphorus and calcium in a molar ratio of up to 0.8, suggesting mineralization by calcium phosphate rather than calcium carbonate. Nanoindentation reveals that the elastic modulus is very low in the epicuticle, highest in the exocuticle and intermediate within the endocuticle. Overall the elastic modulus of the cuticle increases from 0.75 GP at the tip to about 5 GP at the base of the Pars incisiva.

☐83 Hans Peter Katzmann A 702 / 14:30

Comparative SEM studies of the anterior ventral head region in maxillopod and branchiopod representatives of the Euentomostraca (Crustacea, Entomostraca)

Authors: *Hans Peter Katzmann*[1], *Andreas Maas*[1], *Dieter Waloszek*[1]
Affiliation: [1]*University of Ulm, WG Biosystematic Documentation, Germany*

The origin of the arthropod head and affiliation of its ventral appendages has been a matter of debate in the scientific community for several decades already. Especially the appendages of the anterior region were subject to considerable dissent among scientists. Two of the critical structures there are of special interest to us, usually referred to as hypostome and labrum. The use of these terms is inconsistent, clear definitions of the terms are lacking. Our current hypothesis is that hypostome and labrum are two different, but closely allied structures: The labrum is hereby a more sclerotized and bulged plate extending from the rear of the hypostome and overhanging the recessed mouth. Sometimes the labrum bears chemo-sensillae, the openings of slime glands and fine hairs laterally and distally, indicating the use of the labrum in food handling, ingestion and in grooming of the anterior appendages. The labrum has been in the focus of various molecular and developmental studies over the last years, but none of these studies have considered its morphological and structural appearance in detail so far. In our study we are investigating the anterior ventral head region of representatives of several crustacean groups, such as *Cirripedia, Copepoda, Ostracoda, Cephalocarida, Anostraca* and *Phyllopoda* (all belonging to the Entomostraca), using scanning electron microscopy. We are comparing the different surface structures in order to distinguish between those belonging to the hypostome and those belonging to the labrum, in order to shed light on the functional significance of these structures and the distinction of the two head parts.

☐84 Sukhum Ruangchai A 702 / 14:45

Local variations of cuticular architecture in the basis joint head of *Porcellio scaber peraeopods*

Authors: *Sukhum Ruangchai*[1]*, Christian Reisecker, Sabine Hild, Andreas Ziegler*[1]
Affiliation: [1]*University of Ulm*; [2]*Johannes Kepler University of Linz*

The cuticle of crustaceans is an interesting model for the study of structure-function relationship in biological composite materials because of the hierarchical organisation of its organic matrix, which is generally arranged in a twisted plywood structure, and variations in type and phase of the mineral compound. In our study the basis's joint head of *Porcellio scaber Latreille*, 1804 was chosen due to its apparently different function from the tergite, which was already studied in detail. Our results show that the cuticle architecture of the joint head has local variations in structure and composition. In the central region the joint head cuticle is similar to that of the tergite. However, towards the edges, where the cuticle is connected to the flexible arthrodial membrane, the epi- and exocuticle are much thicker. The endocuticle remains as thick as in the central region but, interestingly, the chitin-protein fibrils run parallel to one another forming no twisted plywood structure. The mineral distribution in the central region is also similar to that in tergites, with calcite located distally and amorphous calcium carbonate (ACC) more proximally. Higher amounts of phosphate are located in the endocuticle suggesting the coexistence of ACC and ACP (amorphous calcium phosphate). In the edge region phosphate in the distal exocuticle is as high as that in the endocuticle at a cost of diminishing calcium carbonate. The overall difference in the cuticular architecture of the edge in comparison to the central region might be an adaptation to different mechanical strains it has to sustain and due to the structural transition from the edge to the connecting arthrodial membrane.

☐85 Michael Heethoff A 702 / 15:00

Functional morphology and bite performance of raptorial chelicerae of camel spiders (Solifugae).

Authors: *Michael Heethoff*[1], *Franz Langer*[1], *Arie van der Meijden*[2]
Affiliation: [1]*Institute for Evolution and Ecology, University of Tübingen*; [2]*CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Campus Agrário de Vairão, Portugal*

Solifugae are an understudied group of relatively large arachnids. These highly active predators utilize their large chelicerae for feeding, defense, burrowing and mating. We investigated the differences in cheliceral morphology and performance of two ecologically divergent species from North-Africa; the cursorial *Galeodes* sp. and the burrowing *Rhagodes melanus*. Bite force measurements show *Rhagodes* to be a much stronger biter than *Galeodes*, both in absolute maximum force (*Rhagodes* 5,63 N, *Galeodes* 2,12 N) and relative to cheliceral size. Synchrotron-µ-tomographies of one specimen for each species reveal large differences in physiological cross sectional area (PCSA) and estimated muscle stress, resulting in a higher muscle stress in *Rhagodes*. Relative bite forces of both species were in the range of pedipalpal pinch forces of scorpions, but lower that pinch forces of crabs.

☐86 Stefan Blazek A 702 / 15:15

Impact of UV-radiation on the bending resistance of barn owl and pigeon feathers

Authors: *Stefan Blazek*[1], *Hermann Wagner*[1]
Affiliation: [1]*RWTH Aachen University, Institute for Biology II*

The wings of the barn owl (*Tyto alba*) are constantly subjected to wearing. Feathers are exposed to stress like turbulences in air, UV-radiation, degradation by bacteria and collision with obstacles.

It was shown that most individuals of species with body weights below 0.5 kg replace their feathers every year. The barn owl has a body weight of 400-500g. However, the barn owl has an untypical moulting cycle extending over 2-3 years. Feathers are replaced one by one sequentially.

The keratin of feathers is rich in cysteine. This amino acid includes sulfur and is able to build disulfide bonds which underlie the high stability of the protein. It has a peak in the absorption spectrum for wave lengths ranging from 280 to 310nm. An exposure of UV-B radiation may destroy the disulfide-bonds and leads to a lower stability of the protein.

With this study we aim to investigate the impact of UV-B radiation on the bending resistance of barn owl feathers. Further we want determine whether the duration of the moulting cycle is related to the change of the bending resistance induced by UV exposure. For comparison we included the domestic pigeon (Columba livia), which has an annual moulting cycle, in our study. The bending resistance is determined by a 2 point bending test. It was performed before and after the exposure to a UV-B radiation dosage corresponding UV-B exposition in Germany for 2.5 years.

We will present data on the influence of UV-radiation on the bending resistance of the feathers of both species.

11. Morphology POSTER

♦111 David Altrock

Dynamics and functional morphology of contraction and expansion in the calcareous sponge *Clathrina clathrus*

Authors: *David Altrock*[1]*, Christopher Arnold*[1]*, JörgHammel*[1]*, Felix Beckmann*[2]*, Alexander Ereskovsky*[3]*, Michael Nickel*[1]

Affiliation: [1]*Institut für Spezielle Zoologie, Friedrich-Schiller-Universität Jena*; [2]*Zentrum für Material- und Küstenforschung, Helmholtz-Zentrum Geesthacht*; [3]*Institut Méditerranéen de Biodiversité et d'Écologie, Aix-Marseille Université, France*

The body of the calcareous sponge *Clathrina clathrus* (Schmidt, 1864) (Porifera, Calcarea, Calcinea, Clathrinidae) consists of an anastomosing network of even tubes. Like most sponges, *C. clathrus* is contractile, however its contractile strength exceeds most other species by far. This enormous shrinkage of the body in contracted animals was already observed in first in situ studies during the last century and where misinterpreted as necrotic events.The contraction-expansion cycle, however, takes much more time than in most demosponges (comparative data for other calcareous sponges is not available to date). The aim of our project is to characterize the dynamics and functional morphology of contraction in *C. clathrus*. Further on we will compare it to data on well-studied demosponges, like Tethya wilhelma. We used time-lapse imaging, histology, SEM and SR-µCT to characterize body dynamics as well as anatomical traits in 2D and 3D. Our preliminary results confirm the hypothesis of pinacocyte contractility with a clear body shape change from extended thin pinacocytes in expanded stage to t-shaped pinacocytes in contracted stage. However, in contrast to demosponges, the mesohyl displays prominent changes during contraction, too. Surprisingly, the mesohyl increases in thickness during contraction, while the canal lumen almost collapses completely. Whether the volume of the mesohyl is altered by incurrent water (swelling = volume increase) or thickening is simply an effect of an overall 3D deformation of the tube walls due to overall shortening will have to be proven.

♦113 Christoph Bleidorn

Immunocytochemical investigations of anterior regeneration in *Chaetozone caput-esocis* (Cirratulidae, Annelida)

Authors: *ChristophBleidorn*[1]*, Michael Weidhase*[1]*, Conrad Helm*[1]

Affiliation: [1]*University of Leipzig, Institute for Biology, Molecular Evolution and Systematics of Animals*

A remarkable characteristic of many annelids is their ability to regenerate lost body parts. It is also known that many taxa are capable of regaining their anterior body after decapitation. Although this ability is known to be present within many members of the Annelida, only few investigations deal with distinct regenerative patterns concerning the re-development of different organ systems so far.

In order to gain more data regarding patterns of neural and muscular re-development in annelids, we analyzed different stages of anterior regeneration in *Chaetozone caput-esocis* (Cirratulidae, Sedentaria, Annelida) by using immunocytochemical staining techniques combined with subsequent confocal laser scanning microscopy (cLSM). With focus on different stages of anterior regeneration in adult specimens, we used neuronal antibodies (e.g., against serotonin and FMRFamide) and muscular markers (phalloidin) to reconstruct the process of tissue and body formation after decapitation. Our investigations help to understand basic patterns of reorganization within annelid organ systems and provide fundamental knowledge for further investigations. Here we present a summary of our findings and draw conclusions regarding basic regenerative patterns of Annelida in general.

♦114 Angelina Bösemann

Body stalk morphology and cell dynamics of the carnivorous sponge Asbestoplumahypogaea during starvation, prey capture and digestion

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The carnivorous sponge *Aspestopluma hypogaea* Vacelet & Boury-Esnault, 1996 (Demospongiae, Poecilosclerida, Cladorhizidae) lacks a canal system. Instead of filtering particulate organic matter like other sponges, it feeds upon small crustaceans which are caught by microscleres on the surface of long dynamic body filaments. The millimeter-sized club shaped body of A. hypogaea sits on a centimeter-long thin stalk which anchors the sponge upon the hard substrate in a relatively small disc-like holdfast structure. While the morphology and dynamics of the prey-capturing filaments during starvation, prey capturing and digestion is well known, the role of the body stalk has not been investigated before. Recent time-lapse imaging series revealed a high cellular dynamics within the stalk with a bi-directional cellular traffic between the stalk and the body. The aim of the present study is to understand the functional morphology of the stalk under its constraints to mediate stability and to allow for nutrient transfer between sponge body and holdfast. We used time-lapse imaging, histology, SEM, cLSM and SR-µCT to characterize body and cell dynamics as well as anatomical traits in 2D and 3D. Our preliminary results characterize the stalk as structure highly stabilized by macroscleres, collagen, the pinacocytes and eventually other positionally stable cell types. Spherulous cells seem to be the most prominent motile cell type. Bi-directional movement of cell clusters at velocities of 205 µm h-1 (±36 µm h-1) occurs simultaneously regardless of the feeding state. However we found a tendency during digestion for increased downstream movement towards the holdfast.

◆115 Christiane Casper

The morphology of the female genitalic region in libelluloid Odonata (Insecta: Pterygota)

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Libelluloidea (ca. 1400 species) is a monophyletic subgroup of Anisoptera. Most species belong to the clade Libellulidae + Macromiinae+ Corduliinae (MCL-clade). We described and compared the exoskeleton ofthe female genitalic region in 15 species from 14 genera of the MCL-clade. In Sympetrum vulgatum we additionally studied the musculature. Homology hypotheses between the structural elements of the plesiomorphic female genitalia of Odonata (with an ovipositor) and those of the simplified female genitalia of Libelluloidea were established based on all available evidence. In Libelluloidea the various original sclerites of the odonatan genitalic region are mostly fused into largerones, and the processes forming the ovipositor are more or less reducedor vestigial. Sympetrum has several muscles that in ovipositor-bearing Odonata are present in the larvae but resorbed in the adults. This indicates that simplification of female genitalia in Libelluloidea is due to paedomorphosis, leading to assimilation with pregenital segments. In addition, structural differentiations typical for pregenital segments appear to undergo expansion to the genitalic segments; this mainly concerns the dorsal parts of the segments. Despite simplification, female genitalia in the MCL-clade show a strongstructural diversity both in the external parts and in the (cuticulised) gonoducts. Based on the comparison among the sampled species and between these and selected ovipositor-bearing Odonata, a list of 48 characters and a character matrix were compiled. The dataset is quite conflicting and with the present sample it yielded little phylogenetic resolution. This situation might be improved with an expanded taxon sample.

◆116 Fabian Deister

Providing a more complete overview of the rotifer nervous system: an example using *Brachionus calyciflorus* (Pallas, 1766)

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Our knowledge regarding the nervous system of rotifers is fragmentary. To date, only a few species scattered across the group have been examined using modern methods (e.g., electron or confocal laser scanning microscopy) and then only for specific subcomponents of the nervous system. However, through the use of differential staining, it is possible to obtain a more complete overview for a given species, a possibility that we explore here for *Brachionus calyciflorus*. Using antibodies specific for nervous system structures (5H-T, RF-amide and α-tubulin), cell nuclei (nuclear markers) and musculature (phalloidin), we were able to not only obtain a more complete visualization of the nervous system as such, but also to place it within the context of the overall body morphology. In addition, we also examine the benefits and trade-offs associated with visualizing morphological structures as two-dimensional drawings versus three-dimensional models (e.g., greater accuracy versus

more complete perspective, respectively). Moving forward, application of our protocol will help fill in the many gaps present regarding the rotifer nervous system and then in a standardized fashion, facilitating both cross-species comparison and investigations into the evolution of this system within the group.

◆117 Martin Heß

Das Fischgehirn in 3D: ein neuer Ansatz des funktionsmorphologischen Arbeitens

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Um zu verstehen wie Fische sehen, müssen die am Sehvorgang beteiligten Strukturen auch morphologisch untersucht werden. Wir haben die Europäische Sardelle (Engraulis encrasicolus), deren Retinastruktur auf Polarisationssehen hindeutet, mit der Europäische Sardine (Sardina pilchardus), einem nahen Verwandten und Vertreter des viel weiter verbreiteten Farbkontrastsehens verglichen.
Es wurden zahlreiche Gehirne fixiert, präpariert, in unterschiedlichen Medien eingebettet und lückenlose Schnittserien angefertigt. Mit Richardson/OsO4 gefärbte Eponschnittserien wurden am Lichtmikroskop digital fotografiert, die Bilder unter Photoshop bearbeitet und unter Amira® aligniert, segmentiert, gerendert und morphometrisch analysiert. Historesinschnitte dienten der Untersuchung zusätzlicher mikroanatomischer Strukturen. Mit lipidgängigen Fluoreszenzfarbstoffen versetzte Vibratomschnitte wurden fluoreszenzmikroskopisch untersucht. Es wurde jeweils für die Sardelle und die Sardine ein 2D-Histo-Atlas und ein 3D-Oberflächenmodell erschaffen und miteinander verglichen.
Die lückenlosen Schnittserien ermöglichten es in den 3D-Oberflächenmodellen morphometrische Daten (Strecken-, Dicken- und Volumenmessungen) zu erheben, verschiedene Gehirnstrukturen und Regionen herauszuarbeiten und zu benennen: Nervus opticus NO, Telencephalon, Diencephalon, Mesencephalon, Tectum opticum TO, Cerebellum, Medulla oblongata, Blutgefäße und Ventrikel etc. Der Gehirnaufbau von Sardelle und Sardine unterscheidet sich hinsichtlich des Chiasmatypus, der äußeren Form des TO, dem Übergang NO zum TO und der Platzverteilung einiger Strukturen innerhalb des Gehirns (z.B. variieren Ventrikelanteile).
Die vorliegenden Datensätze bestätigen den Grundaufbau der am Sehvorgang beteiligter Komponenten. Die Möglichkeit Strukturen frei im dreidimensionalen Raum bewegen und daran morphometrische Daten erheben zu können, ist ein gänzlich neuer und zukunftsweisender Ansatz für ein funktionsmorphologisch vergleichendes Arbeiten. Die Darstellung retinotoper Projektionen über Sehnerv und Chiasma ins optische Tectum (DiI-Tracing) und die Entschlüsselung des feinstrukturellen Aufbaus ausgewählter Strukturen mittels TEM-Aufnahmen sind in Bearbeitung.

◆118 Katja Jaszkowiak

The mouthpart apparatus of Lithodesmaja - functional morphology and evolution

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Within crustaceans, decapods are one of the species-richest groups. Being able to utilize many different food resources is probably an important aspect of their success. This phenomenon is facilitated by their complex mouthpart apparatus, which is able to perform various movements including transporting, aligning, crushing and cutting and processes sensory information from the food before it is swallowed. Although the main set of mouthparts is the same in many species, differences in form and function have evolved according to lifestyle. Studies into the functional morphology of mouthparts have already been carried out for some decapod species, and to complement the available taxon sampling a species of the hitherto unstudied king crabs (Lithodidae), Lithodes maja, was analyzed here. Individuals were filmed while being presented with different kinds of food. To obtain structural information on the individual mouthpart elements in their natural position to one another, the mouthparts were 3D-reconstructed from micro- CT scans. These data were complemented by scanning electron microscopy, permitting the surface structures, such as setae, to be analyzed in detail. As indicated by studies into other species, there is evidence that the mouthparts of Lithodes maja can be sorted into functional groups. By analyzing movement patterns six of these groups could be found: 1 transporting mouthparts, 2 aligning/sorting mouthparts, 3 clutching/holding mouthparts, 4 tearing/cutting/crushing mouthparts, 5 current-generating mouthparts, and 6 grooming mouthparts. According to the 3D reconstruction there seem to be differences in morphology and relative position - which might implicate functional differences - between the mouthparts of Lithodes maja and those of even closely related species. The data presented is discussed in comparison to data from the literature to create a picture of the evolutionary transformations undergone by the functional feeding apparatus in decapod crustaceans.

◆119 Johanna Kaidel

The morphology of the female postabdomen of Apachyuschartaceus (Insecta: Dermaptera: Apachyidae)

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The probed species Apachyus chartaceus (de Haan, 1842) is one of 15 species, belonging to the higher dermapteran family Apachyidae. Because of its similar wing structures and reproductive organs, this palaeotropical earwig is thought to be close to the basal" Dermaptera (Jarvis et al. 2004). On the contrary, Klass (2001) mentions the chance of a relation between the highly derived Hemimeridae and Apachyidae. In order to solve this conflict the morphological investigation of the female postabdomen of A. chartaceus was undertaken, focussing on its genitalic region and comparing it to Hemimerus vosseleri Rehn & Rehn, 1935. Two postabdomens of Malaysian A. chartaceus were studied using common methods (maceration in 5%

KOH, dorsal dissection, observation under stereo-microscope). Our research indicated that Apachyidae strongly resemble Hemimeridae when looking at the overall structure of the postabdomen, though A. chartaceus does also show characteristics of "basal" dermapterans like the presence of accessory glands. As the genitalic region is a key character for inter-species relationship, we expect to facilitate the forthcoming phylogenetic analysis and taxonomic descriptions."

♦120 Sabrina Kaul-Strehlow

The formation of muscles in the medusa of Clytiahemisphaerica, Hydrozoa

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In bilaterians, the mesoderm gives rise to almost all muscles. The sister group of the Bilateria, the cnidarians, are diploblastic and lack a mesoderm. However, most medusae feature well developed striated muscles, exhibiting a sarcomeric organization similar to bilaterian striated muscles, from ectodermal precursor cells. We investigated muscle formation and morphology in the medusal buds of different stages of Clytia hemisphaerica (Hydrozoa, Leptomedusae) using a variety of methodological approaches. We combined 3D reconstructions based on serial sectioning for transmission electron microscopy (TEM), F-actin staining and marker gene expression to get a detailed picture of muscle development. We found that the myosin light chain kinase- and ?striated-type? myosin heavy chain-expressing striated ring muscles of the bell develop from four initially separate anlagen within the ectoderm that gradually expand and fuse. The contractile parts of the cells, the myonemes, grow out basally and adopt a parallel organization rather late in development. In F-actin stainings, striation is first visible when the medusa formation is almost accomplished. In reconstructions of serial sections we currently investigate whether striated muscles of the subumbrella retain an epithelial organization or whether they are subepithelial, in contrast to most cnidarian epithelial muscle cells

♦121 Matthes Kenning

An Ancestor's Tale: woodlice, slater and the conquest of land: insights from brain morphology of *Saduriaentomon Linnaeus*, 1758 (Valvifera, Isopoda)

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Besides the ancestors of Hexapoda, within the Crustacea at least five lineages independently succeeded in colonizing land, and the Isopoda are considered to be the most successful terrestrial crustacean group.

Our current understanding of the organization of the olfactory system, as well as its immanent chemotactic behavior of crustaceans, is heavily biased towards members of the Decapoda. Therefore, in this study the Isopoda were taken into consideration. Although, the deutocerebral organization of land living and semi-terrestrial isopods has been investigated already, the brains of marine representatives have rarely been considered. The current study focuses on the brain of the marine Saduria entomon using immunohistochemistry and confocal laser scan microscopy. Previous studies have shown that in the course of isopods? terrestrialization the first antennae have been greatly reduced with a concomitant reduction of corresponding neuronal substrate. In contrast, marine isopods such as Saduria entomon still possess well developed first antennae and defined olfactory centers. These centers are divided into spherical neuropil compartments, the olfactory glomeruli, which a clustered into distinct groups. Additional structures that we describe in gretater detail include the optic neuropils and the central complex. We discuss our findings with regard to brain morphology in the ground pattern of malacostracan crustaceans.

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♦122 Verena Kutschera

Is there a coxa in malacostracanpleopods?

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Malacostraca is a species-rich taxon of crustaceans, characterised by a unique tagmosis: the head comprises five appendage-bearing segments and is followed by a subdivided trunk (thorax): Thorax I consists of eight segments each carrying a pair of so-called thoracopods, each built of a basal coxa and a basipod distal to it, which carries the two rami, endopod and exopod. Thorax II comprises six segments bearing limbs, which seem to consist only of basipod, endopod, and exopod. The body is completed by the telson posteriorly, basically carrying a pair of furcal rami. We examined the pleopods of representatives of various malacostracan taxa via staining with alizarin, which tinges calcified parts of the cuticle purple while non-calcified, membranous parts remain white. By this we were able to detect several small sclerites in the membrane of the limb-body articulation of these species. Most of the sclerites correspond to each other in relative position to the basipod and shape and have internal apodemes where muscles can attach. This conserved morphology allows the hypothesis that these sclerites might be remains of a coxa also in the pleopods, with this contradicting previous assumptions.

♦123 Tobias Lehmann

Retinula axons and visual neuropils of the median and lateral eyes of *Euscorpius italicus* (Herbst, 1800) (Scorpiones: Euscorpiidae)

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Lately sets of neuroanatomical characters have contributed important arguments to the discussion about the phylogeny of Arthropoda. Especially the visual system of Arthropods is well studied, which is underlined by the Tetraconata concept (Crustacea + Insecta), where the structure of the eyes is eponymous. In contrast the visual system of Scorpiones is studied so far only in a neurophysiological context, and no morphological features are described to date making the visual system accessible for a phylogenetic comparison.

Hence in this study we analyse the visual system of *Euscorpius italicus* (Herbst, 1800). The visual neuropils of the median and lateral eyes are identified with Cobalt backfills and the basic structure of the protocerebrum is described by means of osmium-ethyl gallate Procedure.

The findings allow a detailed comparison with the situation found in other basal Chelicerates like Xiphosura and Pycnogonida. Hence the ancestral ground pattern of the visual system of amandibulate Arthropods is discussed.

♦124 Fanny Leubner

The thorax of Comicus. Morphology and systematics of a strange bushcricket.

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Schizodactylids form a presumably relict group with unresolved phylogenetic affinities among the highly diverse orthopteran subgroup Ensifera (crickets and katydids) comprising the only two extant genera Schizodactylus and Comicus. Due to specialized features of the tarsi that are broadened by lobe-like processes allowing for convenient movement on sandy territory, these insects are commonly referred to as splay-footed crickets or dune crickets. Represented by seven described species, the genus Comicus is an endemic of Southern Africa. In contrast to the Indian Schizodactylus, the representatives of Comicus are flightless with fully reduced fore and hind wings.

The Namibian Comicus calcaris was described in 1986 and no further studies providing descriptions of morphological and anatomical features have been conducted ever since. Here we present the first detailed study of the sceletomuscular system of the thorax of C. calcaris based on numerous non-invasive investigation methods such as CLSM, SEM and µCT imaging, yielding a highly informative three-dimensional reconstruction of the thoracic exoskeleton and musculature. The obtained results were thoroughly compared with the recently reconstructed neopteran groundpattern (Friedrich F, Beutel RG 2008, Arthropod Structure & Development 37, 29-54) in order to reveal morphological adaptations to the loss of flight and to generate a phylogenetically informative set of anatomical traits that will illuminate the systematic position of the Schizodactylidae among Ensifera.

♦125 Elisabeth Lipke

Primary sperm conjugation in the spider family Caponiidae (Araneae) and its implication on the evolution of sperm transfer forms in spiders

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Sperm competition influence motility, size and morphology of sperm, but also can lead to a cooperation between single sperm. One cooperation strategy is sperm conjugation, a process in which two or more sperm physically unite to positively influence motility or translocation through the female reproductive tract. Sperm conjugations are rare, but known from all major lineages across animal taxa. Based

on their developmental mechanisms, two different types of conjugation can be distinguished (primary and secondary). In spiders both types of sperm conjugation are present. Particularly, haplogyne spiders are of special interest because all known sperm transfer forms common in spiders occur in this group. Nevertheless, the evolution of sperm conjugations in Haplogynae is not understood. Whereas, Filistatidae, the sister to all remaining haplogynes, use coenospermia (secondary sperm conjugation) for transferring sperm, synspermia (primary sperm conjugation) are only known from few dysderoid and sicarioid taxa, two main lineages within haplogynes. The family Caponiidae is suggested to be the sister-group of Dysderoidea and thus of particular interest with regard to the evolution of transfer forms. Here, we investigated a representative of Caponiidae, *Caponina alegre*, using light, electron microscopy and computer-based 3D reconstruction. Males of *C. alegre* transfer sperm via synspermia, which are formed at the end of spermiogenesis and consists of four fused sperm cells. Our results suggest that synspermia are more widespread than assumed in former studies and evolved already in basal taxa in at least one of the main lineages of Haplogynae.

◆126 Gerd Mayer

Coexistence of native and non-indigenous gammarideans (Crustacea, Amphipoda) in Lake Constance - functional morphology of mouthparts

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In the last two decades, the amphipod communities of German inland waters have changed dramatically. Especially the Ponto-Caspian gammarid Dikerogammarus villosus caused severe effects on the biocoenosis of the concerned waters, e.g. in decreasing or even eliminating populations of native or earlier established gammarideans. Therefore, this invasive species was even named killer shrimp". In 2002 D. villosus was recorded in Lake Constance for the first time. Within only five years it spread in the littoral of the entire lake and is now the dominant gammarid on hard substrates. But, unlike in many other Middle European waters the native Gammarus lacustris and the earlier established G. roeselii seem to co-exist well with D. villosus in Lake Constance. Moreover, since 2007 a local population of another amphipod, Crangonyx pseudogracilis, is co-existing here with D. villosus too. In our SEM study of structures involved in food acquisition of these gammaridean species inhabiting Lake Constance we discovered morphological differences between the species, apparently enabling them to use different food resources. In spite of its ecological impact, D. villosus turned out to be not a specialized predator, but is also able to collect detritus, sieving particles out of the respiration water current and sweeping in periphyton. G. lacustris does the same but has additional specializations to feed on macrophytes, while the mouthparts of G. roeselii in addition possess specializations for scraping periphyton off the substrates. In contrast, the morphology of the mouthparts of C. pseudogracilisis implies that this species is a specialized detritus feeder."

♦127 Roland Meyer

Morphology of the first zoeal stage of the spotted bumblebee shrimp *Gnathophyllum elegans* Risso, 1816 (Decapoda: Caridea: Gnathophyllidae) studied with light and scanning EM microscopy

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The morphology of the first stage zoea of *Gnathophyllum elegans* (Risso, 1816) raised in the laboratory is illustrated and described for the first time. Larvae were obtained from an ovigerous female, caught in shallow waters west of the isle of Solta, Croatia. Descriptions are based on dissected larvae analysed with both the light microscope and the SEM. The morphological characters are compared to *Gnathophyllum americana* (Guérin-Méneville, 1855), the only other species of the genus Gnathophyllum (Latreille, 1819) with a larval description present. The systematic relationships between the Gnathophyllidae and the Palaemonidae are discussed. We tried to find larval characters that are family specific for the Gnathophyllidae and help to solve controversies in the taxonomy of Palaemonidae (Pontoniinae) and Gnathophyllidae.

♦128 Benjamin Ott

The impact of mechanically induced wearing on the bending resistance of barn owl feathers

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Most birds depend vitally on their plumage in their everyday life. Especially predators like the barn owl (*Tyto alba pratincola*) need an intact plumage in order to hunt silently for prey. Feathers are susceptible to various ageing factors that may cause damage, among these are UV-radiation and mechanical strain. Worn or missing feathers would not only lead to raised energy expenditure due to insufficient heat insulation but to poor flight performance, too. That makes moulting, the regular replacement of feathers, necessary.

Most birds with a mean bodyweight below 500 g, for example the domestic pigeon (*Columba livia domestica*), moult once a year. Even though the barn owl that has a mean body weight around 500 g, it moults over a period of 2-3 years, replacing feather sequentially. This gives rise to the question whether ageing proceeds slower in barn owl feathers compared to feathers of other birds of similar weight. Previous studies have shown that mechanical strain has an impact on the bending resistance of feathers. This work focusses on the impact of mechanical strain as an ageing factor for barn owl flight feathers.

The bending resistance of the feather vane was measured prior to artificial ageing and afterwards by a two-point bending test. The decrease of bending resistance is a sound measure for ongoing ageing. Artificial ageing of 2.5 years was induced by recurrent deflection of the feather vane.

We will present preliminary data of the impact of mechanical induced ageing on the bending resistance of barn owl feathers.

◆129 Caren Pawlowski

Reconsidering hypotheses of cell constancy in rotifers using modern microscopic methods

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In the early 20th century, light microscopic observations combined with stained serial sections led several scientists to conclude that many rotifer species reach a fixed number of cells (nuclei) at the end of development (i.e., are eutelic). Thereafter, increases in body size could only occur through cell enlargement. Although the hypothesis of eutely in rotifers is widely accepted, it could be that it might not truly hold (e.g., as recently discovered for Gastrotricha) and, even if it does, its extent across the 2000+ species of rotifer is unknown. For the last point in particular, traditional methods are far too labour-intensive to permit large-scale sampling and we examine the potential for modern methods for facilitate this process. In particular, we use a combination of confocal laser scanning microscopy with computer software to stain all nuclei and to reconstruct their three-dimensional positions. The increased sampling enabled by these new methods will make it easier to address a number of outstanding questions regarding eutely in rotifers. For instance, should eutely truly exist, how conserved is the number of nuclei among individuals of a species or among species within a clade (and does the number of nuclei show phylogenetic signal)? What are the factors that determine the number of nuclei for a given species (e.g. size of the ovary and/or body size)? Providing the answer to these and other similar questions will prove valuable for reinvestigating the issue of eutely in rotifers by improving/upgrading the results from the last century.

◆130 Felix Quade

The Chelae of Anomala: Function and Evolution

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New techniques are driving functional morphology to be a powerful tool for understanding complex structures and their evolution. In this study µCAT and computer based 3D reconstruction are used as base for in silico simulation of mechanical properties and advanced geometric morphometrics of crustacean chelae. The group of Anomala is particularly interesting because of its economic and ecologic importance and jet uncertain phylogenetic relationships. We performed µCAT scans of the right chela of 14 Anomalan species and one Brachyuran representative, covering nearly the entire diversity of the phylum and one outgroup taxon. 3D models were built from the µCAT data. These models were used for analyses by the finite element method (FEM) and 3 dimensional geometric morphometrics. Cluster analysis of the morphometric data was performed to categorize chela forms and identify functional groups which were compared with the data from FEM. Our investigations provide inspiring new insights into the relation of Anomalan chela functionality, mechanic properties and structure which we analyze from an evolutionary perspective.

◆131 Jendrian Riedel

Subdigitalmicroornamentation of leaf chameleons (Brookesia, Rhampholeon and Rippeleon)

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Climbing locomotion requires friction maximization for prevention of slipping. In many lizard clades mircroscopic hairy structures (setae) have been evolved convergently on the ventral epidermis of the feet as adaptation to the arboreal lifestyle. Also in the arboreal grade of Chamaeleonidae, tree chameleons friction maximizing setae on the ventral side of the feet (subdigital) have been found. Comparative studies on subdigital pads in all lizard clades showed that subdigital structuring reflects phylogenetic relationship as well as the animal‘s ecological adaptation to the substrate.

Leaf chameleons are a grade of ground-dwelling Chamaeleonidae. Thus, they can be expected to show differend subdigital structuring than tree chameleons. Previous studies on single species of the leaf chameleons revealed a highly diverse subdigital structuring which ranges from hairy and honey-comb structures to thorned scales.

We compared the subdigital epidermis of representatives of all three leaf chameleon genera Brookesia, Rhampholeon and Rippeleon using scanning electron microscopy.

We found microornamentation and scale modifications, specific for the single genera and partly for the single species. In contrast the correlation with the animals´ habitat or locomotion was weak. Additionally to thorned scales Brookesia have honey-comb structures below the thorn, but lack hairy structures. Rhampholeon show scales with short spines on the marginal areas and different kinds of fused spines on the centre of it. The scales of Rippeleon also have a strong thorn in the centre. However, below they have small uprisings. Additionally, they bear honey-comb structures around the thorn and spines on the scale margins.

◆132 Sven Rossel

Characterization of a novel musculature in Mytilinamucronata Müller 1773 (Rotifera) responsible for anti-predator behaviour

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The rotifer *Mytilna mucronata* lives as a detritivore mostly on aquatic plants and the bottom of lakes. It is characterized in part by a relatively thick shell that covers the whole body except for the foot and anterior of the head, which can be withdrawn in a turtle-like fashion when being disturbed or attacked by a predator. Potentially facilitating this behavior is a longitudinal sulcus that is present in all members of the

genus on the dorsal aspect of the shell and that is bordered by two keels. SEM pictures reveal that this sulcus can be opened and closed according to the contraction of the specimen under examination; hence, closing the sulcus might represent an evolutionary adaptation against predation. To date, however, no structures have been described, either internally or externally, to account for this motion. Using a combination of confocal laser scanning microscopy and 3D reconstruction, we describe a novel set of four muscle bundle pairs located on either side of the sulcus along the longitudinal body axis. In combination with an examination of the complete body musculature, the close relationship of these bundles with the sulcus leads us to hypothesize that they might be responsible for opening and closing the sulcus in Mytilina mucronata. Further investigations in other members of the genus will help to test this hypothesis in the future.

◆133 Andy Sombke

New insights into the brain of *Scutigera coleoptrata* (Chilopoda): optic neuropils, central body, and mushroom bodies

Authors: *Andy Sombke*[1]*, Steffen Harzsch*[1]
Affiliation: [1]*Ernst-Moritz-Arndt-Universität Greifswald, Zoologisches Institut und Museum, Cytologie und Evolutionsbiologie*

The Scutigeromorpha are the sister group to all other chilopod families. Furthermore, it is assumed, that they represent the most basal taxon within Myriapoda which are the sistergroup to Tetraconata. Our knowledge of the chilopod nervous system largely relies on studies from the 19th and early 20th century using light microscopy. However, we recently investigated the organization of deutocerebral neuropils in representatives of the Chilopoda with contemporary neuroanatomical methods (Sombke et al. 2010, 2012). Like in Tetraconata, the (first) antennae innervate the primary chemo- and mechanosensory neuropils (olfactory lobe and corpus lamellosum). The architecture of the protocerebrum is, however, in many respects insufficiently understood. In *Scutigera coleoptrata*, it expands dorsally to the deutocerebrum and projects laterally towards the compound eyes. It comprises the unpaired midline neuropil (or central body), the optic neuropils, and the corpora pedunculata (mushroom bodies sensu lato). These structures are of particular importance for phylogenetic comparisons with the brain of other Mandibulata.
In the present study on *S. coleoptrata*, we analyzed the organization of protocerebral neuropils with serial semi-thin sectioning and immunofluorescence combined with confocal laser-scanning microscopy and 3D reconstruction. Our results reveal as yet unseen architectural details of the two visual neuropils and a putative optic chiasm, of the mushroom bodies and of the central body.

This study was supported by DFG Ha 2540/8-2.

12. Neurobiology TALKS

Saturday, September 22, 2012

Invited speaker 1: Chair – Jacob Engelmann A 701 / 11:00

Boris Chagnaud (München)

Temporal patterning of vocalizations and prevention of acoustic reafference– a lesson from vocalizing fish

Author: *Boris Chagnaud*[1]
Affiliation: [1]*Division of Neurobiology, Department Biology II, Ludwig-Maximilians-Universität München*

Vocalizations require perfect neuronal control to be executed in a meaningful way. While we have a basic understanding of the way vocalizations are patterned in higher brain centers, we almost entirely lack information about the final patterning of vocalizations that occurs in the hindbrain. This is mainly due to respiratory influence on vocalizations and the difficult accessibility of hindbrain structures in birds and mammals. Using vocalizing fish, that share an evolutionary ancient and conserved hindbrain compartment in all vocalizing vertebrates, we have elucidated the neuronal elements that contribute to the patterning of vocalizations in singing fish. Our results show that separate hindbrain compartments code for vocalization frequency and duration respectively. The duration encoding nucleus not only serves a function in motor control but also informs other hindbrain nuclei about the onset and duration of vocalizations in order to prevent reafferent signalling.

Invited speaker 2: Chair – Christoph Kleineidam A 704 / 11:30

Jörg T. Albert (London)

From circadian time keeping to species-specific hearing: chordotonal contributions to mechanosensory behaviours in *Drosophila*

Author: *Jörg T. Albert*[1]
Affiliation: [1]*Ear Institute, University College London, UK*

A major type of insect mechanosensors is formed by chordotonal organs (ChOs). ChOs are located at virtually every joint of the insect body and they contribute to a plethora of different behaviours. Most famously perhaps, Johnston's Organ (JO), a specialized ChO located in the second antennal segment of Diptera, underlies the auditory behaviours of mosquitoes and fruit flies. During the last decade, the *Drosophila* JO has been subjected to in-depth analyses, establishing it as one of the prime model organs for the molecular, and mechanistic, study of mechanotransduction.

This presentation will present recent data on the molecular composition of mechanosensory transduction machineries in the fruit fly antenna, and on how this

machinery contributes to sensitive hearing and species-specific tuning in Drosophilid flies. Also, data will be presented on how ChOs, on a more systemic level, contribute to a fly's 'sense of time' by providing sensory input for the animals' circadian clocks.

Chair: Jakob Engelmann

☐87 Adrian Klein A 701 / 14:00

Medullary lateral line units of the common rudd, Scardinius erythropthalmus, are sensitive to Kármán vortex streets in terms of spike rate and spike pattern

Authors: *Adrian Klein*[1]*, Jan Winkelnkemper, Horst Bleckmann*
Affiliation: [1]*University of Bonn, Institute for Zoology*

Fish can sense water motions with their mechanosensory lateral line. Fish use the lateral line for the detection of predators and prey, for schooling, collision avoidance and energy efficient locomotion in unsteady flow. A cylinder placed in running water alternatingly sheds columnar vortices (a Kármán vortex street) in a wide range of Reynold numbers. Fish use Kármán vortex streets to reduce locomotory costs. Navigating in hydrodynamic perturbations ? like those in a Kármán vortex street - is complex and information about the hydrodynamic flow field is advantageous. Peak spike frequency of primary lateral line afferents coincide with the vortex shedding frequency, no increase in spike rate was found, however. Up to now it was not clear whether and how vortex street information is processed in higher brain areas. Therefore rudd, Scardinius erythropthalmus, were exposed to Kárman vortex streets. Activity of medullary lateral line units correlated with unsteady flow signatures in terms of spike pattern or spike rate or both. In contrast to the noisy spiking activity of primary lateral line afferents, some medullary units showed a sharp representation of each vortex in the vortex street. Synchronously obtained particle image velocimetry was used to uncover a correlation map between the flow field and the neuronal activity. A correlation map was found with peak similarity between the flow field close to the fish and the neuronal responses of medullary lateral line units. Our data show that some medullary units selectively process vortex street information.

Supported by the DFG (GRK1572)

☐88 Hendrik Herzog A 701 / 14:15

Respiratory noise and lateral line function

Authors: *Hendrik Herzog*[1]*, Joachim Mogdans*[1]*, Horst Bleckmann*[1]
Affiliation: [1]*Institut für Zoologie, Universität Bonn*

The lateral line system of fish responds to hydrodynamic stimuli and to hydrodynamic noise. In electrophysiological experiments one source of noise that contaminates the physiological data are the water motions generated by artificial respiration. Visualization of the respiratory flow of Ide, Leuciscus idus, revealed a complex pattern of turbulences with a predominantly rostrocaudally oriented flow of approximately 3 cm/s. The belly of the Ide was more affected by the flow than the back. Fluorescence staining revealed that neuromasts were not found directly in the area of the highest velocities caused by the respiratory water flow.

Under still water conditions, 43 out of 88 primary lateral line afferents of the Ide changed their discharge rate by more than 10 % when artificial ventilation was turned on. Afferents that innervated a cephalic neuromast or a trunk neuromast near the tail changed their rates by about 10 to 11%. In contrast, afferents innervating neuromasts located between gill cover and dorsal fin changed their rates on average by 23 to 26%. These neuromasts most likely were stimulated by the fading turbulences caused by the respiratory water flow. When artificial ventilation was switched off, most of the 43 units showed a reduced on-going activity and more regular spike patterns.

The effect of the respiratory water flow on unit activity decreased with increasing velocity of a superimposed bulk water flow. As a consequence, unit responses to the bulk flow, especially to low flow velocities, were more prominent without ventilation than with ventilation.

Our physiological data raise the question how Ide cope with the noise caused by natural breathing. Our performed behavioral studies showed a smart strategy for solving this task.

This work was supported by the federal ministry of education and research (BMBF).

☐89 Peter Machnik A 701 / 14:30

Functional stability: Archerfish compensate temperature effects that occur at the level of the Mauthner-cell

Authors: *Peter Machnik*[1], *Stefan Schuster*[1]
Affiliation: [1] *Department of Animal Physiology, University of Bayreuth*

Temperature variation can affect the behavioural performance of cold-blooded animals, even if the behaviour is critical for survival. In archerfish the accumulation of visual information is of outstanding importance for hunting. Archerfish use their Mauthner (M)-cell-associated C-start network not only for driving escapes like most teleosts do, but also for their precisely tuned predictive start in their unique hunting behaviour. The M-cell integrates incoming sensory information and decides, if a precise predictive start is possible to reach the point of prey impact on the water surface. Temperature takes effect on reaction time of the predictive start, but precision stays unaffected. This is surprising, because M-cell-triggered flight reactions are known to be less precise at lower temperature. Therefore, we analysed the effect of temperature on visually induced postsynaptic potentials at the level of the M-cell in archerfish using electrophysiological intracellular in vivo recording techniques. Here we show integration time of visual information is affected by temperature at the level of the M-cell. Latency and duration of visual induced postsynaptic potentials increase with decreasing temperature. Latency observed at the M-cell level corresponds well with behavioural observations. We suppose behavioural flexibility is obligate for successful M-cell-triggered hunting in archerfish. Therefore, the provided flexibility is also available to compensate temperature-induced effects.

☐90 Carlos Mora-Ferrer A 701 / 14:45

Full-field motion vision: From photopic to scotopic conditions

Authors: *Carlos Mora-Ferrer*[1]*, Cornelis Steger*[2]
Affiliations: [1]*University Bayreuth;* [2]*University Mainz*

Full-field motion vision in fish is color blind and either L-cone dominated (photopic conditions) or rod dominated (scotopic cond.). The change from cone to rod vision includes an increase in convergence and much higher sensitivity at photoreceptor level. However, do these changes have an effect on threshold contrast of motion perception? Goldfish were adapted for min. 30 min to 5, 1.5, or 0.2 lux and then tested in an optomotor set-up (Mora-Ferrer et al., 1995). Laminated black-white pattern paper cylinder of 0, 10, 20, 40, 60, and 80% modulation depth, 4 cm/cycle, and 10 RPM stimulus velocity were used to elicit an optomotor response that was taped with a video system and observed on a monitor. Illumination was generated with a slide projector and adjusted with ND-filters. Resting activity was recorded for a resting stimulus pattern and did no differ from an optomotor response of 0 (zero). Under all illumin. conditions animals reacted to stimuli of 20% and more mod. depth. with increasing optomotor responses of max. 6 RPM. Overall, responses were smaller than under photopic illumin. conditions. For high mod. depths optomotor responses were ‘saturated’. The range of mod. depths which elicited a dynamic optomotor response was reduced by ~37% for 0.2 and 1.5 lx and by 50% for 5 lx ambient illumin. Threshold mod. depths increased from 22% to 30% with decreasing ambient illumin. conditions. Despite an increase in convergence and much more sensitive receptors, behavioral sensitivity and overall max. behavioral responses decrease with ambient illumin. intensity.

☐91 Silke Künzel A 701 / 15:00

Linking behavior and sensory processing: analysis of distance estimation capability in neurons of the Mormyrid ELL

Authors: *Silke Künzel*[1]*, Volker Hofmann*[1]*, Juan Ignacio Sanguinetti Scheck*[1]*, Jacob Engelmann*[1]
Affiliation: [1]*Univerisity of Bielefeld, Faculty of Biology, AG Active Sensing*

Weakly electric fish use active electrolocation for orientation, and navigation tasks. They emit short electric signals and perceive changes of the electric field with electroreceptors distributed across the fish?s skin. Objects lead to modulations of the current distribution at the skin, termed electric images. Using these images, Gnathonemus petersii can determine three-dimensional depth using a unique mechanism [1].

While this ability has been studied extensively at the behavioral level, studies on the underlying neuronal mechanism are missing. Recent studies have addressed to which degree of reliability electric image properties are conveyed from the electrosensory periphery to the first stage of central processing, the electrosensory lateral line lobe (ELL), showing that the physical properties of electric images are transmitted reasonably well. Additionally, behavioral and modeling studies strengthen the view that relative motion between fish and objects, leading to spatiotemporal changes in electric images and the distance discrimination metric [2], need to be considered to fully understand how fish reach the stunning behavioral discrimination performance [3].

We here present our analysis of object detection and object discrimination performance of single neurons recorded in ELL. As a stimulus we used a metal cube (1 cm3). It was presented at fixed distances from the receptive field centre of individual neurons (1 - 23 mm distance). We quantified the neuronal performance in cube detection and distance discrimination with a ROC analysis.

With increasing distance, detection probability showed exponential decrease, with spike latency being the more sensitive measure. Regarding discrimination, our data show that with increasing object distances, the minimal distance to a second object needed to be increased for a successful discrimination. However, in a number of single cells distance discrimination thresholds (17 to 1 mm) are comparable to behavioral data.

In a next step we will compare the physical basis of the differences in electric images to both the single neuronal and the animal performance, using methods currently established in our labs.

☐92 Vanessa Kassing A 701 / 15:15

Monitoring single cell responses via calcium imaging in the optic tectum of the adult zebrafish (Danio rerio)

Authors: *Vanessa Kassing*[1]*, Jacob Engelmann*[1]*, Rafael Kurtz*[1]
Affiliation: [1]*Univerisity of Bielefeld, Faculty of Biology, AG Active Sensing*

During the last years the zebrafish (Danio rerio) became a popular model organism in neurophysiology and developmental neurobiology. The optic tectum is the main center for processing visual information in fish and it is well known for its role in coordinating voluntary movements with multimodal sensory input. To achieve this, several sensory modalities are mapped within the tectum.

We have established a method of in-vivo calcium imaging of tectal neurons in adult zebrafish. This approach is extensively used in larval zebrafish but only up to the age of 9 days post-fertilization. Skin pigmentation and the development of a bony cranial roof after day 9 limited the technique to early larvae thus far. Moreover, we use conventional widefield fluorescence microscopy, in contrast to previous studies, in which two-photon imaging was necessary to resolve somatic signals from individual neurons. To this end, we use dextran-coupled dyes, which can be loaded into small groups of cells by a mechanical procedure or via local electroporation. Compared to the previously used procedure of pressure injection of a membrane-permeable dye, which stains numerous of neurons, our methods reduce crosstalk between individual neurons. The experiments show that our new approach for this technique leads to convincing results in the optic tectum of adult zebrafish. We were able to characterize direction and orientation selective cells with different stimuli, e.g. moving bars and dots, full field and counter phase flicker.

Our further experiments deal with short-term plasticity of visual computation in the adult zebrafish, and may in the future open a way to ask how maps of different modalities are integrated at the level of the optic tectum.

Sunday, September 23, 2012

Chair: James Poulet

☐93 Christian Schopf A 701 / 12:00

Hearing in aging grey mouse lemurs (Microcebus murinus)

Authors: *Christian Schopf[1], Andrej Kral[1], Julia Tünsmeyer[1], Sabine B. R. Kästner[1], Elke Zimmermann[1]*

Affiliation: [1]*Institute of Zoology, University of Veterinary Medicine Hannover, Foundation, Hannover*

Mouse lemurs are small nocturnal primates, communicating in the high-frequency and ultrasonic range. They are discussed as an emerging new primate model for aging and genomic research. The aim of this study was to gain first empirical information on auditory thresholds and hearing sensitivity in mouse lemurs during aging. We applied brainstem evoked response audiometry (BERA) a cost-efficient method traditionally used for screening hearing sensitivity in human babies and animal models in hearing research such as cats. To asses the effect of age, we determined frequency dependent auditory thresholds in the range between 500 Hz and 100 kHz of two age groups of mouse lemurs (young animals: 1 to 5 years of age; old animals: 6 years or older). Audiograms were established individually based on auditory thresholds detected visually. Findings indicate that mouse lemurs show broadband frequency sensitivity from 500 Hz to 80 kHz. Although they exhibit better hearing in the ultrasonic range than most primates, their best frequency of hearing is about 8 kHz. High frequency hearing loss in the ultrasonic range was found in aged animals. Long-term measurements will characterize the progress of that hearing loss more exactly. For assessing hearing capabilities and deficiencies in small primates, such as mouse lemurs, BERA is a promising, cost- and time-efficient technique.

☐94 Alexander Fischer A 701 / 12:15

GABA - relevant for hearing cues?

Authors: *Alexander Fischer[1], Matthew Xu-Friedman[2], Eckhard Friauf[1], Désirée Griesemer[1]*

Affiliations: [1]*TU Kaiserslautern, Biology department, Animal physiology group*; [2]*University at Buffalo, Department of biological sciences*

The brain utilizes subtle sound intensity and time differences between the two ears to localize sound sources. We focus on the murine lateral superior olive (LSO), a nucleus in the auditory brainstem, whose function is to integrate excitatory and inhibitory signals for detection of interaural level differences. In rats and gerbils inhibitory input to the LSO is mediated by GABA, together with glycine. To analyze the specific role of GABA during development, whole-cell voltage-clamp recordings were obtained from LSO principal neurons in acute brainstem slices around postnatal days (P) 4 and 11. While electrical stimulation of inhibitory fibers in P4 mice revealed ~10% of inhibitory synaptic transmission to be mediated by GABA, we did not detect

any remaining GABAergic component at P11. However, focal application of GABA (100 µM) onto LSO cell somata evoked large inhibitory currents at both ages. These currents displayed a strong dependence on GABA transporter (GAT) activity. During repetitive GABA application, pharmacological blockade of GATs resulted in a strong depression of amplitudes and prolonged kinetics of the evoked currents. In addition metabotropic GABABRs may also constitute a role in auditory processing in the LSO. Indeed, using a presynaptic calcium imaging assay, application of a GABABR agonist led to a decrease of calcium influx during synaptic activity. Although the GABA proportion of synaptic inhibitory LSO inputs disappears within the first two postnatal weeks, many functional GABA-related proteins, like GABAARs, GABABRs and GATs persist. Therefore, we hypothesize GABA-mediated modulation to remain important for detection of interaural level differences.

Chair: Christoph Kleineidam

☐95 Norbert Boeddeker A 701 / 14:00

Cue integration for navigation in bees, wasps and humans

Author: *Norbert Boeddeker*[1]
Affiliation: [1]*Department of Cognitive Neuroscience & Center of Excellence Cognitive Interaction Technology, Bielefeld University*

Bees and wasps learn the location of rich food sources and their nests. The task of travelling between the hive and these food sources technically requires them to learn and estimate a vector between the two places and then travel along the connecting beeline. This navigation method is known as path integration (PI): many animals, while searching for food, keep a running total of their distance and direction to calculate a vector pointing home. Here we focus on the question how directional cues are integrated into place memories and what directional cues can be use to estimate travel direction en route.

We investigate cue integration for navigation in humans, bees, and wasps. Whereas blindfolded human subjects were asked to complete an L-shaped path with the aid of acoustic landmarks, the experiments in bees required extended training with a food reward. Bees, like several other animals, systematically confound the correct corner and the diametrically opposite one when trained to relocate a particular corner in a rectangular arena. This rotational error has been interpreted to demonstrate the use of the geometry of space to obtain directional information. We ask here what features are relevant and how are they acquired and processed? The third part of the work reported here will focus on how insects keep their eyes aligned with the world and how they reorient gaze while solving a navigation task.

☐96 Matthias Wittlinger A 701 / 14:15

Odometry during passive transport in the desert ant Cataglyphis

Author: *Matthias Wittlinger*[1]
Affiliation: [1]*Institute of Neurobiology, University of Ulm*

Desert ants Cataglyphis employ path integration to return to their nest, a navigation feat that requires continuous updating of a home vector. The angular component of this vector is provided by a celestial compass (Wehner 2003 J Comp Physiol A 189: 579). Distance estimation is performed by a stride integrator (Wittlinger et al. 2006 Science 312: 1965). However ventral optic flow, if present, does also provide distance information to the odometer. It has been challenging to separate both inputs to the odometer experimentally, stride integration and optic flow integration, in a behavioral paradigm.

Here I present an experiment where the role of the ventral optic flow integrator on odometry can be tested without interference with the stride integrator. Experienced foragers of Cataglyphis bicolor regularly transport indoor workers between two nest locations of a colony. When separated during transport, the transported ant returns to the nest of origin. Although it has previously been shown that the transportees gain directional information during their transport (Duelli 1973 Rev Suisse Zool 83:413), the odometer mechanism was still unclear. In a formicine fashion, the head posture, and notably head angle, of the transportee correspond to the head posture of the transporter, only the looking directions are opposite. Hence the ventral optic flow field during transport appears to be the same for both animals, even though pointing into opposite directions.

Transportee/transporter pairs that travelled in a channel set-up were caught and separated after approximately 10m of transport and the transported ants were tested in a parallel test channel. The tested ants searched for the nest entrance after the corresponding distances that they were carried.

In summary, the ants' distance estimator can work without any active locomotion and hence without stride integration exclusively relying on optic flow integration.

☐97 Eva Berg A 701 / 14:30

Single perturbations cause sustained changes in searching behavior of stick insects

Authors: *Eva Berg*[1]*, Joachim Schmidt*[1] *, Ansgar Büschges*[1]
Affiliation: [1]*Universität zu Köln*

Walking stick insects that do not find a foothold perform stereotypic cyclic searching movements (SMs) with the respective leg (Bässler, 1993; Dürr, 2001). We are interested in the control of SMs that are continued after a one-time leg contact with an object.

Experiments were performed on stick insects (Cuniculina impigra) with a single intact foreleg that was restrained to move in the vertical plane. A stick was moved into the leg's movement path such that it was touched one time by the distal tibia. After touching, animals modified their SMs by (i) shifting them towards the position of contact and (ii) significantly decreasing SM amplitude. These changes were independent of where in the leg's trajectory the stick was touched. Only slowly the movements shifted back to the original position accompanied by a simultaneous increase in amplitude. This targeted response outlasting a single stimulus for several seconds expresses properties of a short term memory in the insect leg muscle control system.

We investigated the role of leg sense organs for the successful execution of the targeted motor response by means of ablation experiments: (i) no influence on SMs was detected following removal of sensory signals distal to the femur. (ii) SMs were impaired when proprioceptors reporting position of femur and tibia were ablated.

To study the underlying changes in motor output, leg muscle activity was monitored by EMG recordings from levator and depressor trochanteris. Changes in muscle activities were related to the direction of shift of SMs. Currently, we explore the mechanisms underlying the targeted response by intracellularly recording leg moto- and premotor interneurons.

☐98 Reinhold Hustert A 701 / 14:45

Leg-to-mouth coordination of locusts feeding on loose grass.

Authors: *Reinhold Hustert*[1]*, Anh-Vu Nguyen*[1]

Affiliation: [1]*Universität Göttingen*

Guiding food with hands or forelimbs to the mouth for biting off pieces is observed in many animals. It is a good example of kinesthetically guided coordination between different body parts, specifically object manipulations that require fine-tuned and adaptive sensory-motor coordination under mechanosensory (kinesthetic), haptic and often also under visual control. Locusts can hold a loose or dangling blade of grass vertical between the tarsi of both their forelegs and guide it to their mouthparts for biting off pieces. The legs position the food precisely for the mandibles and raise the grass blade with fine motor control. That presents a model for relative coordination with mainly the limbs controling the behavior and it is also a model for bilateral haptic motor control between the forelegs. Myograms from foreleg muscles demonstrate the positioning control of food pieces for the biting mandibles.

☐99 Carmen R. Smarandache-Wellmann A 701 / 15:00

Network mechanisms of coordination for distributed neural oscillators

Author: *Carmen Smarandache-Wellmann*[1]

Affiliation: [1]*Institute of Zoology, University of Cologne*

The abdominal nerve cord of crayfish coordinates the movement of the four pairs of swimmerets. It is the ideal model system to study in vitro the cellular mechanism of central pattern generator (CPG) organization and coordination of a chain of CPGs.

In the system a metachronal wave can be observed in vitro and in vivo, such that the movement of the swimmeret starts in the last segment and the anterior modules follow with a latency of a quarter of a cycle. The activity of each swimmeret module is generated through reciprocal inhibition of two sets of nonspiking local interneurons, the Int1?s and Int2?s, which form the CPG core. Their alternating oscillations control directly the firing of the two antagonistic pools of motor neurons that move the swimmerets. From each module two types of coordinating neurons, ASCE and DSC, send detailed information about the status of their home module to neighboring modules in other segments. The coordinating information of ASCE is encoded through the direct synaptic inhibition from one of the nonspiking CPG interneurons, Int1. It is important to mention that Int1 shapes ASCE-activity through graduate transmitter release and has only an effect in a small window (10mV) around its resting potential. Additionally it is known how each module decodes coordinating activity: a single nonspiking interneuron (ComInt1) integrates this information and forms a gradient of synaptic strength, in a way that neighboring modules elicit the biggest depolarization in ComInt1. To close the loop ComInt1 synchronizes the activity of the oscillator through its electric synapse to one of the CPG interneurons, Int2.

Supported by grants from DFG SM206/3-1

☐100 Matthias Gruhn A 701 / 15:15

Body Side-specific Control of Motor Activity during Turning in an Insect

Authors: *Matthias Gruhn*[1], *Philipp Rosenbaum*[1], *Anke Borgmann*[1], *Ansgar Büschges*[1]
Affiliation: [1]*University of Cologne*

The neural control of forward walking in insects is well studied. However, the mechanisms underlying the flexibility of motor programs between the segmental neural networks that control the individual legs during behaviors such as curved or backward walking remains largely unknown (Büschges & Gruhn, 2008).

We first investigated how middle leg muscle activity of tethered, intact animals, walking freely on a slippery surface changes during optomotor induced curved walking (Gruhn et al., 2009a). No marked changes in cycle period, duty cycle distribution, or the average stepping frequency occurred with a change in function of the leg as outside (oL) or inside legs (iL). Muscle activity and timing in all muscles was virtually the same between the two behaviors except for a small increase in flexor activity and the occasional reversal of phasing in protractor and retractor activity during inside steps. We then studied the influence of descending signals from rostral segments, including front legs, on mesothoracic coxal MN activity in the otherwise deafferented mesothoracic ganglion. During optomotor-induced turning with the front legs (N=17), the mesothoracic protractor and retractor neurons on the inside showed alternating activity, while they often generated tonic activity with rarely occurring alternation on the outside. Results of split bath experiments using the muscarinic agonist pilocarpine (N=5) support the notion of a task-dependent descending influence on mesothoracic motor activity for oL and iL walking activity. Our results indicate that turning kinematics of single legs are under individual segmental control and that descending signals from the brain not only affect sensorimotor processing (Hellekes et al., 2012) but also central premotor networks in a hemi-segment-specific fashion to generate flexible locomotor behavior.

Supported by DFG grant Bu857.

Monday, September 24, 2012

Chair: Joachim Schachtner

☐101 Martin Kollmann A 701 / 14:00

The different stages of the olfactory pathway of the red flour beetle *Tribolium castaneum*

Authors: *Martin Kollmann*[1]*, Stefan Dippel*[2/3]*, Sergius Frank*[1]*, Stephanie Crombach*[1]*, Stefan Schütz*[3]*, Ernst A. Wimmer*[2]*, Joachim Schachtner*[1]

Affiliations: [1]*Philipps-University Marburg, Dept. of Biology, Animal Physiology, Marburg*; [2]*Georg-August-University Göttingen, Dept .of Developmental Biology, Johann-Friedrich-Blumenbach-Institute of Zoology and Anthropology, Göttingen*; [3]*Georg-August-University Göttingen, Institute for Forest Zoology and Forest Conservation, Göttingen*

The olfactory pathway of *Tribolium castaneum*, as well as of most other insects, starts with the olfactory sensory neurons (OSNs) in the chemoreceptor sensilla of the antenna, which project into the glomeruli of the antennal lobe (AL). From the AL projection neurons send their axons in higher olfactory integration centers, the mushroom body (MB) and the lateral protocerebrum / lateral horn.

By creating a Gal4-UAS line, expressing tGFP in all ORNs, which contain the ORCO (the general olfactory receptor), using an antibody against ORCO, electron raster microscopy of the antenna, immunostainings of the brain und backfills of the antenna and maxillary palps, we characterize the olfactory pathway of the red flour beetle *Tribolium castaneum* in high detail.

Analyzing the anatomical features of the pathway revealed no sexual dimorphism at the level of the antenna and the AL. Interestingly, backfills from the antenna not only label olfactory glomeruli but additionally suggest a connection with the accessory medulla of the optical lobes, which serves as circadian clock in the insect brain. Backfills of the maxillary palps resulted in only one glomerulus in the AL.

Supported by the DFG priority program SPP 1392 ‘Integrative analysis of olfaction’ (SCHU 1135/13-1, WI 1797/4-1, SCHA 678/13-1)

☐102 Christoph Kleineidam A 701 / 14:15

Processing of simple and complex odor patterns within the antennal lobe of social insects

Author: *Christoph Kleineidam*[1]

Affiliation: [1]*University of Konstanz*

The perception of odors guides animal behavior probably more than any other sense. This is particularly true for social insects like ants and bees, which not only perceive and discriminate a vast number of different odors, but also are able to produce odors (pheromones) for communication. Following a pheromone trail to a profitable food source is the primary example of extreme odor sensitivity in ants, and the adaptation to detect minute amounts of a chemical may even exceed the high sensitivity of moths' perception of sex-pheromones. Another amazing ability of social insects is their chemical recognition system that allows colony-specific recognition of individuals.

I will demonstrate how the olfactory system of leaf-cutting ants is adapted for high sensitivity to detect the trail pheromone, and how distinct neuroanatomical phenotypes of the olfactory pathway may contribute to division of labor in this highly derived social insect species (Kuebler et al. (2010) JCompNeurol. 518). In a second example, I will introduce the neuronal basis of nestmate recognition in the Florida carpenter ant. Surprisingly, the results we obtained in our studies on the neuronal representation of CHCs and the classification of an odor, as being 'nestmate' or 'non-nestmate', is not consistent with the current notion that in the antennal lobe, the spatio-temporal representation itself has coding properties to assess the quality of an odor (Brandstaetter et al. (2011) JNeurophysiol. 106:). This illustrates how powerful the diverse adaptations found in the olfactory system of social insects are to address even very basic questions in olfaction.

☐103 Marlene Binzer A 701 / 14:30

Neuropeptides in the antennal lobe and the mushroom body of Tribolium castaneum: direct peptide profiling and immunohistology

Authors: *Marlene Binzer*[1]*, Carsten Michael Heuer*[1]*, Joachim Schachtner*[1]
Affiliation: [1]*Philipps-Universität Marburg, Dept. Biology, Animal Physiology*

Among the signaling molecules involved in neuronal communication, neuropeptides represent the largest and most diverse group. They are able to shape the activity pattern of neuronal circuits and are thus accepted to be of major importance for the functional condition and output pattern of the central nervous system. Furthermore, neuropeptides are thought to be involved in processes related to neuronal plasticity, the substrate for learning and memory.

In the presented project we aim to characterize the neuropeptide repertoire of two integrative neuropils in the olfactory pathway of the red flour beetle *Tribolium castaneum*, the antennal lobes (ALs) and the mushroom bodies (MBs). The ALs act as primary olfactory centers that receive direct input from olfactory receptor neurons and are involved in early processing and modification of olfactory signals They are intimately linked to higher integrative brain centers such as the MBs, which also receive information from other sensory modalities. In *T. castaneum*, the MBs comprise a single knob-shaped calyx, a stalk-like peduncle, and a medial and vertical lobe, each consisting of distinct subdivisions formed by Kenyon cell processes.

To further reveal the principal repertoire and the potential role of neuropeptides in the AL and the MB, these neuropils were investigated by two complementary methods. To assess the full range of the AL and MB neuropeptidome, isolated tissue samples of these brain centers were subjected to MALDI-TOF mass spectrometry by direct peptide profiling. Immunohistochemical stainings allowed us to confirm the presence of neuropeptide transmitters and to localize sites of expression in the ALs and MBs of *T. castaneum*.

In another approach, we examine developmental changes in the ALs neuropeptide repertoire of adult beetles. To quantify those changes we use stable isotope-labeled peptide analogues as an internal standard.

Supported by the DFG priority program SPP 1392 “Integrative Analysis of Olfaction” (SCHA 678/13-1)

☐104 Ricarda Scheiner A 701 / 14:45

Biogenic amine receptors, response thresholds and division of labor in honeybees

Authors: *R. Scheiner*[1], *T. Reim*[1], *A. Toteva*[1], *M. Thamm*[1], *P. Chatterjee*[1], *S. V. Yi*[1]
Affiliation: [1]*University of Potsdam*

Honey bees are well-known for their complex division of labor. But how does a bee know which task she has to perform? A prominent current theory assumes that differences in individual sensory response thresholds are the basis for division of labor. Workers of a colony differ in their response thresholds for task-related stimuli and therefore perform different tasks.
Experimental evidence for differences in sensory response thresholds is rare. We demonstrate that both age-independent division of labor among pollen and nectar foragers and age-dependent division of labor between hive bees and foragers is accompanied by respective changes in sensory response thresholds for visual and gustatory stimuli.
But which mechanisms regulate sensory responsiveness and division of labor? Our data strongly suggest that division of labor is regulated via differential expression of octopamine and tyramine receptors. Age-independent division of labor among foragers correlates with differential methylation and splicing of the honeybee tyramine receptor. Age-dependent division of labor, in contrast, seems to be mediated by differential expression of the honey bee octopamine receptor. In addition, we show that both tyramine and octopamine significantly affect sensory responsiveness to gustatory and visual stimuli, locomotion and learning behavior. These findings imply that tyramine and octopamine receptors have decisive regulatory functions in honey bee division of labor.

☐105 Marc Spehr A 701 / 15:00

Mitochondrial calcium mobilization is a key element in olfactory signaling

Authors: *Marc Spehr*[1], *Daniela Fluegge*[1], *Lisa M. Moeller*[1], *Annika Cichy*[1], *Monika Gorin*[1], *Agnes Weth*[1], *Sophie Veitinger*[1], *Silvia Cainarca*[1], *Stefan Lohmer*[1], *Sabrina Corazza*[1], *Eva M. Neuhaus*[1], *Werner Baumgartner*[1], *Jennifer Spehr*[1]
Affiliation: [1]*Department of Chemosensation, Institute for Biology II, RWTH Aachen University, Aachen*

In olfactory sensory neurons (OSNs), cytosolic Ca2+ controls the gain and sensitivity of olfactory signaling. Important components of the molecular machinery that orchestrates OSN Ca2+ dynamics have been described, but key details are still missing. Here, we demonstrate a critical physiological role of mitochondrial Ca2+ mobilization in mouse OSNs. Combining a novel mitochondrial Ca2+ imaging approach with patch-clamp recordings, organelle mobility assays, and ultrastructural analyses, our study identifies mitochondria as key determinants of olfactory signaling. We show that mitochondrial $Ca2+$ mobilization during sensory stimulation shapes the cytosolic $Ca2+$ response profile in OSNs, ensures a broad dynamic response range, and maintains sensitivity of the spike generation machinery. When mitochondrial function is impaired, olfactory neurons function as simple stimulus detectors rather than intensity encoders. Moreover, we describe activity-dependent recruitment of mitochondria to olfactory knobs, a mechanism that provides a context-dependent tool for OSNs to maintain cellular homeostasis and signaling integrity.

☐106 Andreas Thum A 701 / 15:15

Learning and Memory in Drosophila Larvae

Author: *Andreas Thum*[1]
Affiliation: [1]

Animals as well as humans need to organize their behavior. Thereby the brain uses past experience to evaluate environmental stimuli in the background of an individual’s state to select for an appropriate behavior. For centuries, researchers in the functional brain sciences have been mapping properties of behavior to areas of the brain. But a mechanistic understanding of brain and behavior is still lacking.
Based on its neuronal simplicity the Drosophila larvae has turned into an elementary model system for studying brain functions and even allows for meaningful comparisons with other insects or mammals. For this work we used anatomical, behavioral and molecular approaches to identify the fundamental processes involved in larval associative conditioning. The results will provide insights into how learning and memory is organized on multiple levels within a simple brain.

13. Neurobiology POSTERS

♦134 Gerd Bicker

A dog is man's best friend, but can its olfactory ensheathing cells help human neurons?

Authors: *Gerd Bicker*[1/6], *F. Roloff*[1], *S. Ziege*[2], *S. Strauss*[3], *K. Reimers*[3], *J.D. Kocsis*[4/5], *C. Radtke*[3], *W. Baumgärtner*[2/6],*K. Wewetzer*[2/6]

Affiliations: [1]*Division of Cell Biology, University of Veterinary Medicine Hannover*; [2]*Department of Pathology, University of Veterinary Medicine Hannover;* [3]*Department of Plastic, Hand- and Reconstructive Surgery, Hannover Medical School;* [4]*Department of Neurology and Center for Neuroscience and Regeneration Research, Yale University School of Medicine, New Haven, Connecticut*; [5]*Neuroscience Research Center, Veterans Affairs Connecticut Healthcare System, West Haven, Connecticut*; [6]*Center for Systems Neuroscience Hannover*

Transplantation of olfactory ensheathing cells (OEC) and Schwann cells (SC) is a promising therapeutic strategy to facilitate axon regeneration and remyelination after spinal cord injury. However, the close phenotypic resemblance of OECs and SCs including the expression of marker molecules, e.g. the neurotrophin receptor p75 (p75NTR) and S100 so far did not allow selective identification and purification of OECs. Using magnetic activated cell sorting, we depleted contaminating SCs from OEC preparations and purified canine OECs from olfactory bulb (OB-OECs), olfactory mucosa (OM-OECs), and SCs from fibular nerve for in vitro analysis. To compare the motility of the purified glial cells, we used a scratch migration assay which measures cell migration during the closure of a ?wound? that is scratched into a confluent cell monolayer. Closure of the gap was followed by monitoring the advancement of the cell front over 8 hrs. Because this time interval is too short for significant cell proliferation, the presence of cells in the gap reflects migration. A quantitative evaluation shows that OB-OECs and SCs migrated faster than the OM-OECs. The OB-OECs and SCs covered a distance of about 120 µm in 8 hrs, as compared to about 80 µm for the OM-OECs. We then investigated whether motility could be up-regulated by pharmacological agents. So far, we found no evidence that glial migration is regulated by cGMP or cAMP signaling, but activating PKC enhances motility. Further experiments address the improved neurite outgrowth of human model (NT2) neurons in a co-culture system with OECs and SCs. The cell culture experiments using canine OECs and SCs serve to evaluate the potential therapeutic impact of the three glial cell types for repair of spinal cord injuries in a large animal model.

This study was supported by a DFG grant (FG 1103, BI 262/16-1)

♦135 Stefanie Blankenburg

Characterization of 2 GABA Receptor Subtypes involved in Cockroach Salivation

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In the American cockroach, Periplaneta americana, it is well-known that the secretion of saliva by the acinar-type salivary glands is under neuronal control. The glands are innervated by two salivary neurons (SNs) originating from the subesophageal ganglion (SEG). SN1 contains dopamine as a neurotransmitter. SN2 however is GABAergic. The application of GABA during salivary duct nerve stimulation enhances the electrical response of acinar cells and leads to a higher rate of fluid and protein secretion. The effect on the electrical response can be mimicked by the application of GABAB receptor agonists and blocked by GABAB receptor antagonists. The pharmacological evidence for the involvement of GABAB receptors in mediating the effects of GABA has to be substantiated by the molecular identification of these receptors and their localization in the model organism.
In the current study, I used PCR with degenerate primers followed by RACE-PCR in order to isolate cDNA fragments encoding the full-length GABAB receptor subtype 1 and part of the GABAB receptor subtype 2 (PeaGB1 and PeaGB2). The deduced amino acid sequences show a high degree of conservation to vertebrate and invertebrate GABAB receptor subtypes. In order to investigate the distribution of the GABAB receptor subtypes in P. americana I am currently raising polyclonal antisera directed against selected regions of these receptors. For a functional analysis, the receptor subtypes are supposed to be heterologously expressed in HEK293 cell lines.

This work was supported by the German Research Foundation (BL 469/4).

♦136 Ann-Juliane Breitenbach

Octopaminergic modulation of synaptic transmission between antennal mechanoreceptors and descending giant interneurones in the cricket brain

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In insects and many other animals descending brain neurones are decisively involved in recruiting suitable motor responses to the current sensory events. We investigate in the cricket how the responsiveness of identified descending giant interneurones to mechanical stimulation of an antenna is modulated by the biogenic amine octopamine. In response to lightly touching the antenna, one descending brain neurone (DBNc1-2) reliably generates a single spike with a short and constant latency, which indicates monosynaptic mechanosensory inputs (Schöneich, Schildberger, Stevenson, J Comp Neurol 519:1677-1690, 2011). After bath application of octopamine, or its agonist chlordimeform (CDM), this neurone then responds to the same touch stimulus with several spike (the most effective agonist concentration was 10 mM, but there was no clear dose-response relationship. This octopaminergic modulation was reversed by washing, and reversibly blocked by the octopamine antagonist epinastine. During these experiments, we never observed any effect on the afferent response as recorded from the antennal nerve. Interestingly, application of epinastine alone led to a conspicuous lengthening of the response latency. This suggests that the mechanosensory input synapses of this interneuron are controlled by endogenously released octopamine. Supporting these findings, octopamine-like immunoreactive varicosities were found to occur in the brain neuropile where antennal-mechanosensory afferents overlap with the dendritic ramifications of DBNc1-2 and its functional sibling neurone DBNc2-2. We are currently working to unravel the mechanism of octopamine‘s action in this system, and the extent to which octopamine shapes the crickets? behavioural response to mechanical antennal stimulation.

Supported by the German Research Council (DFG: FOR 1363, STE 714/4-1).

♦137 Martin Brill

Parallel processing within the bee's dual olfactory pathway

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Animals face complex and highly dynamic olfactory input in their natural environment. This demands fast and reliable information processing in olfactory systems of both, vertebrates and invertebrates. Parallel processing was shown to improve processing speed and power in other sensory systems and is characterized as extraction of different parameters along parallel sensory information streams. Honeybees possess an elaborate olfactory system with unique neuronal architecture, a dual olfactory pathway comprising a medial and lateral projection-neuron (PN) output tract (m-, l-APT) connecting the olfactory lobes with higher order brain centers. This peculiarity is a derived character exclusively found in Hymenoptera (e.g. Rössler and Zube 2011, Arthropod Struct Dev 40:349). Here, we asked whether this specific adaptation could serve as a model system for parallel processing in olfaction.
We employed a novel experimental technique for simultaneous multi-unit recordings from both antennal-lobe output tracts. We revealed detailed response profile characteristics of high numbers of PNs to a variety of tested floral, pheromonal and biological relevant odors. PNs of both tracts responded to all tested odors, but with different characteristics indicating parallel processing. L-APT PNs were activated by multiple odors (broad response profiles) suggesting generalized odor coding, whereas m-APT PNs responded comparatively weaker, less frequent, but with higher complexity indicating higher odor-specificity. Comparison of response latencies of PNs within and across both output streams revealed odor-dependent latency patterns that likely support a dual tract temporal code, possibly promoting coincidence coding at the level of the mushroom body input. We conclude that parallel processing via the honeybee?s dual olfactory pathway enhances performance for sophisticated odor perception as required under complex natural stimulus conditions of a social insect.

Supported by DFG SPP 1392 (RO 1177/5-1).

◆138 Hannah Burger

Have specialized bees evolved neural adaptations to locate their host plants?

Authors: *Hannah Burger*[1]*, Giovanni Galizia, Stefan Dötterl, Sabine Kreissl, Manfred Ayasse*
Affiliation: [1]*University of Ulm, Institute of Experimental Ecology*

Specialized (oligolectic) bees rely on a small range host plants for their pollen collection, in strong contrast to bees like honeybees which forage on a broad and generalized flower spectrum. As compared to generalists, the specialists might have evolved neural adaptations allowing them to effectively locate their specific host flowers. In particular, olfactory cues might be suited for identifying host flowers. To investigate how host odours are processed in their brains, we used calcium imaging experiments and recorded odour-evoked activity patterns in the antennal lobe for the specialist *Andrena vaga* and, for comparison, in the generalist honeybee *Apis mellifera*. Our investigations show that *A. vaga* bees, but not the honeybee *A. mellifera*, had a particularly high sensitivity for a main component of the host-flower odour. Our experiments suggest that *A. vaga* females show correlates between neural organization and host-plant finding behaviour.

◆139 Peter Christ

Activity dependent plasticity in the olfactory system of adult *Tribolium castaneum*

Authors: *Peter Christ*[1]*, Martin Kollmann*[1]*, Joachim Schachtner*[1]
Affiliation: [1]*Philipps-University Marburg, Dept. Biology, Animal Physiology*

Tribolium castaneum offers an excellent system to study development and plasticity of the olfactory system. A previous work on volume of distinct neuropils revealed a pronounced increase of brain volume incl. antennal lobes (ALs) and mushroom bodies (MBs) within the first days of adult life, indicating a pronounced sensitive phase. To further reveal this mechanism, we examined neuropeptidespossibly involved in this postmetamorphic plasticity. We compared the numbers of tachykinin-immunoreactive (TK-ir) AL neurons of females and males directly (A0) and seven days after molt (A7). We found a sexual dimorphism at A0 concerning numbers of TK-ir cells, with females having more TK-ir AL neurons than males. In both sexes, the numbers of AL TK-ir cells increased from A0 to A7. Females, isolated shortly before adult molt and raised to A7, showed no increase in the number of TK-ir cells, in contrast to males held under same conditions. As in T. castaneummales are the main source of pheromone, we concluded, increase in TK-ir cell number can be induced by perception of pheromones. To extend these findings, we added the pheromone Dimethlydecanal (DMD), a food-related odor (cis-3-Hexen-1-ol) or a perception disturbing substance (Deet) to isolated beetles. The pheromone as well as the food related odor led to an increase in number of TK-ir cells in both sexes, while Deet addition prevented an increase in cell number.

This result suggests that the increase of TK-ir cells between A0 and A7 depends on the perception of odor signals and favors an activity dependent mechanism for the maturation of a peptidergic system in the AL of the red flour beetle.

♦140 Stephanie Friederike Crombach

Identification of putative GABAergic neurons in the brain and the olfactory system of the red flour beetle *Tribolium castaneum*

Authors: *Stephanie Crombach*[1], *Martin Kollmann*[1], *Joachim Schachtner*[1]
Affiliation: [1]*Philipps-University Marburg, Dept. Biology, Animal Physiology*

GABA (γ-aminobutyric acid) mediated inhibitory signaling plays an important role in information processing in the insect brain. Amongst the most extensively investigated neural networks governed by GABA signaling is the insect antennal lobe (AL), the first integration center for olfactory information. Here we present data on the localization of GABA in the brain of the red flour beetle of Tribolium castaneum, based on stainings against glutamate decarboxylase (GAD), a crucial enzyme in GABA biosynthesis.

In the olfactory pathway, GAD antibody stainings revealed about 300 immunoreactive cells associated with the AL. These neurons give rise to prominent staining throughout the whole AL neuropil. The majority of the GAD-ir neurons are certainly local interneurons. A subpopulation of the GAD-ir neurons of the AL are projection neurons ascending via the medial antenna cerebral tract (mACT) to the calyces of the mushroom bodies. GAD immunoreactivity was also detected in the mushroom bodies, the higher integration centers of the olfactory pathway. GAD immunostaining revealed a fiber network in the calyces, the peduncles and in the lobes, very likely stemming from extrinsic neurons.

Apart from neuropils of the olfactory pathway, we also detected immunoreactivity in the lower unit of the central body and the lateral accessory lobes, the optical lobes, the pars intercerebralis, as well as in other areas of the beetle brain.

To further confirm the presence of GABA in the identified neuronal populations, we are currently performing anti-GABA immunostaining (direct identification) in combination with GAD antibody staining (indirect identification). The current study will serve as a prerequisite to investigate plasticity of the GABAergic network of the central olfactory pathway of T. castaneum, e.g. whether and how age, odor environment or RNAi knockdowns of the olfactory receptor co-receptor (Orco) influence the neuroarchitecture of this network.

Supported by the DFG priority program SPP 1392 ‘Integrative analysis of olfaction’ (SCHA 678/13-1)

♦141 Max Diesner

Allatostatin A expressing interneurons in the adult and larval antennal lobe of *Drosophila melanogaster*.

Authors: *Max Diesner*[1], *Joachim Schachtner*[1]
Affiliation: [1]*Philipps University Marburg*

The fruit fly, *Drosophila melanogaster*, is dependent on its olfactory sense in search of food and reproduction. Processing of odorant information takes place in the antennal lobes (ALs), the primary olfactory center in the insect brain. Recent studies indicated that apart from classical neurotransmitters multiple neuropeptides, including Allatostatin A (AstA), short neuropeptide F, tachykinin related peptide

(TKRP), myoinhibitory peptide, SIFamide, IPNamide and myosuppressin are present in the AL. AstA, MIP and TKRP were identified in local interneurons of the AL. We tested two different GAL4-GFP expressing interneuron strains, NP 1227 (LN1) and NP 2426 (LN2), for their peptidergic composition. In ALs of adult flies, AstA is present in only 3 interneurons, which we can exclusively attribute to the LN2 strain, whereas TKRP is present in both strains in a different number of interneurons. MIP immuno-reactive interneurons are not present in both strains. The LN2 strain expresses GFP in 10, the LN1 in no larval interneurons. We are currently examining whether AstA is already expressed in larval AL interneurons in LN2 flies or whether AstA occurs during metamorphic development of the AL. To further elucidate the role of AstA during olfactory driven behavior and during antennal lobe development we are crossing a novel AstA-GAL4 strain with the LN2 strain to knock out the AstA expressing interneurons.

♦142 Roland Ferger

Adaptation in the auditory midbrain of the barn owl induced by double stimulation

Authors: *Roland Ferger[1], Philipp Tellers[1], Martin Singheiser[1], Mark von Campenhausen[1], Hermann Wagner[1]*
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Neurons in the external nucleus of the inferior colliculus (ICX) of the barn owl (*Tyto alba*) are arranged in a map of auditory space. Each neuron responds to a broad frequency range and represents information about the interaural time difference (ITD) and the interaural level difference (ILD) of a stimulus. The typical response behavior is phasic-tonic. In other words, these neurons exhibit spike-frequency adaptation. Similar to this effect are the neurons' responses to two subsequently presented stimuli: Neurons will respond with a higher rate to the first stimulus (called masker) than to the second one (called probe). This effect is known as response adaptation.

In this study we investigate how the inter-stimulus-interval between masker and probe (ISI) and the stimulus-level of the probe relative to that of the masker (2nd level) influences response adaptation. The ISI needed to obtain equal response rates to marker and probe, and the increase in level of the probe needed to obtain the same response rate as to the masker are determined. All stimuli consist of broadband noise. We compare our results to those from narrowband neurons.

DFG Wa606/16-1

♦143 Jonas Finck

Identification and localization of TRP channels in the antenna of leaf-cutting ants (Attavollenweideri)

Authors: *Jonas Finck[1], Ewald Grosse-Wilde[1], Christoph J. Kleineidam[1]*
Affiliation: [1]*University of Konstanz*

Ants show various fine-tuned behaviors in response to environmental temperature, and all of them require precise thermo-reception and the detection of minute temperature differences. In the context of brood care, the ants can detect differences of only 0.2 °C, and physiological measurements of one receptor neuron type revealed an incredible resolution of only 0.005°C for temperature fluctuations (Ruchty et al. (2010) J. Neurophysiology 104). Thermo-reception takes places in peg and pit sensilla located at the tip of the ants' antenna. Several studies in other insects revealed that members of the TRPA subfamiliy are involved in thermo-reception. Interestingly, the number of TRPA members is expanded in Hymenoptera (Matsuura et al. 2009). Therefore, we hypothesize that the TRP channels are important for thermo reception in ants, and that modulation and adaptation of diverse TRP channels contribute to the highly evolved thermo-reception system. In order to understand the underlying mechanism of thermo-reception, we address the following questions: i) which members of the TRP family are expressed in the ants' antenna, and ii) which sensilla types house the TRP expressing neurons?

Antennal transcriptome analysis revealed the expression of different TRP channels. Based on these transcripts, we built TRP-specific probes for fluorescence in situ hybridization (FISH). For establishing FISH, we used a specific probe for the olfactory co-receptor ORCO, which is expressed in most of the antennal chemosensory neurons. Currently, we are testing various probes on cryosections of the ants' antenna to co-localize the expression of TRP channels with their specific sensilla types.

♦144 Judith Förster

Determining Mode of Action of Pymetrozine - From Single Cell to System Level

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Pymetrozine is one selective insecticide against aphids. It induces a stretched posture of the legs and proboscis. This effect vanishes over time after application. Experiments in locusts indicate that pymetrozine affects gross sensitivity of sensory neurons in the fCO (Ausborn et al., 2005; Kaufmann et al., 2004). However, the mode of action of Pymetrozine is presently unknown. That means it is not known how single sensory cells of the fCO are affected and which target sides in the fCO exist.

So far two possible explanations exist: (1) Pymetrozine affects the mechanoelectrical transduction process or (2) affects transformation of receptor potential towards action potentials.

The stick insect, *Carausius morosus*, that has well characterized sensory organs, is also affected by Pymetrozine by lifting its legs. Potent concentrations of pymetrozine start at 100nM. Single fCO sensory cells are sensitive to changes of position (P), velocity (V) and/or acceleration (A) of the tibia (Hofmann et al., 1985). The reactions of these sensory cells to pymetrozine can be recorded intracellularly in the segmental ganglion (n=10). We show that P-sensitive (n=2) and V-sensitive (n=4) cells become tonic during stimulation after pymetrozine application. Active sensory cells as well as silent sensory cells become tonically active with pymetrozine treatment already in the absence of fCO-stimulation. This was independent of cell type (P: n=2; V: n=5; A: n=1). On average 25sec after the tonic activation, 70% of sensory cells became inactive. These results suggest that pymetrozine influences the transformation of receptor potentials into action potentials because the effect occurs without mechanical stimulation.

♦145 Ruth Maren Frings

Adaptive responses of peripheral lateral line units to dipole stimuli

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Fishes and aquatic amphibians detect minute water movements with the mechanosensory lateral line. The sensory units of the lateral line system are the neuromasts which consist of hair cells covered by a gelatinous cupula. Lateral line hair cells are innervated by afferent nerve fibres of the anterior and posterior lateral line nerves (ALLN and PLLN, respectively). In previous studies, the responses of lateral line afferents to the sinusoidal water motions generated by a dipole source have been described as non-adapting. This is surprising since afferent fibres in the auditory system of vertebrates have been shown to adapt to sinusoidal stimuli.

Here, we investigated whether responses of fibres in the PLLN of goldfish, Carassius auratus adapt to sine wave stimuli and how adaptation depends on stimulus frequency and amplitude. Single unit recordings were made from 18 PLLN fibers while the lateral line was stimulated with a 3 s sine wave stimulus generated by a stationary vibrating sphere (10 mm diameter). Vibration frequencies were 50, 70, 100 and 130 Hz und peak-to-peak displacements ranged from 4 to 247 µm.

Twelve units (67%) exhibited adapting responses to at least one of the stimulus frequencies, i.e. they increased discharge rate after stimulus onset (Onset response) and decreased discharge rate by at least 30 % for the remainder of the stimulus (Steady-State response). The degree of adaptation and the number of adapting units increased with increasing displacement and frequency of the dipole stimulus. In fourteen units, responses were recorded to step stimuli, during which the stimulus amplitude was increased abruptly, i.e., in a single step. All units exhibited adapting responses and responded to the amplitude step with an additional increase in discharge rate, indicating that the decrease in discharge rate between Onset and Steady State was not due to neuronal fatigue.

Our results show that the primary lateral line afferents can adapt to dipole stimuli. This allows the lateral line periphery to adjust its dynamic range to constant amplitude stimuli and rescale its responses to novel sensory stimuli.

♦146 Katrin B. Gehring

Characterization of the cAMP response element binding protein (CREB) in the honeybee brain

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Affiliation: [1]*Freie Universität Berlin*

The transcription factor CREB (cAMP response element binding protein) is involved in regulation of growth, differentiation, neuronal viability and circadian rhythms. It also plays an essential role in the formation of long term memory (LTM). CREB induces gene expression after being phosphorylated by several kinases. A huge body of work analyzed this CREB phosphorylation but little is known about its role in the honeybee (Apis mellifera), a well-known invertebrate model system for learning and memory. Our aim is to characterize Apis mellifera CREB and localize CREB dependent processes in the honeybee brain.

We use different antibodies to detect CREB and phosphorylated CREB (pCREB) in bee homogenate and in fixed bee brain slices. Counterstaining of synaptic proteins and DNA were performed to further characterize pCREB containing neurons.

pCREB immunoreactivity can be observed in a wide range of cell nuclei including nuclei of neurons known to be involved in processing sensory information, for example intrinsic mushroom body neurons (Kenyon cells). In contrast to the assumed distribution of pCREB, which, as a transcription factor, is thought to be predominantly located in the nucleus, we also find strong immunoreactivity in axonal and dendritic parts of Kenyon cells.

We investigated the distribution of pCREB immunoreactivity in the honeybee brain in bees with different age. We compared one day old bees with more experienced bees and found increased pCREB levels in aged bees and, focusing on specific brain neuropils, an ongoing redistribution and sharpening of the pCREB signal in distinct neuronal subsets.

Since the antennal lobes and the mushroom bodies are involved in processing sensory information, ongoing experiments focus on changes of pCREB and CREB levels in these neuropils after learning.

◆147 Jens Goldammer

Calcium imaging of retrogradely labeled retractor coxae neurons in the stick insect Carausiusmorosus

Authors: *Jens Goldammer*[1], *Cathleen Rotte*[1], *Joachim Schmidt*[1], *Peter Kloppenburg*[1], *Ansgar Büschges*[1]
Affiliation: [1]*Universität zu Köln*

Calcium ions (Ca2+) play an important role in various neuronal processes, e.g. release of neurotransmitters or as 2nd messengers (for review see Berridge 1998). We are interested in the potential contribution of Ca2+ transients to rhythmic motor activity in stick insect leg motoneurons (MNs). Neuroanatomical data in the stick insect Carausius morosus showed that MN neurites are mainly found in dorsal ganglion regions, especially neurites of retractor coxae MNs that have axons in nervus lateralis 5 (nl5; Goldammer et al. 2012) and therefore are suited for calcium imaging studies.

We retrogradely labeled mesothoracic nerve nl5 with the Ca2+ sensitive dye Oregon Green 488 Bapta-1 dextran. Measurements of Ca2+ transients in retractor coxae MNs were combined with extracellular recordings of the antagonistic protractor coxae MNs or of the backfilled nl5, respectively. We induced either rhythmic activity in the MNs through application of the muscarinic receptor agonist pilocarpine (Büschges et al. 1995) onto the mesothoracic ganglion or activity was induced by tactile stimulation of the animal. Our results show spatially uniform Ca2+ transients in primary neurites and higher order branches in antiphase with the activity of excitatory protractor coxae MNs (N=5) and in-phase with activity of the labeled nl5 MNs (N=3). Currently we are investigating the role of Ca2+ transients in mediating the tonic depolarization of MNs during walking movements.

♦148 David Goyer

Giant Synapses in Vitro: A Co-Culture of Chicken Cochlear Ganglion and Auditory Brainstem Neurons

Authors: *David Goyer*[1], *Hermann Wagner*[1], *Thomas Künzel*[1]
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In birds, the axons of cochlear ganglion neurons project into two subdivisions of the cochlear nucleus in the auditory brainstem, the nucleus magnocellularis and the nucleus angularis. Nucleus angularis neurons are contacted by bouton-like synapses. In nucleus magnocellularis however, collaterals of the same fibre can form giant axosomatic terminals, the Endbulbs of Held. The molecular basis for the determination of this giant synapse during development is yet to be found. We established a primary culture of cochlear ganglion neurons of the embryonic chicken as a starting point for the design of a co-culture system, consisting of cochlear ganglion and auditory brainstem neurons.

Tissue from the chicken basilar papilla of Hamburger and Hamilton stage 36 was explanted. Serum-free cell culture media were used. Immunocytochemical stainings against neurofilament revealed a distinct bipolar morphology of the neurons, reminiscent of the in vivo situation. The neurons showed a profound axon outgrowth and were viable up to eight days in vitro. Electrophysiological recordings additionally confirmed the identity of the cochlear ganglion neurons. We also could demonstrate the existence of synaptic markers like synaptic-vesicle protein 2 in the axon terminals, showing that these neurons already express and transport the machinery for synapse formation as early as E10. Preliminary results of the co-culture system show viable brainstem and cochlear ganglion neurons and indicate that in vitro innervation of brainstem neurons by cochlear ganglion neurons is possible, making this co-culture system an excellent tool for further investigation of molecular aspects of Endbulb-formation and developmental control of synaptic terminal size.

♦149 Silvia Gruhn

A neuro-mechanical model for curve walking in the stick insect

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The coordination of the movement of single and multiple limbs is essential for the generation of locomotion. Movement around single joints and the resulting stepping patterns are usually generated by the activity of antagonistic muscle pairs. In the stick insect, the three major muscle pairs of a leg are the protractor-retractor, the levator-depressor and the flexor-extensor. The protractor-retractor moves the coxa and thereby the leg forward and backward, the levator-depressor moves the femur up and down and the flexor-extensor flexes or extends the tibia around the femur-tibia joint. The underlying neuronal mechanisms for a forward stepping middle leg have been intensively studied in experimental and theoretical studies. However, details about neuronal and mechanical mechanisms driving a single stepping leg in situations other than forward walking remain largely unknown. Here, we present a neuro-mechanical model of the coupled three joint control system of the stick insects middle leg. The neuro-mechanical controller is able to walk forwards, backwards or sidewards. Switching between these three different behaviors is achieved by minimal changes to the central control to the neuro-mechanical model. By attaching two such middle legs to the thorax and fixing hind and front legs, we are able to generate curve walking with two different mechanisms: In the first, the inner middle leg is switched from forward to sideward and in the second to backward walking. Backwards stepping in the inner middle leg is thereby much more effcient in producing sharper turns than sideward stepping. Both behaviors are observed in the animal.

♦150 Volker Hofmann

Spatiotemporal analysis of static electric images: a tool to investigate electric flow?

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Active electrolocation enables weakly electric fish to explore and analyze their environment based on the modulations in a self-generated electric field. These are induced by nearby objects and result in an altered voltage distribution across the body, the so called electric image (EI), that can be sensed by a distributed array of electroreceptors situated in the skin. EI properties depend on object material, volume, shape and distance, making the information within EIs ambiguous. A feature that has received relatively little attention so far is the degree to which EIs are subjected to changes induced by ego-motions and how known cues extractable from these images under stationary conditions are translated into dynamical cues.

Here we report on a mutual modeling and experimental study of the stimuli available during active electrolocation of Gnathonemus petersii. We validate model results by reproducing earlier key findings showing that the ratio of the maximal EI slope to the maximal EI amplitude provide an unambiguous cue for distance estimation. We show that this metric is subjected to systematic changes dependent on the body position at which an EI is cast at.

We further extent this approach to the analysis of electric images in temporal space introducing a new temporal metric for distance estimation that is based on the spatial properties of electrical images. This metric might be a useful tool for spatiotemporal analysis of electric images in quasi-natural object exploration sequences which could facilitate the understanding of electric flow in the electrosensory system.

◆151 Jennifer Ignatious Raja

Odor response profiles of Drosophila olfactory receptors from heterologous expression in HEK293 cells

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Olfaction plays a major role in insects and mediates behavioral and physiological responses. Drosophila is an excellent model insect to study various biologically important aspects of olfaction. For these studies the odor response profile of all odorant receptors (ORs) to a wide range of odor molecules should be known. Though Drosophila ORs (dORs) were studied extensively, still the olfactome is not complete. Our group recently developed a database called DoOR (Database-of-Odor-Responses; see http://neuro.unikonstanz.de/DoOR) by integrating all data sets (single sensillum recordings and in vivo calcium imaging) published until 2010. DoOR provides information about many Drosophila OR response profiles. However some ORs have not yet been characterized or have only been tested with a limited number of odor stimuli. We developed an in vitro olfactory receptor assay to characterize the odor response profiles of all ORs, ultimately striving towards the complete olfactome for Drosophila. Preliminary experiments were done with Or22a and Or92a receptors to validate the assay. The transfection efficiency of dORs was about 50-60% and the majority of the transfected cells (greater than 78%) responded to the odor by increasing the levels of intracellular calcium. Calcium response to the odor was transient and reproducible and required co-expression of Orco. The calcium response of individual cells in a population was analyzed semi-autonomously by using the user defined workflows in the open source software ? KNIME (Konstanz Information Miner - http://www.knime.org/). This image analysis method is robust and faster than other methods. By this method we aim at characterizing the odor response profile of all dORs whose response profiles are as of yet unknown.

◆152 Mirta Jacobs

Sensory physiology of thermoreception in Bombusterrestris

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Bumblebees can counter unfavorable nest temperatures by either incubating and heating or by wing fanning to cool down nest temperature. Thereby, bumblebee colonies maintain stable temperature conditions that are crucial for proper brood development (Heinrich B. (1979) Thermal warriors). Within a colony, workers differ in their response thresholds to temperature; some workers consistently respond to lower temperatures, while others have high response thresholds (Weidenmüller (2004) Behav. Ecol.). This inter-individual variability promotes the emergence of division of labor and collective thermoregulation. The proximate mechanisms underlying the inter-individual variability in behavior are unknown, and we address this question with a sensory physiology approach on worker of Bombus terrestris. Temperature reception takes place at different peg-in-pit sensilla on the antennae and various thermo sensitive neurons have been described in ants and bees (Ruchty et al. (2009) Arthropod Struct. & Dev.; Yokohari (1983) Cell Tiss. Res.). Based on these studies, we focus our investigation on thermo sensitive neurons, associated with the sensillum coeloconicum and sensillum coelocapitulum, which also have been found in bumbelbees (Fonta (1987) Chem. Senses). Using sharp electrodes for extracellular recordings, we measure the rate of action potentials in response to temperature and temperature changes. Following a detailed description of the physiological responses of the thermo sensitive neurons (dose-response curves), we combine physiological and behavioral measurements. The individual response threshold of bumblebees will be assessed in a behavioral assay and subsequently the sensitivity and working-range of the thermo sensitive neurons will be measured.

Our hypothesis is that differences in sensory physiology of receptor neurons underlie the differences found in behavior. Our study will help to better understand the proximate mechanisms of adaptive thermoregulation and emergent division of labor in bumblebee colonies.

♦153 Felix Kaldenbach

Infrared vision in snakes: How neurons in the rattlesnake's tectumopticum respond to amoving warm object

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Rattlesnakes can perceive infrared radiation with their pit organs. This enables them to detect and precisely strike towards warm blooded prey even under dark conditions. It is also used to find suitable places for thermoregulation.

All thermal objects of interest to the snake either move (e.g. prey) or produce moving infrared images, when the snake performs scanning movements with its head. Surprisingly, it has not been investigated yet, how the infrared system responds to a moving thermal object.

Electrophysiological recordings of infrared sensitive neurons in the tectum opticum of rattlesnakes (*Crotalus atrox*) were performed. A thermal object was moved in a horizontal direction in front of the snake at various velocities while neuronal activity was measured.

The neurons showed very low or no activity at slow object velocities (even though the object was presented for a long period of time). With increasing velocities neuronal activity increased and reached a maximum followed by a slight decrease at very high object velocities.

These results, obtained from single neurons, may also be of importance to the snake’s infrared detection abilities in general: as opposed to fast moving objects, slow or even stationary objects may not be detected at all when the snake is e.g. motionless couching for prey. In an environment, in which all objects of interest produce moving infrared images, such a sensory system sustainably deals with the precious resource of alertness.

◆154 Lutz Kettler

A double-stimulus paradigm for investigating adaptation in the barn owl (Tytoalba): a behavioral approach

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During hunting barn owls attend to sounds as for example rustling generated by prey. The birds typically do not attack upon hearing the first sound, but wait for a second sound. This situation was mimicked with a double-stimulus paradigm. It was tested behaviorally whether and how a first or reference sound influenced the head turning of the birds towards a second sound or probe. The delay between reference and probe was varied between 100 ms and 3200 ms. Preliminary data collected with three adult barn owls indicate a reduction in the number of behavioral reactions compared with a situation where only the probe was presented. Furthermore, head turning latencies were increased in double-stimulus condition. This indicated response adaptation. Latencies returned to the level of the probe-only condition if the reference-probe delay was increased. The time constant of recovery from adaptation coarsely matched time constants that were determined in electrophysiological experiments. Thus, a first stimulus rather lowers than facilitates the response to a second stimulus under the conditions examined.

◆155 Nicholas Kirkerud

APIS - a new approach towards automatic conditioning of honey bees

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For more than 50 years, honeybees have been widely used model organisms for the study of learning, memory and the underlying neuronal substrates and mechanisms because they combine a rich behavioral repertoire with an easily accessible brain of 1mm^3 in size. The well-established Proboscis Extension Response-paradigm (PER, Kuwabara, 1957) has been used to quantify appetitive learning in nectar feeding insects for decades. Recently, an aversive paradigm based on Sting Extension Response to electric shocks has been developed (SER, Vergoz et al. 2007). These methods, in which the bees are harnessed, are technically challenging, vary to different extents from lab to lab, and demand an inconveniently large test group because of the binary data they produce.

Here we introduce a novel method of honeybee conditioning: APIS, the Automatic Performance Index System. In an enclosed walking arena where bottom and top is covered with an electric grid, the bee is presented with odors from either end coupled with the presence of weak electric shocks to form aversive associations. The movement of the bee and its responses to the stimulus and the electric shocks are monitored continuously by an automatic tracking system. From the tracking data output, several factors of the bee's behavior in the chamber can be used to calculate a new index accessing the bee's learning ability, response threshold and response profile, expressing the bee's fitness in a single number - the BeeQ.

Preliminary data shows that the BeeQ correlates well with learning indices obtained from conventional conditioning methods. Thus, the advantages of this automatic system makes it ideal for assessing learning rates in a standardized and convenient way, and its flexibility adds to our toolbox for studying mechanisms behind learning and memory.

Vergoz V, Roussel E, Sandoz JC, Giurfa M. 2007. Aversive learning in honeybees revealed by the olfactory conditioning of the sting extension reflex. PLos One 2: e288. doi: 10.1371/journal.pone.0000288.
Kuwabara M. 1957. Bildung des bedingten Reflexes von Pavlovs Typus bei der Honigbiene Apis mellifica. Hokkaido Univ Zool J Fac Sci 13:458-464.

◆156 Thomas Laudes

New data for the Database of Odorant responses - DoOR

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In the olfactory world, organisms have to deal with thousands of different odorants and have evolved sophisticated chemical olfactory systems to perform this task. These systems differentiate meaningful stimuli from background thereby enabling a given animal to locate and navigate even in a turbulent surrounding to a food source or find mating partners. The coding of thousands of different odorants with a relatively low number of input channels is achieved by an ensemble response that arises due to activation of an individual set of olfactory sensory neurons (OSN) by a particular odorant. Each OSN is expressing a given olfactory receptor (OR) which defines its sensitivity to a set of odorants. In order to decipher the olfactory code one would ideally want to know all of these response profiles, the so called olfactome. Of all olfactory systems, that of Drosophila melanogaster is the one in which most receptor ? ligand combinations are already measured. But there are still some OSNs which were only tested with a few ligands so far or are not even characterized yet.

Here we present response profiles of the four Drosophila Ors Or10a, Or42b, Or56a and Or 69a. We measured calcium concentration changes directly in the antenna of genetically modified flies which expressed the calcium sensor G-CaMP exclusively in Or10a, Or42b, Or56a and Or69a carrying neurons. Among the best ligands for Or69a we found 4-Methylphenol, a-Terpineole, ß-Citronellol and Ethyl-3-hydroxyhexanoate. For Or56a we found both, strong excitatory and inhibitory responses. (1R)-(?)-Fenchone and ?-Ionone, being the two best excitatory ligands and 2,3-butanedione and ethanoic acid leading to strong inhibitory responses. The response profile of Or42b revealed 3-Octanol, Linalool and 2-Heptanol as inhibitory stimuli and 3-Hexanone, Ethyl-3-hydroxybutanoate and 3-Pentene-2-one as excitatory ligands. For Or10a we found Methyl tiglate and Ethyl tiglate as strong excitatory ligands, 2-Propylphenol and Isoeugenol elicit inhibitory responses.

This new data will be included into DoOR, the Database of Odorant Responses, an open access database (http://neuro.uni.kn/DoOR). DoOR is able to integrate heterogeneous data-sets from different labs and no matter what technique was used for measuring them (e.g. action potentials, calcium influx or in situ measurements vs. heterologous expression), thereby getting one step closer to the complete olfactome.

Software and data is freely available, with tools for data visualization or integration of new response profiles, among others. The framework can be used to create a DoOR to the olfactome of another species as soon as enough data is available.

♦157 Kathrin Leupolz

Neuroanatomyofthearcherfish Mauthner-cell

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Most teleosts use their Mauthner (M)-cell-associated network to initiate a rapid C-type escape start. The M-cell is unique in its characteristics within the vertebrate central nervous system. It receives incoming sensory information and decides if a C-start should be triggered. Hence, there is a rigorous causal connection between the activity of a particular cell and the onset of a quantifiable behavioural reaction. Interestingly, archerfish use their M-cell-associated C-start network not only for driving escapes, but also to initiate their precisely tuned 'predictive start'. In this behavior hunting archerfish integrate - within a brief interval - information on the initial motion of a dislodged prey to release a C-start that turns the fish right to the later point of impact of their ballistically falling prey and pushes it off at a speed matched to the respective distance. Because inaccurate starts are costly, demands on not prematurely triggering a start are high. This makes the archerfish M-cell an interesting target for studying decision-making at the single cell level. As we show, the two archerfish M-cells are deeply buried inside the Medulla oblongata. Upon antidromic stimulation they produce an extracellular all-or-none negative field potential with its maximum in the axon hillock region of the M-cell. This field potential can be conveniently used to guide an electrode to the M-cell-soma and to fill the cell. Based on this, we present here, the first neuroanatomical characterisation of the archerfish M-cell.

♦158 Alja Lüdke

Prolonged odor information in the antennal lobe of *Drosophila melanogaster*

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In classical conditioning, animals learn to associate a neutral stimulus (CS) with a reinforcing stimulus (US). Associative learning is effective both when CS and US are overlapping in time (delay conditioning), or when there is a temporal gap between the stimuli (trace conditioning). In order to associate stimuli which are separated in time the sensory systems must keep a neural representation of the first stimulus after its termination (i.e. a stimulus trace). *Drosophila* and other insects are able to solve the olfactory trace conditioning task. However, the neural substrate of the underlying odor trace is not known. To address this issue, we investigated whether and how olfactory information is kept in the first olfactory brain area, the antennal lobe, of *Drosophila*. Using *in vivo* calcium imaging and the GAL4/UAS system, with OR83b/Orco and GH146 as driver lines, we selectively measured responses from two types of olfactory neurons: the olfactory receptor neurons and the projection

neurons, which pass odor information to higher brain areas. We analyzed the spatio-temporal response patterns of odor responses and post-odor responses in olfactory glomeruli, which are the functional units of the antennal lobe. For both neuron populations odors evoked specific response patterns of activated and inhibited glomeruli, which corresponded to the previously described combinatorial response patterns (see http://neuro.uni.kn/DoOR). After odor offset, the odor response patterns turned into prolonged post-odor response patterns of activated and inhibited glomeruli, which were dissimilar to the initial odor response patterns, but still odor specific. Variation of the stimulus length had only minor effects on the post-odor activity patterns. Taken together, these results show that there is a physiological odor trace in the antennal lobe of *Drosophila*. Whether this physiological trace is the substrate of the behavioral trace remains to be determined.

◆159 Shouwen Ma

Neural mechanism of auditory-vocal coupling in HVC for calling communication of Zebra finch (Taeniopygiaguttata)

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Zebra finches are social animals that communicate with each other using calls and songs. To facilitate the social communication a precise mechanism of auditory-vocal coupling is required. Previous studies have shown that the song communication involves a specific higher vocal pathway, but the neural mechanism of calling communication is at present poorly known. In this study, a radio neural telemetric system was used for simultaneous measurements of neural activity and vocalization in freely behaving zebra finches with social interaction. We report that the sensorimotor nucleus HVC of male zebra finches displays a rigid pattern of activity in calling production and auditory representation, whereas the auditory response to calls of conspecifics in HVC is regularly coupled. We further show a correlation between local field potential and the firing patterns, indicating that the auditory processing and vocal control are mediated through the local circuits in HVC. The neural mechanism of auditory-vocal coupling allows the animals to maintain the sensitivity to sensory input while vocalizing during social communication.

◆160 Joachim Mogdans

Adaptation to dipole stimuli in brainstem lateral line units

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The responses of brainstem lateral line units to constant-amplitude dipole stimuli are generally described as having a higher degree of adaptation than those of primary afferents. This, however, has never been shown quantitatively. Here, we recorded the responses of lateral line units in the brainstem medial octavolateralis nucleus (MON) to a dipole stimulus, i.e. a sinusoidally vibrating sphere (Ø 8 mm). Stimulus frequencies were 50 Hz and 100 Hz with peak-to-peak displacement amplitudes of

845 µm and 545 µm (50 Hz) and 255 µm (100 Hz). Stimulus duration was 1 s with on- and off-ramps of 100 ms.

In 45 out of 51 units, discharge rates increased during stimulus presentation (maximum evoked rates to 50 Hz 31.1 ± 17.1 spikes/s, average ongoing rates 8.5 ± 9.3 spikes/s). About half of the units (n=27, 53%) exhibited adapting responses to at least one of the two stimulus frequencies, i.e. discharge rate increased during the first 150-200 ms of the stimulus to a maximum (onset response) and thereafter decreased by at least 30% to a steady state response (range of response decrement 32-90%). The strength of adaptation and the number of adapting units increased with increasing stimulus frequency. Across 18 units stimulated with 50 Hz and 100 Hz sphere vibrations of comparable velocities (0.17 and 0.16 m/s, respectively), average response decrement was 29% to the 50 Hz and 47% to the 100 Hz stimulus. Seven units (37%) exhibited adaptation to the 50 Hz and twelve (67%) to the 100 Hz stimulus.

Our data are in fair agreement with those reported for primary afferent nerve fibers, suggesting that adaptation at the level of the MON may reflect mechanisms already implemented at the level of the lateral line periphery.

♦161 Daniel Münch

Mixture interactions in the periphery of the olfactory system - What does banana smell like?

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The olfactory world consists of thousands of odors, most of which convey important information for a given organism. Almost all odors appear as multi component mixtures, which makes it an even more demanding task for the olfactory system to differentiate between these stimuli.

Olfactory sensory neurons (OSN) have response profiles generated by the receptors they express. Different OSNs have overlapping profiles. Thus, a given odorant molecule will always activate a set of OSNs. As a consequence, not only will the different components of a mixture activate a pattern across OSNs, but even a single OSN is likely activated by several of these components. However, the components differ in their activation properties for a receptor and occur in varying concentrations. How will a cell respond to such a mixture? Will the responses of different ligands sum up or, if mixture interactions occur between the components, what kind of interactions are they? Will the highest concentrated compound dominate the response and what is the contribution of minor components?

To address these questions we chose the very well characterized *Drosophila melanogaster* receptor Or22a and an odor blend with high relevance for the fly: banana. *Drosophila melanogaster* is an ideal model for studying questions like these, as many genetic tools are available to manipulate cell properties. With its only ~ 50 olfactory receptor types expressed in the adult animal, the olfactory system is rather simple, though still able to encode thousands of odors.

We created an artificial banana blend from 15 of its major components and studied how they contribute to the mixture response by applying them individually, in binary mixtures or all together in their natural banana concentration. We started by studying a single receptor that responds vigorously to a presented banana: Or22a. We performed calcium imaging recordings on the flies antenna by selectively expressing the Ca2+ sensitive dye G-CaMP under the control of the Or22a promoter using the GAL4/UAS expression system.

We found that five out of 15 components elicited a significant response when presented alone at the concentration in which they naturally occur in banana. The response strength towards one component (isopentyl-acetate) alone did not differ from that to the full blend whereas the other four elicited significantly lower responses. Thus for Or22a the single odorant isopentyl-acetate is equivalent to the full bouquet, but how do the other components contribute?

Thus, even adding good ligands did not increase the isopentyl-acetate odor response, indicating that hypoadditive mixture effects where taking place. In order to analyze the underlying mechanism, we characterized the full dose-response curves for mixtures and components, and modeled different mixture-interaction scenarios. These models show that the observed mixture effects arise from syntopic interaction at a single interaction site with the receptor Or22a. While we cannot exclude intracellular interactions or multiple interaction sites, they are not necessary to explain the full extent of the effects that we observed. In addition, we found that syntopic interaction is ideally suited to ensure a stable response across a range of mixture concentration.

♦162 Manuel Nagel

Thermosensation in the carpenter ant Camponotusrufipes

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Ants have a distinct sense of the environmental temperature, and they show this amazing sensory ability by various fine-tuned thermo-guided behaviors, e.g. during brood-care behavior. Interestingly, thermal preferences of individuals are not fixed but depend on previous experience and time-of-day (circadian rhythmicity) as well as on their own pupal temperature during development (Weidenmüller et al. (2009) CurrBiol 19).

We are investigating the sensilla and associated thermo-sensitive neurons in the ants' antenna to address the following questions: Which of the thermo-sensitive neurons provide the necessary information for i) precise brood temperature assessment, ii) detection of minute differences of temperature and iii) measurement of ambient temperature over a wide range?

In this study, we identified two thermo-sensitive receptor neurons associated with the sensillum coelocapitulum in the carpenter ant Camponotus rufipes.

One neuron function as a warm-receptor (activity increases with increasing temperature) with a non-adapting tonic response and a working range of more than 10°C. This neuron continuously codes for mean environmental temperature, comparable to a thermometer (TM-neuron).

The co-localized second neuron function as a cold-receptor (activity decreases with increasing temperature) within a small temperature range that only covers the most prevailing brood-temperature of 28-32°C. Within this temperature range, the neuron is highly sensitive to differences in temperature. We propose that this neuron provides the ants with precise information about the broods' temperature, which ultimately leads to brood translocation at unfavorable conditions (thermal switch; TS-neuron).

Currently, we investigate the physiological properties of both thermo-sensitive neurons with respect to circadian rhythmicity and thermal experience.

♦163 Peter Bräunig

How locusts perceive cold feet

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Previous studies on the central projections of extero- and proprioreceptors of insect legs resulted in the notion that all afferent axons project into their segmental ganglion, they do not form projections into adjacent ganglia. Only the afferents of specific chordotonal organs that span the joint between thorax and coxa form collaterals that may ascend as far as the suboesophageal ganglion. Using Neurobiotin staining, we detected additional afferent axons in one of the major leg nerve branches (nerve 5B2) that ascend towards the brain where they form conspicuous terminals in a special neuropile region. An intensive search for the cells forming these projections resulted in the identification of special neurons that are located in the proximal tibia (1 neuron) and the second tarsal segment (2 neurons). Usually the cells are not visible when unstained because in most cases they are located within the leg nerve or its side branches. In electron microscopic images the cells look very similar to infrared receptors as described in certain beetles, but recordings from the tibial cell show that responds to drops in temperature. Additional stainings show that such cells are located in all legs, the maxillary palps, and the antennae. Thus locusts, and perhaps other insects, possess a system of thermoreceptors within the appendages that feed directly into brain circuits.

♦164 Anna Reifenrath

Neuropeptides in the Brain of Aedesaegypti - A Quantitative Analysis

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The yellow fever mosquito, Aedes aegypti, is the major vector of several arboviral diseases, e.g. dengue fever and yellow fever. The gonotrophic cycle of A. aegypti females consists of distinct behavioral and physiological phases, including host seeking, blood feeding and oviposition. These changes in behavior depend on changes in the processing of sensory information, especially the processing of olfactory information. A multitude of chemical signaling molecules modulates processing of odor information in the central nervous system, including the primary olfactory centers of insects, the antennal lobes (AL). The most occurring and diverse group of neuromodulators, in vertebrates and invertebrates, are the neuropeptides. In the present study we analyzed neuropeptides in the antennal lobes of female Ae. aegypti at different times during the gonotrophic cycle using direct MALDI-TOF mass spectrometric peptide profiling. For a quantitative analysis of changes in the concentration of specific neuropeptides we used isotope labeled peptides as internal standards.

♦165 Tina Reim

Octopamine and division of labor in honey bees

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Honey bees show a complex division of labor. Young bees perform tasks in the center of the hive. Approximately one week after emergence, many bees are nurse bees and provide the brood and the queen with nutrients, while two weeks later bees leave the hive to forage for pollen, nectar, water and propolis. Nurse bees and foragers not only differ in the tasks they perform, they also differ in their responsiveness for task-related sensory stimuli. Biogenic amines like octopamine can modulate the sensory responsiveness of honey bees. Octopamine, for example, increases responsiveness to gustatory and visual stimuli and induces precocious foraging. In addition, foragers have higher levels of octopamine in the whole brain than nurse bees.

The underlying mechanisms of division of labor with regard to biogenic amines and their receptors are not yet clear, but octopamine receptors are promising candidates for regulating division of labor by setting sensory response thresholds.

We studied the mRNA expression of all octopamine receptors in the brains of honey bees of different ages performing different social roles. Most receptors show a significantly lower expression in nurse bees and foragers compared to one-day-old bees but do not differ between foragers and nurse bees. Only Amoa1 mRNA is significantly stronger expressed in foragers than in nurse bees. These expression differences are due to a different receptor expression in the subesophageal ganglion and possibly other neuropiles. This makes AmOA1 a promising candidate for regulating the transition from hive bee to forager. This study is a starting point for investigating in detail how biogenic amines and their receptors regulate division of labor in honey bees.

♦166 Martin Strauch

ImageBee - A KNIME plugin for analysing calcium-imaging data from the honeybee antennal lobe

Authors: *Martin Strauch*[1], *C. Giovanni Galizia*[1]
Affiliation: [1]*Universität Konstanz, Neurobiologie*

Calcium-imaging with fluorescent dyes is an established technique for recording glomerular odor response patterns in the insect antennal lobe. Here we present ImageBee [1], a software for analysing calcium-imaging recordings from the honeybee antennal lobe.
ImageBee is available as a plugin for the modular data analysis platform KNIME (www.knime.org) that provides a user-friendly graphical interface for constructing signal processing and data analysis pipelines.
Based on the algorithm presented in [2], ImageBee contains the tools to automatically construct functional maps (segmentations) of the antennal lobe, to compute glomerular signals from imaging movies, and to construct denoised versions of the movies.
Preprocessing methods such as spatial and temporal filtering or motion correction are available, and the modular principle of KNIME allows for future extensions of the toolkit, also for application to imaging data from other insects.
ImageBee provides a solid foundation for data analysis in insect brain imaging and is available free of charge [1].

[1]http://tech.knime.org/imagebee-analysing-imaging-data-from-the-honeybee-brain
[2] Martin Strauch, Julia Rein, C. Giovanni Galizia: Signal extraction from movies of honeybee brain activity by convex analysis.

♦167 Johannes Strauß

Spatial arrangement of auditory receptors in Tettigoniidae: a comparative tracing study

Authors: *Johannes Strauß*[1], *Gerlind C. U. Lehmann*[2], *Arne W. Lehmann, Reinhard Lakes-Harlan*[1]
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The auditory organ of Tettigoniidae is located in the proleg tibia and consists of scolopidial sensilla organised in an array called crista acustica. This ear is a highly ordered, tonotopic sensory system: the tonotopy of the receptors is the correlation between the proximo-distal position of a receptor in the crista acustica on one hand, and the distinct characteristic frequency of maximum sensitivity for an individual receptor on the other hand. Detailed anatomical studies reported that the sensory neurons and their dendrites in the distal crista acustica may occur in a double row rather than in a strictly linear arrangement. With the physiological analysis of single receptors and the established concept of tonotopy, the crista acustica became depicted as a linear set of sensory elements. Here, the spatial arrangement of receptor cell bodies and dendrites is shown by retrograde tracing with cobalt chloride solution in six tettigoniid species. In these species, the distal receptor neurons are consistently arranged with double-rows of somata rather than a linear sequence. This arrangement of neurons is found for 30-50% of the overall auditory receptors. Occasionally, dendrites of distal receptors also alternate, or occur massed with no obvious ordering. A double row of receptors and their scolopales is probably more common among Tettigoniidae than previously appreciated. With respect to functional implications, the massed dendrites of distal cells may not allow for a clear frequency discrimination, but could imply similar tuning characteristics.

◆168 Philipp Tellers

Response Variability in Broadband Neurons of the Barn Owl Auditory Pathway

Authors: *Philipp Tellers*[1], *Kerstin Bülles*[1], *Hermann Wagner*[1]
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Barn owls use differences in the time of arrival between the two ears (ITDs) to localize sound sources in azimuth. At the early levels of the auditory pathway ITDs are processed in narrow band frequency channels. This processing leads to phase ambiguities. Phase ambiguities preclude the determination of the real sound source position and have therefore to be solved. The acoustic system accomplishes this by across-frequency integration in the external nucleus of the inferior colliculus (IC).

In 2006 Christianson and Pena (J Neurosci 26: 5948) hypothesized that the auditory system of the barn owl uses the step from nucleus laminaris (NL), where ITDs are detected, to the core of central nucleus of the IC (ICCc) for improving the ITD coding. Noise delay functions of ICCc neurons exhibited a lower variability and a higher peak-to-trough ratio than their NL pendants. We hypothesize that the highly accurate ITD coding is less important for the auditory system upstream of ICCc, resulting, for example in higher response variability. To test our hypothesis, we recorded extracellularly from single units in the external nucleus of the IC (ICx) and the auditory arcopallium (AAr), a forebrain nucleus. Preliminary data support our hypothesis: noise delay functions of ICx and AAr neurons are less stable over repetitions and exhibit lower peak-to-trough ratios compared to ICCc neurons.

◆169 Vincent van Meir

Electrophysiological correlates of vocal plasticity in singing canaries

Authors: *Vincent van Meir*[1], *Manfred Gahr*[1]
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Telemetric electrophysiological measurements in singing canaries can provide new insight on how the production of complex vocal sequences is achieved by the brain. The song behavior of canaries differs substantially from the main model species for this type of research: the zebra finch. Canaries produce long songs containing trills and long syllables with stable and variable spectral and temporal features. The stability of the song production can change in adulthood dependent on light cycle and hormone levels.

Using lightweight transmitters we recorded electrical activity in awake, freely moving animals for up to two weeks after the implantation of an electrode. We recorded mainly from HVC, a telencephalic region with a central role in the production and learning of song. We used short-day male canaries that produced syllables with different levels of stability and testosterone-treated female canaries that developed song over the course of the two weeks during which they were recorded. We found that the timing of the electrophysiological activity was highly correlated to the timing of the vocal output in both male and female canaries. During song development the variation in electrophysiological activity became more related to the variation in acoustic features as the songs became more stable. However, whereas the variation in acoustic features between syllables seems to change over time, the variation in electrophysiological activity between syllables remains the same.

♦170 Michiel Vellema

Experience-dependent recurrence of vocal motor patterns

Authors: *Michiel Vellema*[1], *Sabrina Bascones*[2], *Annemie van der Linden*[2], *Manfred Gahr*[1]

Affiliations: [1]*Max Planck Institute for Ornithology*; [2]*Bio-Imaging Lab, University of Antwerp*

The development of birdsong is dependent on the ability to precisely coordinate the respiratory system with the muscles of the vocal organ, the syrinx. Seasonally breeding birds such as the canary (*Serinus canaria*) annually go through a period in which they do not sing, and therefore the fine motor control necessary for producing the complex vocal patterns needs to be re-acquired each year.

To investigate the dynamic acquisition of vocal motor patterns and re-acquisition after a period of non-use, we recorded the complete vocal ontogeny of female canaries after repeated testosterone treatments. In parallel, anatomical changes to a song nucleus involved in vocal learning and production, area X of the basal ganglia, were repeatedly examined using Magnetic Resonance Imaging.

In our study we observed that female canaries re-acquire the exact same vocal patterns with identical temporal precision after recurring hormone-induced behavioral stimulation. After a second stimulation, these vocal patterns emerged much faster than after the first stimulation, indicating that songbirds can retain and reuse information from previously acquired motor skills to shape future motor behaviors. Area X volumes increased during song development, but did not retain its increased size after hormone down-regulation and the associated termination of song production. Thus hormone-induced restructuring of brain areas involved in vocal learning and production are not maintained between emergence, loss, and re-emergence of motor patterning, suggesting that the long-term storage of vocal motor patterns must be looked for outside the traditional song control system.

◆171 Hannah Wasser

Quantification of antennal afferent regeneration in the locust brain after nerve crush

Authors: *Hannah Wasser*[1]*, Michael Stern*[1]
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We study neuronal regeneration in the olfactory pathway of the locust (*Locusta migratoria*). Olfactory afferents are axotomized in adult locusts and 5th instar nymphs by crushing the base of one antenna, leaving the other antenna as an internal reference. We quantify the resulting degeneration and subsequent regeneration in the first olfactory processing center, the antennal lobe, by means of anatomical size measurements, quantitative immunofluorescence of cell surface markers, anterograde labeling, and intracellular recording.

In the antennal lobe of postembryonic locusts, the cell adhesion molecule Fasciclin I is exclusively expressed by olfactory receptor neurons. Thus, after degeneration of axotomized distal segments of sensory neurons, Fasciclin I staining vanished in the antennal lobe within two days following the deafferentation. The reappearance of Fasciclin I during the following days proved a valuable quantitative marker for the regeneration process. Olfactory receptor neurons of 5th instar nymphs regenerated faster than those of adults.

To describe the neuroanatomical changes during regeneration the ingrowing afferents were labeled anterogradely with neurobiotin through the scraped-off olfactory sensilla on individual antennal segments (annuli). Normally, fibers from individual annuli grow together as discrete bundles in the antennal nerve and innervate the antennal lobe in a conspicuous ring-shaped pattern. Such an ordered pattern of growth and innervation is not observed in regenerated fibers, despite their precise confinement to the antennal lobe.

Intracellular recording from olfactory interneurons in the antennal lobe revealed the first regenerated synaptic connections seven days after axotomy.

◆172 Georg Welzel

Direct analysis of activity-dependend changes in gap junction conductivity in the leech

Authors: *Georg Welzel*[1]*, Stefan Schuster*[1]
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It is well established, that gap junctional conductance can be affected by a variety of mechanisms. However, activity-dependent modifications, such as LTP, have been much less studied in electrical than in chemical synapses and have mostly been assayed in rather indirect ways. Here we directly measure the electric coupling between the two Retzius-cells of the leech *Hirudo medicinalis* by using a dual-cell voltage-clamp technique. We show that the prolonged depolarization of any one of the two cells causes a lasting increase in gap junction conductivity. These findings make the well-accessible electrical synapses of the leech an attractive model to study mechanisms of plasticity in electric synapses.

◆173 Andrea Wirmer

Neurons in the insect corpora allata

Authors: *Andrea Wirmer*[1], *Alexander Heni*[1], *Harald Wolf*[1]
Affiliation: [1]*Universität Ulm, Institut für Neurobiologie*

The insect corpora allata (CA) are the releasing sites of juvenile hormone, a key regulator of insect development and reproduction. They receive innervation by the pars intercerebralis/lateralis region of the brain and neurons in the subesophageal ganglion. Stainings against horseradish peroxidise (HRP), a neuronal marker in insects, revealed a new feature of the corpora allata. They contain HRP positive cells with long projections into the nervus corporis allati I (NCA I), connecting brain and CA. Electrical recordings from the NCA I show action potentials propagated from the CA toward the brain and demonstrated a yet unknown way of mutual communication between brain and CA.

◆174 Anne Wosnitza

Interleg Coordination in the Control of Walking Speed in Drosophila

Authors: *Anne Wosnitza*[1], *Till Bockemühl*[1], *Michael Dübbert*[1], *HenrikeScholz*[1], *Ansgar Büschges*[1]
Affiliation: [1]*University of Cologne*

Legged locomotion can be regarded as the most important behavior of terrestrial animals. It is assumed to have become highly optimized over the course of evolution and that the neural structures controlling locomotion reflect this process. Quadrupeds, for instance, use distinct and easily identifiable gaits and it has been shown that these are optimal with regard to metabolic cost.

In six-legged animals, i.e. insects, the situation is not as unambiguous. For various species of insects, tripod and tetrapod walking patterns have been described; however, it is still not clear if these are true gaits or if they are merely prominent patterns that are part of a speed-dependent continuum. Distinguishing between these alternatives has been difficult due to the poor dissociation of species, size, and weight in the literature.

Here, we have addressed this issue and investigated four strains of Drosophila (WT strains Berlin, Canton-S, and w1118, and mutant strain TbH). Individuals of these strains are of similar size and weight, but tend to walk at different speed ranges, thereby covering a broad speed spectrum, ranging from 1 up to 18 body lengths s-1 (BL s-1).

Our data suggest that Drosophila controls its walking speed almost exclusively via step frequency while keeping stride length constant. At high speeds we invariably found tripod coordination. This finding was also supported by a simple measure of tripod coordination strength (TCS) which increased with higher walking speeds. In contrast, at speeds below 5 BL s-1 walking patterns were more flexible and animals used tripod as well as tetrapod coordination; occasionally even wave gait was observed.

◆175 Lydia Zopf

Temperature and infrared detection in the blood sucking bug Rhodniusprolixus

Authors: *Lydia Zopf*[1], *Claudio R. Lazzari*[2], *Harald Tichy*[1]
Affiliation: [1]*Faculty of Life Science, University of Vienna, Department of Neurobiology, Austria*; [2]*IRBI, UMR 7261 CNRS – Université François Rabelais, Faculté des Sciences et Techniques; Parc Grandmont, Tours, France*

Triatomine bugs are obligate blood feeders and act as vectors of Chagas disease, a protzoan infection of man and other mammals in South America. They use different sensory cues to locate a warm blood host, including CO2, infrared (IR) radiation and odor stimuli. Lazzari and Nùñez (1989) and more recently Schmitz et al. (2000) have established that triatomine bugs sense infrared radiation and approach a thermal source in complete darkness guided solely by infrared radiation. McIver and Siemicki (1985) described by means of SEM and TEM techniques a type of sensillum on the bug's antenna that has structural features adapted for thermo- and hygroreception. The aim of the present study was to determine with electrophysiological techniques the modalities which stimulate the sensory receptor neurons associated with this sensillum type. We identified hygro- and thermoreceptive rceptor neurons, the latter of which responding to IR radiation as well as convective heat provided by an air stream flowing over the antenna. To elucidate the contribution of these receptor neurons during orientation to an infrared source we studied their response charateristics to temperature to temperature changes and infrared stimulation.

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◆175a Susanne Seltmann

Hormone dependent electrical properties in freely behaving zebra finches

Authors: *Susanne Seltmann*[1], *Lisa Trost*[1], *Andries ter Maat*[1], *Sebastien Derégnaucourt*[2], *Manfred Gahr*[1]
Affiliation: [1]*Department for Behavioral Neurobiology, Max Planck Institute for Ornithology, Seewiesen*; [2]*Laboratory of Compared Ethology and Cognition, Université Paris Ouest Nanterre La Défense*

Song learning in songbirds has striking parallels to speech acquisition in humans. Both songbirds and humans must hear adult tutors as well as their own vocal production during a distinct learning period. A specific brain area is responsible for language / song learning and memory consolidation, the speech centre in humans and its equivalent in birds, the so called song control system. To get a closer view on those neural mechanisms we have chosen the Zebra finch as a role model for perceptual and sensorimotor learning in birds.

Melatonin is well known for its role in entrainment of circadian rhythms but Melatonin receptors are also expressed in the song control system, a structure without known clock function.

In the current project we are looking at the influence of this hormone on the regular spiking patterns occurring in RA, an important nucleus of the song control system, involved in learning as well as in producing song. Additionally we investigate the influence of Melatonin on the temporal pattern of birdsong itself.
Telemetric devices developed in our institute are used to gain insight into both temporal patterns of song and learning related brain activity. So far our work shows changes due to Melatonin treatment in the temporal pattern of song and its neuronal correlates. Melatonin seems to have the same effect on song and neuronal activity in RA as sleep.

14. Physiology TALKS

Saturday, September 22, 2012

Invited speaker 1: Chair – Thorsten Burmester A 701 / 12:00

Miriam Götting (Hamburg)
Stress tolerance in fish and the role of globins
Author: Miriam Götting
Affiliation: [1] *Biocenter Grindel and Zoological Museum, University of Hamburg*

Aquatic ecosystems experience daily and seasonal changes of abiotic and biotic variables. Physiological adaptation to a changing environment is an essential feature of aquatic organisms. Most of the threats to aquatic ecosystems (e.g., eutrophication, pollution, global warming) affect the level of dissolved oxygen and induce hypoxic periods of variable lengths.
In the first part of this talk, I will present data from our studies investigating the mechanisms of hypoxia tolerance in the three-spined stickleback (*Gasterosteus aculeatus L.*). Just as critical as the need to survive periods of oxygen limitation is the ability to cope with subsequent rapid restorage of tissue oxygen levels (reoxygenation). We anticipated that adaptive molecular responses to oxygen limitation and reoxygenation might occur in pathways related to energy metabolism, ROS neutralization and redox balance. The responses were studied on the transcript and protein level in different stickleback tissues. In particular, we were interested in the specific role of globins in the acclimatization to adverse environmental conditions.
The second part of the talk will focus on the function of globins. Globins are small heme-proteins that reversibly bind oxygen, and are instrumental in various aspects of oxygen supply and hypoxia adaptation. Our in vitro studies mainly focused on globin X which is restricted to lower vertebrates and is acylated at its N-terminal extension. This addition of fatty acids results in an association with the cellular membranes,

suggesting a specific role in signalling processes or protection to oxidative stress. Another so far unrecognized globin function is also conceivable for globin X.

Chair: Wolf-Michael Weber

☐107 Annika Herwig A 704 / 14:00

The role of hypothalamic thyroid hormones in energy balance

Authors: *Annika Herwig*[1], *Anita Boelen*[1], *Perry Barrett*[1]

Affiliation: [1]*University of Hamburg*

In seasonal mammals it has been demonstrated that thyroid hormone (T3) availability to the hypothalamus is crucial for controlling centres of long-term energy balance in the brain. The aim of this study was to identify novel mechanisms regulated by T3 that underpin energy balance and appetite in both, seasonal and non-seasonal species. We chemically thyroidectomised a cohort of Sprague Dawley rats that was then divided in two groups. At the end of the experiment one group of the cohort received a single T3, the other group a single saline injection. A third group of animals was run without treatment as a naive control group. We have characterized physiological parameters and the expression of known relevant genes in the brain of this model, and assessed changes in hypothalamic gene expression using microarrays. The animals showed marked differences in food intake, body weight, body composition, serum fatty acid and thyroid hormone levels. In situ hybridisation revealed distinct changes in crucial components of the hypothalamic thyroid hormone system as well as in gene expression related to the regulation of food intake in the hypothalamus. Microarray analysis indicated pronounced changes of novel candidates that are potentially regulated by T3. Our experimental design provides a model to identify mechanisms of T3 actions in the brain and further studies will reveal the significance of candidate genes in the regulation of energy balance.

☐108 Ina Hermann A 704 / 14:15

The role of paxillin in alpha-hemolysin induced reorganisation of focal adhesions in human airway epithelial cells

Authors: *Ina Hermann*[1], *Susann Räth*[1], *Sabine Ziesemer*[1], *Jan-Peter Hildebrandt*[1]

Affiliation: [1]*Ernst Moritz Arndt University of Greifswald, Animal Physiology and Biochemistry*

Because of a thick mucus layer protecting the human airway epithelium against direct contact with bacteria, it is likely that the first interaction between inhaled Staphylococcus aureus and the airway epithelial cells is through soluble bacterial virulence factors. We could recently show that the staphylococcal alpha-hemolysin (Hla) induced the opening of paracellular gaps and changes in cell shape in confluent monolayers of immortalized human airway epithelial cells.

To investigate potential effects of Hla on the stability of cell-matrix-connections we used immune fluorescence and cLSM to study the structure, organisation and distribution of focal adhesions and actin stress fibres in 16HBE14o- cells in the absence or presence of 2.000 ng/ml recombinant Hla (rHla). We also examined the phosphorylation status and changes in subcellular localization of the focal adhesion component paxillin in 16HBE14o- cells under rHla-treatment by quantitative Western blotting.

rHla induced a loss of paxillin- and vinculin-positive focal adhesions in the lamellipodia and a disorganisation of cytosolic stress fibres within the cells resulting in changes in cell shape and reduction in cellular protrusions. These alterations coincided with a higher phosphorylation status of paxillin on Y31 and Y118, a decline in the amount of membrane-bound paxillin, and translocation of paxillin from the membrane to the cytosol.

Our results indicate that rHla alters the signalling in focal adhesions, promotes the disassembly of mature focal adhesions and prevents stabilization of native focal contacts and formation of actin stress fibres. We conclude that such changes may impair epithelial barrier functions in airways in early stages of an infection with Staphylococcus aureus.

☐109 Ulrich Hoeger A 704 / 14:30

Evidence for a common precursor in two Crustacean high density lipoproteins, the large discoidal lipoprotein and the beta-glucan binding protein

Authors: *Steffi Stieb[1], Ziv Roth[2], Isam Khalaila[2], Amir Sagi[2], Ulrich Hoeger[1]*
Affiliations: *[1]Institute of Zoology, Johannes Gutenberg University, Mainz; [2] Dept of Life Sciences and the National Institute for Biotechnology in the Negev, Ben Gurion University, Beer Sheva, Israel*

The large discoidal lipoprotein (dLP) of is a novel Crustacean hemolymph lipoprotein only known from the decapod *Astacus leptodactylus* so far. Its gene and amino acid sequence and its relationship with other lipoproteins are not yet known. To investigate its molecular structure, MALDI-TOF measurements were carried out after in gel digestion of the two apoproteins of the dLp. Eighteen peptides were found matching sequences in another lipoprotein, the high density lipoprotein/?-glucan binding protein (HDL/BGBP). These peptide fragments were located adjacent to two putative furin cleavage sites enclosing a 1108 amino acid region of the HDL/BGBP sequence with a calculated MW of 126 kDa. Four peptide fragments specific for the large (280 kDa) dLp subunit were located on N-terminal side before the first furin cleavage site, while 11 peptides specific for the small (75 kDa) subunit were found C-terminal after the second cleavage site. No matches were found in the sequence between the two furin sites. Our results thus suggest that the sequence of the HDL/BGBP is also part of the dLP sequence and that both lipoproteins originate from a common precursor which is cleaved into the BGBP and the two apoproteins of the dLp, respectively, before lipoprotein assembly. However, the mature HDL/BGBP has a lower molecular weight (105 kDa) than the apoprotein enclosed by the furin cleavage sites suggesting its further processing before secretion in the hemolymph.

The presence of the same furin cleavage sites in the homologous HDL/BGBP sequences of other decapods suggests a wider occurrence of dLP like proteins in crustaceans.

☐110 Andreas Ziegler A 704 / 14:45

The effect of saline and organic matrix proteins from *Porcellio scaber* sternal deposits on CaCO3 precipitation under near physiological conditions

Authors: *Andreas Ziegler*[1]*, Sigrid Hennig*[1]*, Helge-Otto Fabritius*[1]*, Sabine Hild*[1]
Affiliation: [1]*Central Facility for Electron Microscopy, University of Ulm, Germany*

The terrestrial isopod *Porcellio scaber* stores CaCO3 within a confined ecdysial space in the first four anterior sternites. The deposits consist mainly of amorphous calcium carbonate (ACC), little amorphous calcium phosphate and an organic matrix. In order to study precipitation of CaCO3 under near physiological conditions we measured the cationic composition and the pH in the ecdysial fluid of the sternites using ion selective microelectrodes and isolated the soluble protein fraction of the organic matrix from the deposits. We designed a near physiological, but phosphate-free saline and developed a method that allows precipitation of CaCO3 in volumes as small as 20 µl. Structure, mineral phase and composition of the precipitates were analysed by FE-SEM, Raman spectroscopy and EDX. Within near physiological saline the total soluble protein fraction leads to precipitation of ACC. Agglomerations of ACC granules and the dried soluble fraction of the organic matrix are virtually devoid of organic phosphates. The agglomerations mimic several aspects in the architecture of native sternal deposits and were stable for at least one month. The saline alone has no effect on the crystal phase but leads to changes in calcite crystal morphology due to the effects of Mg2+. BSA that was used as a control protein has virtually no effect on the mineral phase, but in the presence of Mg2+, severe effects on the surface structure of calcite crystals, suggesting a combined effect of BSA and Mg2+ on crystal growth.

☐111 Saskia Lieberei A 704 / 15:00

Identification of carriers for the uptake of plant secondary substances in *Longitarsus jacobaeae* (Coleoptera, Chrysomelidae)

Authors: *Saskia Lieberei*[1]*, Susanne Dobler*[1]
Affiliation: [1]*Biozentrum Grindel, Molekulare Evolutionsbiologie, Universität Hamburg*

Several host plant adapted herbivorous insects are able to use toxic plant secondary compounds for their own chemical defense and protection. These insects sequester the plant defense compounds and store them in their own tissue. Accumulation of these substances guarantees a powerful deterrent against their predators.

Several species of leaf beetles (Chrysomelidae) use this defense strategy. The species *Longitarsus jacobaeae* e.g. accumulates the pyrrolizidin alkaloid (PA) senecionin. In non-adapted organisms the non toxic N-oxides are transferred to the highly toxic tertiary PAs under the mildly reducing conditions in the intestine. *L. jacobaeae*, in contrast, takes up the N-oxide from the plant tissue and transfers it unchanged into the hemolymph (Narberhaus et al. 2004). Obviously this transport of the labile N-oxide is realized by highly efficient carriers. We assume that carriers of the family organic anion transporting polypeptides (Oatps) are highly likely candidates for this process. In addition, it could be proven by PCR, that there is a tissue specific distribution of Oatps, especially in the intestine. In order to further investigate our hypothesis, Oatp-genes have been isolated from cDNA of *L. jacobaeae* and have been

cloned into a RNA producing vector for expression in Xenopus-oocytes. Transport studies with selected substances will be carried out to characterize their substrate spectrum. Feeding experiments of *L. jacobaeae* with several potentially harmful substances revealed so far, that these substances were transferred into the hemolymph without causing damage to the organisms.

Invited speaker 2: Chair – Ulrich Hoeger A 704 / 11:00

Alexander Tups (Marburg)

The interplay of leptin, insulin and nutrients in the hypothalamus: A key to understand the pathophysiology of type II diabetes?

Author: *Alexander Tups*[1]
Affiliation: [1]*Department of Animal Physiology, Faculty of Biology, Philipps University Marburg*

More than ten years ago it was discovered that the brain plays a pivotal role in the regulation of whole body glucose homeostasis. The adiposity signals leptin and insulin mediate glucose homeostasis through hypothalamic signal transduction mechanisms. We and others could show that not the body fat per se contributes to the pathogenesis of type II diabetes, rather leptin resistance, typically associated with obesity, appears to be one leading cause of this disease. Employing physiological animal models of leptin resistance such as the Djungarian hamster (*Phodopus sungorus*) or mice fed a high fat diet together with state of the art viral gene therapy, we identified that the WNT/β-catenin pathway, typically involved in tumorigenesis and embryogenesis, acts as a key regulator of glucose homeostasis via integrating the leptin and insulin signal in the hypothalamus. Hypothalamic inhibition of this pathway led to severe glucose intolerance and obesity in mice fed a high fat diet (HFD). Using leptin-deficient mice, we demonstrated that not hyper-leptinemia leads to diabetes, rather diet-induced hypothalamic inflammation disrupts the physiological feed-back to the leptin and insulin signal in the brain. Leptin deficient mice fed a high fat diet surprisingly developed central leptin resistance that was associated with extreme glucose intolerance. Pharmacological inhibition of hypothalamic inflammation reversed leptin resistance and improved glucose tolerance in these mice. Certain dietary flavonoids act as natural inhibitors of the hypothalamic inflammation pathway. Dietary intervention approaches and gene therapy might be an important tool to further understand and combat the patho-physiology of obesity and diabetes.

Chair: Jan-Peter Hildebrandt

☐113 Andreas Vilcinskas M 629 / 14:00

Epigenetic regulation of metamorphosis and immunity in insects

Author: *Andreas Vilcinskas*[1]
Affiliation: [1]*Institute of Phytopathology and Applied Zoology, Justus-Liebig-University of Giessen*

Using the greater wax moth *Galleria mellonella* and the red flour beetle *Tribolium castaneum* we explored the epigenetic reprogramming during metamorphosis and immune responses both at pre- and posttranscriptional level. The transfer of acetyl groups to histones by enzymes known as histone acetyltransferases (HATs) increases DNA accessibility and favors transcription, whereas the removal of these groups by histone deacetylases (HDACs) has the opposite effect. Several HATs and HDACs are regulated during metamorphosis in G. mellonella and we were able to delay metamorphosis by inhibiting HATs and accelerate it by inhibiting HDACs. We also found that the same approach could increase or reduce the survival of insects after wounding, and identified a number of modulated downstream genes suggesting that development and responses to wounding and pathogens are coregulated epigenetically. It therefore appears that the balance between histone acetylation and deacetylation in insects helps to control transcription during metamorphosis and in response to wounding and infection.

MicroRNAs are small non-coding RNAs mediating post-transcriptional regulation of gene expression in eukaryotes. Addressing their role in regulation of physiological adaptations to environmental stress in insects we selected Tribolium castaneum as a model. Differential expression of selected immunity and stress-related genes was quantified using real-time PCR and expression and induction of 455 mature arthropod miRNAs was determined using proprietary microarrays. We found that Tribolium exhibits both gender- and stressor-specific adjustment of immune gene and miRNA expression. Strikingly, we discovered that the number of stressor induced miRNAs in females is remarkably higher than in males (Freitak et al., 2012: Biology Letters, in press).

☐114 Christine Fink M 629 / 14:15

Microbial communities in the fruit fly's intestine - what we can learn about host-microbe interactions and the outcome of disturbing the homeostatic situation

Authors: *Christine Fink*[1]*, Fabian Staubach*[1]*, Sven Kuenzel*[1]*, John Baines*[1]*, Thomas Roeder*[1]
Affiliation: [1]*Zoophysiology II, CAU Kiel*

The intestinal epithelium of the fruit fly *Drosophila melanogaster* harbors many symbiotic microorganisms that are beneficial for the host. The bacterial community increases lifespan and overall fitness and supports e.g. the degradation of polysaccharides fatty acids. Disturbing the host microbe-interaction can lead to an increased incidence for epithelial disruption and the development of chronic inflammation. To check the role of microbial influence in the fly’s intestine we invented a model that allow studying the bacterial communities non-invasively. Thus, we used feces samples as sources for 454-sequencing based 16S rRNA phylotyping of bacterial communities as well as qPCR analyses of selected bacterial species. Using feces samples proved to be advantageous, because it is insensitive towards contamination by infection with Wolbachia and it is nob-invasive allowing for multiple probing of the same cohort of flies. We used these samples to investigate the influence of short periods of endogenous ROS production mediated via activation of the dual oxidase. For this, we ectopically expressed a so-called DREADD receptor (Designer Receptor exclusively activated by designer drugs) in enterocytes only, that induces Ca2+-signaling in response to drug administration. This increase in cytosolic Ca2+-levels is the physiological signal that activated reactive oxygen production. We could show that this defense response has a significant impact on the bacterial community in the intestine that is reversible.

☐115 Julia Hoffmann M 629 / 14:30

sir2 and foxo: mediating effects of dietary restriction in Drosophila?

Authors: *Julia Hoffmann, Thomas Roeder*
Affiliation: [1]*Zoophysiology, University of Kiel*

In the current aging research Sirtuins are controversely discussed to be key players in the mediation of the life span extending effects of caloric/dietary restriction. In their function as NADH-dependent histone deacetylases they provide a promising link between the metabolic state of a given cell and its transcriptional regulation. FOXO, a transcription factor responding to stress signals and insulin-like signalling was also shown to extend life span of flies. Since both molecules integrate information of the cell energy status into the regulation of gene expression they are reasonable candidates to mediate effects of dietary restriction on life span.

We over-expressed both candidate genes in the adult fat body with the help of the GeneSwitch GAL4/UAS System and subjected wild type animals to dietary restriction. We analyzed the fat body transcriptome of the three groups using microarray technology. Also we performed life span experiments with flies over-expressing sir2 in the fat body.

We show for the first time that tissue-specific overexpression of sir2 in the fat body elongates life span of males and females. Furthermore we compared differentially expressed genes induced by either dietary restriction or sir2 or foxo over-expression. We found large intersections in the gene sets regulated by sir2 and foxo. But surprisingly very few genes are shared by gene sets regulated by dietary restriction and sir2 or foxo indicating that both genes do not play a major role in mediating the effect.

☐116 Sebastian Martin M 629 / 14:45

Evolution of the matrixin family of metalloproteinases in arthropods

Authors: *Sebastian Martin[1], Lars Hering[2], Georg Mayer[2], Lars Podsiadlowski[1]*
Affiliations: [1]*Inst. Evolutionary Biology & Ecology, Universität Bonn*; [2]*Inst. Biologie, Universität Leipzig*

During ontogeny of vertebrates, matrix metalloproteinases (MMPs) mainly serve for reconstructing the extacellular matrix (ECM) and tissue remodeling, but additional functions in signaling pathways have also been demonstrated. In contrast to vertebrates, only little is known about these ECM-modifying enzymes in arthropods. To provide insights into the evolution of MMP-containing matrixin domains in this group, we analyzed and compared the genomic and transcriptomic datasets from various arthropods and closely related outgroups. Our phylogenetic analysis of the matrixin domain alignments revealed three major clades in most arthropod species studied, corresponding to three MMP genes. However, in some species, including Drosophila melanogaster, we found only two genes whereas additional candidates are present e.g. in water fleas and in mosquitoes species, indicating independent duplication events. An outgroup comparison with nematodes, tardigrades, and onychophorans suggests that the unique set of MMP genes found in arthropods evolved from a single ancestral gene in the arthropod lineage.

☐117 Anne-Katrin Rohlfing M629 / 15:00

Do Worms pee? New insights into the *C. elegans* excretory system

Authors: *Anne-Katrin Rohlfing[1]*
Affliation: [1]*University of Potsdam*

Sydney Brenner established C. elegans as a model organism in the early 60th. Since these early studies the excretory system of *C. elegans* has been analysed morphologically. It consists of a two-branched excretory canal cell which extends throughout the entire body. It is connected to a duct, a pore cell and two associated gland cells. The system has been used, e.g. as a model for intracellular tube formation. Genetic studies revealed an important function of the gland cells in normal molting. It has been shown that laser ablation of the duct cell leads to fluid accumulation within the excretory cell canal. But so far a real physiological characterisation is lacking and fluid secretion has never been observed.

In his natural environment of rotting fruits, *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 found evidence that the excretory system is involved in coping with high as well as low salt concentrations in the environment. Aquaporines of the excretory cell and the intestine are regulated according to osmotically changes in the surrounding environment. These aquaporines are needed to regulate the water and glycerol accumulation of the animals under stress conditions.

☐118 Bostjan Vihar M 629 / 15:15

The subharenal (under sand) respiration of the Sandfish

Authors: *Bostjan Vihar[1], Werner Baumgartner[1]*
Affiliation: *[1]RWTH Aachen*

The Sandfish (Scincus scincus), a sand dwelling lizard living in the deserts of north Africa and Arabia was given some attention in recent years, due to its sand gliding ability, the underlying mechanisms and their usefulness in technology. A subharenal (below sand) way of life, however has more intriguing features. Possible air unavailability and small but sharp sand particles make submerged breathing one of them. Morphological and physiological assets of the Sandfishs respiratory system were investigated, like lung and tidal volumes and the ventilation patterns, the anatomy and histology of the nasal cavity, but also sand properties of the Sandfishs habitat, like porosity, diffusion and airflow resistance. A finite volume method was developed for simulating a breathing Sandfish under the sand and the sufficiency of diffusion as the only oxygen transport mechanism. The nasal cavity was also reconstructed and experiments for sand filtration due only to its form were done and compared to a simple tube of the same size. The lung as well as tidal volumes in the Sandfish are very small, in fact they are up to 15 fold smaller than lizards of similar size, living in a moderate climate. The ventilation is triphasic and similar to other lizards, with some special features like an extremely rapid exhalation and with seemingly slightly different breathing modes for atmospheric and burried conditions. The nasal cavity has a complex anatomy with sharp turns and capilares. Histologicaly, the surface of the nasal cavity is mostly covered by a respiratory epithelium, localy rich with goblet cells and glands in the anterior part of the cavity, ending with a keratinised stratified squamous epithelium resembling that of the skin. This region is also surrounded by an erectile cavernous tissue, that can alter the diameter of the nasal cavity when filled with blood. The simulations have shown, that diffusion is sufficient in providing the needed oxygen for a low consuming animal like the sandfish. The anatomy of the replica, was somewhat different different, than suggested by the histological experiments, therefore the filtrating properties, based on the replica alone are probably not realistic. Also, the upper respiratory system of lizards is anatomicaly very variable even between animals living in similar conditions, therefore it is hard to make assumptions concerning the functionality of a feature, characteristic only for the Sandfish. Since oxygen availability below sand is not a limiting factor, small lung volumes and low metabolic rates however also result in reduced water loss which is vital in xerix envoirments, especially if the only source of water is animalic food, as is the case for the Sandfish.

Sunday, September 23, 2012

Chair: Andreas Vilcinskas

☐119 Thorsten Burmester A 704 / 16:00

The coelacanth is a 'globin fossil': Conservation of globin genes in Latimeria chalumnae and reconstruction of the evolution of the vertebrate globin family

Authors: *Thorsten Burmester*[1]*, Kim Schwarze*[1]

Affiliation: [1]*University of Hamburg*

The (hemo-)globins are among the best-investigated proteins in biomedical sciences. These small heme-proteins play an important role in oxygen supply, but may also have other functions. In addition to hemoglobin and myoglobin, six other vertebrate globin types have been identified in recent years: neuroglobin, cytoglobin, globin E, globin X, globin Y, and androglobin. Analyses of the genome of the living fossil" Latimeria chalumnae show that the coelacanth is the only known vertebrate that includes all eight globin types. Thus, Latimeria can also be considered as a "globin fossil". Analyses of gene synteny and phylogenetic reconstructions allow us to trace the evolution and the functional changes of the vertebrate globin family. Neuroglobin and globin X split from the other globin types already before the separation of Protostomia and Deuterostomia. The cytoglobins, which are unlikely to be involved in O2 supply, form the earliest globin branch within the jawed vertebrates (Gnathostomata), but do not group with the agnathan hemoglobins, as it has been proposed before. There is evidence from phylogenetic reconstructions and gene synteny that the eye-specific globin E and muscle-specific myoglobin constitute a common clade, suggesting a similar role in intracellular O2 supply. Latimeria possesses two ?- and two ?- hemoglobin chains, of which one ?-chain emerged already before the divergence of Actinopterygii and Sarcopterygii, but has only been retained in the coelacanth. Notably, the embryonic hemoglobin ?-chains of gnathostomes form a common clade, while the embryonic ?-chains display a clade-specific evolution. Globin Y is associated with the hemoglobin gene cluster, but its phylogenetic position is not resolved. Our analyses show an early divergence of distinct globin types in the vertebrate evolution before the emergence of tetrapods. The subsequent loss of globins in certain taxa may be associated with changes in the oxygen-dependent metabolism. "

☐120 Kristin Tietje A 704 / 16:15

Evidence of multidrug resistance transporter (MDR) and multidrug resistance-associated protein (MRP) in the marine platyhelminth Macrostomum lignano investigated using fluorescent dyes

Authors: *Kristin Tietje*[1]*, Ulf Bickmeyer*[1]

Affiliation: [1]*University of Oldenburg*

The marine platyhelminth *Macrostomum lignano* may become a transparent model species for physiological experimentation using fluorescence microscopy. We applied a 2-photon Leica SP5 for gentle optical measurements in this transparent animal. The superfamily of the ABC transporters plays a major role in the transport of drugs and drug conjugates. Homologues of the mammalian multidrug resistance protein (MDR), transporting hydrophobic compounds, and the multidrug resistance-associated protein (MRP), transporting organic anionic conjugates as well as amphiphillic organic anions, have been described in a wide variety of organisms. To determine the presence of MDR and MRP in *M. lignano*, individuals were exposed to three potential substrates of the drug- transporters: Fluo-3 AM and Fura-2 AM, both are calcium indicators, as well Calcein AM, a fluorescent dye indicating cell viability. In the presence of Verapamil, an MDR inhibitor, the fluorescence signal of Fluo-3 AM, Fura-2 AM and Calcein am increased significantly in the worms s tissues. After inhibiting the MRP with MK571 we observed a significant increase in fluorescence intensity of all three dyes. Also with Probenecid, another MRP inhibitor, we could enhance the fluorescence signal of Fura-2 AM and Calcein AM. Contrary, inhibition of MDR and MRP transporters did not increase the cellular fluorescence of Rhodamine B and other dyes, which are no substrates of these drug transporters. These results suggest that the flatworms express functional homologues of the mammalian MRP and MDR transporters shown by pharmacological tools.

☐121 Sabine Schleicher A 704 / 16:30

Ca2+-dependent outward currents in identified olfactory neurons of the cockroach antennal lobe

Authors: *Sabine Schleicher*[1]*, (Cathleen Rotte, Ben Warren, Andreas Klein, Viktor Bardos, Peter Kloppenburg)*
Affiliation: [1]*Universität zu Köln*

Local interneurons (LNs) mediate complex inhibitory and excitatory interactions between the glomerular pathways, ultimately restructuring the olfactory information in the antennal lobe and shaping the tuning profile of projection neurons. In *Periplaneta americana*, we found three types of LNs with fundamentally different intrinsic firing properties, implying that these neurons serve distinct functions in the olfactory system. Type I LNs fire Na+-driven action potentials in response to odour stimulation. Type II LNs lack voltage dependent transient Na+ currents and accordingly could not trigger synaptic release by action potentials. By their morphology and physiological properties, we further differentiated two subtypes of non-spiking LNs, namely LN IIa and LN IIb. Considering that the electrophysiological properties are determined by cell type specific ion channel composition, our long term goal is to elucidate the distinct sets of ionic currents of each cell type. Recent studies revealed that in the non-spiking LN II, consistent with graded transmitter release, the voltage dependence for activation of ICa was shifted to more hyperpolarized membrane potentials. Here we have started to characterize Ca2+-dependent potassium currents (IKCa). All antennal lobe neurons investigated so far possess IKCa as shown by its Cd2+-sensitivity. IKCa in different antennal lobe neuron subtypes had differential Ca2+-dependence. In order to pharmacologically dissect the different currents, we investigated their sensitivity to specific toxins. Currently we are studying the role of IKCa in firing properties of projection neurons and LN I.

☐122 Gunnar Broehan A 704 / 16:45

Functional Analysis of the ATP-binding Cassette (ABC) Transporter Gene Family of Tribolium castaneum

Authors: *Gunnar Broehan*[1]*, Tobias Kröger*[1]*, Marcé Lorenzen*[2]*, Hans Merzendorfer*[1]
Affiliation: [1]*University of Osnabrück*; [2]*North Carolina State University*

The ATP-binding cassette (ABC) transporters belong to a large superfamily of proteins that have important physiological functions in all living animals. Most of them are integral membrane proteins that transport a broad spectrum of substrates across lipid membranes. In insects, ABC transporters raised special interest due to their role in insecticide resistance. We have identified 73 genes in the genome of the red flour beetle, *Tribolium castaneum*, which group into eight different subfamilies (ABCA-H). The gene family in *T. castaneum* is significantly larger than reported for insects belonging to other taxonomic groups. Phylogenetic analysis revealed that this high number of genes is due to gene expansion in one clade of subfamily ABCC. We further performed RNA interference (RNAi) screening to study the function of ABC transporters during the development of *T. castaneum*. In seven cases, injection of double-stranded RNA (dsRNA) into larvae caused developmental phenotypes, which included eye pigmentation defects, abnormal cuticle formation, egg laying and hatching defects, and lethality due to abortive molting and desiccation. Some of the ABC transporters we studied in closer detail, to examine their physiological role in lipid, ecdysteroid and transport of eye pigment precursor. The results from our study provide new insights into the physiological function of some ABC transporters in *T. castaneum*, which may help to establish new target sites for insect control.

15. Physiology POSTERS

♦176 Victoria Diedrich

Spring fever in Djungarian hamsters is not triggered by the uptake of 6-Methoxy-2-benzoxazolinone

Authors: *Victoria Diedrich*[1]*, Frank Scherbarth*[1]*, Susanne Jähnig*[1]*, Sabine Kastens*[1]*,
Stephan Steinlechner*[1]
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Seasonal breeding is an important adaptational trait in annually changing environments. The most important external cue enabling an accurate prediction of the beginning of the reproductive season in spring is the annual cycle of day length. However, other factors may also serve as predictors for favourable breeding conditions. The secondary plant metabolite 6-Methoxy-2-benzoxazolinone (6-MBOA), occurring in newly growing plant parts, was found to stimulate gonadal growth and to induce spring fever in several rodent species. In order to investigate the potential

influence of 6-MBOA on the reproductive system of Djungarian hamsters (*Phodopus sungorus*), several experiments have been conducted. We first examined whether 6-MBOA could counteract the delay in puberty seen in hamsters exposed to a short photoperiod soon after birth. The development of testes (palpation) and ovaries (vaginal smears) as well as final gonadal weights were examined as indicators for reproductive competence, however, no influence of 6-MBOA was found. Neither different dosages and routes of application nor variations of the treatment time showed an effect of 6-MBOA. The assumption that the photoperiodic signal possibly overruled the effect of 6-MBOA was tested by treating photorefractory male and female hamsters. Again, no effect of 6-MBOA was found and we conclude that Djungarian hamsters do not rely on secondary plant metabolites, at least not on 6-MBOA, to time their reproductive activity.

♦177 Miriam Götting

Protein expression under changing oxygen availability in three-spined stickleback

Authors: Miriam Götting[1], Jessica Tiedke[1], Julia Chuttke[1], Thorsten Burmester[1], Christine Vogel[1]

Affiliation: [1]*University of Hamburg, Biocenter Grindel and Zoological Museum*

Hypoxia is an increasing threat in aquatic ecosystems and an important stressor in the environment of fish. Acute and chronic hypoxia is caused by natural and anthropogenic factors, such as eutrophication, climate- and season-dependent increase of water temperature and pollution. Organisms living in aquatic environments face changes in oxygen availability periodically, and they must continuously adjust their behavioural and physiological responses to these variations. At the cellular level, mRNA and protein expression as well as enzyme activities are modified accordingly. In particular, during the restoration of normal oxygen levels in tissues, there is an increase in the production of reactive oxygen species (ROS), which are main effectors of cellular damage (e.g. through lipid peroxidation).

We analysed the metabolic consequences of changes in oxygen availability in brain, gill and liver of the three-spined stickleback *Gasterosteus aculeatus L. by* measuring the activities of key enzymes from energy production pathways. In addition, we estimated ROS production, the activities of antioxidant enzymes, and the level of lipid peroxidation in these tissues. Furthermore, we estimated global protein expression changes through 2D-PAGE analysis, and quantified expression changes in several hundreds of proteins via nano-LC tandem mass spectrometry.

♦178 Wencke Reiher

Peptidomics of the agriculturally damaging larval stage of the cabbage root fly *Delia radicum*

Authors: *Judith Zoephel[1], Wencke Reiher[1], Karl-Heinz Rexer[1], Jörg Kahnt[1], Christian Wegener[1]*

Affiliation: [1]*Dept. Neurobiology and Genetics, Biocenter, University of Würzburg*

The larvae of the cabbage root fly *Delia radicum* (Diptera: Anthomyiidae) induce serious damage to cultivated crops of the family Brassicaceae (e.g. rapeseed, cabbage and turnip) by feeding on the plant's roots. Due to this largely subterranean life of the larvae and the long emergence period of the adult flies, control of *D. radicum* with pesticides is quite ineffective.

We have chemically characterized numerous neuropeptides from the central nervous system and neurohemal organs, as well as regulatory peptides from enteroendocrine midgut cells of the *D. radicum* larva. By RP-HPLC and Maldi-TOF/TOF mass spectrometry, combined with chemical peptide labeling using 4-sulfophenyl isothiocyanate, 38 peptides could be identified, representing major insect peptide families: allatostatin A, allatostatin C, FMRFamide-like peptides, kinin, CAPA peptides, pyrokinins, sNPF, myosuppressin, corazonin, SIFamide, sulfakinins, tachykinins, NPLP1-peptides, adipokinetic hormone and CCHamide1. We also found a new peptide (Yamide) without characterised homologs in other insects.

The immunohistochemical analysis of the distribution of several classes of peptide-immunoreactive neurons and enteroendocrine cells in the larva revealed a very similar but not identical peptide distribution to *Drosophila melanogaster*.

Since peptides are regulators of many physiological and behavioural processes in insects such as molting or feeding, our data may provide a basis for the development of new specific peptide-based protection methods against the cabbage root fly and its larva.

◆179 Yvonne Knieper

mRNA-based 'gene transfer' as a new tool in CF therapy

Authors: *Yvonne Knieper*[1], *Nadine Bangel-Ruland*[1], *Barbara Leciejewski*[1], *Katja Sobczak*[1], *G. Leier*[1], *J.* Rosenecker[2], Wolf-*Michael Weber*[1]

Affiliation: [1]*Institute of Animal Physiology, WWU* Münster; [2]*Ludwig-Maximilians University, Department of Pediatrics, Munich*

Cystic Fibrosis (CF) is caused by a mutation of the cystic fibrosis transmembrane conductance regulator (CFTR), a Cl- channel in the apical membrane of airway epithelial cells. The most common mutation ?F508 leads to an impaired processing, following degradation of the protein, preventing the functional expression of the CFTR channel.

In this study we transfected human CF airway epithelial cells (CFBE41o-) with wild type (wt) CFTR-mRNA to investigate the insertion and functional expression of CFTR into the apical membrane. Therefore, we carried out Ussing chamber measurements to demonstrate the restoration of CFTR function and in parallel performed protein biochemical experiments to verify the increase of CFTR protein amount in the apical plasma membrane.

After transfection with wtCFTR-mRNA Ussing chamber experiments revealed an increased CFTR current following cAMP activation (74%) when compared to untransfected cells. This current appeared to be almost identical to the current of control cells expressing wtCFTR (16HBE14o-). Furthermore, the CFTR activation was sensitive to the specific Cl- channel blocker CFTRinh172, which decreased nearly 100% of the generated CFTR current and also reduced the electrophysiological parameters capacitance and conductance, significantly.

In addition, the protein biochemical approaches showed a markedly increased CFTR protein amount in the apical membrane. Using immunofluorescence techniques we demonstrated that the transfection of CFBE41o- cells using wtCFTR-mRNA led to an increase of CFTR expression by about 220% in comparison to untransfected CFBE41o-cells.

These data clearly indicate a successful restoration of impaired CFTR function in CF epithelia cells by transfection with wtCFTR-mRNA.

◆180 Bernhard Leonhard

The role of proline in honeybee flight

Authors: *Bernhard Leonhard[1], Claudia Weber[1], Sandra Riepl[1]*
Affiliation: [1]*Institut für Zoologie, Universität Graz*

Although carbohydrate is well established as the primary energy source in honeybee flight, we propose a secondary, intermediate pathway of energy transfer to the flight muscle mitochondria. Proline, whose concentration is high in tissue and haemolymph, is metabolized rapidly during flight. This is shown by a decrease in radioactive label after injecting 14C labeled proline into the abdomen. Yet, the overall concentration of proline shows less fluctuation- indicating a concomitant resynthesis of proline from carbohydrate, presumably in the fat- body. The rationale behind this proposed intermediary proline shuttle could be seen in the transfer of glycolytic capacities from the flight muscle to the fat body, thus enhancing mass based energy output of the former. In contrast to proline based energy pathways reported in other insect species, alanine appears to have no role in this mechanism in honeybees. Alanine is present at low concentration and no radioactive label could be observed to shift from proline to alanine during flight. Presumably the detoxifying role of transamination ammonia to pyruvate is not necessary in honeybees as the simultaneous resynthesis of proline does not lead to a significant rise in free ammonia.

◆181 Hans Merzendorfer

A Comprehensive Study on the Effects of the Insect Growth Regulator Diflubenzuron in the Model Beetle Species Tribolium castaneum

Authors: *Hans Merzendorfer[1], Marco Kelkenberg[1], Hee Shin Kim[2], Sujata S. Chaudhari[2], Meera Kumari[2], Charles A. Specht[3], Susan J. Brown[2], Subbaratnam Muthukrishnan[2]*
Affiliations: [1]*University of Osnabrück*; [2]*Kansas State University*; [3]*University of Massachusetts*

Benzoylurea such as diflubenzuron (DFB) are in wide use to control insect pests. To gain a broader insight into the mechanism underlying their insecticidal effects, we conducted a comprehensive study with the model beetle species and stored product pest Tribolium castaneum (red flour beetle) utilizing genomic and proteomic approaches. DFB was added to a wheat flour-based diet at various concentrations and fed to larvae and adults. We observed abortive molting, hatching defects and reduced chitin amounts in the larval cuticle, in the peritrophic matrix (PM) and in eggs. Electron microscopic examination of the larval cuticle revealed major structural changes and a loss of lamellate structure of the procuticle. We used a genomic tiling array to determine relative expression levels of about 11,000 genes predicted by the GLEAN algorithm. Genes encoding enzymes involved in chitin metabolism were unexpectedly unaffected, but several genes encoding cuticle proteins were affected. In addition, several genes presumably involved in detoxification pathways were up-regulated. A proteomic approach revealed that DFB affects the protein composition in larval midguts. To examine possible changes of the PM's barrier function in response to DFB, we established an in vivo assay based on FITC-dextrans. The results of this study demonstrate that DFB-treatment disrupts the barrier function of the PM in the midgut of T. castaneum. In summary, the red flour beetle turned out to be a good model organism for investigating the global effects of bioactive materials such as insect growth regulators and other insecticides.

♦182 Christian Müller

Amounts of salivary proteins transferred to a host during feeding of the medicinal leech *Hirudo sp*.

Authors: *Sarah Lemke*[1]*, Christian Müller*[1]*, Gabriele Uhl*[2]*, Jan-Peter Hildebrandt*[1]
Affiliations: [1]*Animal Physiology and Biochemistry, University of Greifswald*; [2]*General Zoology and Zoological Systematics, University of Greifswald*

Hirudo sp. is a hematophagous ectoparasite and uses vertebrates as hosts. Leeches secrete complex mixtures of salivary proteins and peptides into the mechanically inflicted wound to suppress defensive biochemical and cellular reactions in the host. Only a very limited number of salivary proteins and peptides have been identified and only one compound (hirudin) has been mechanistically characterized as yet, although leech therapy has been used for hundreds of years to treat many different ailments (Mory et al. 2000). We investigated distribution and structure of the unicellular salivary glands in leeches. We used Azan-stained serial sections (5 µm) of leech tissue from the anterior part of the body for 3D-modeling of internal leech tissues to determine individual volumes of gland cells and to extrapolate to the total number of cells present in one animal. Since we have previously observed that leeches empty their reservoir of salivary proteins almost completely during a blood meal (Hildebrandt & Lemke (2011) Naturwiss 98, 995 pp), we were able to assess the total amount of salivary material that is transferred to the host during feeding. This information will be used in combination with results from biochemical studies on the composition of the salivary gland content using gel-based analyses of the high molecular mass proteins and HPLC-analyses of the low molecular mass fraction to calculate maximum concentration ranges for the individual salivary compounds that may be reached in the host. Such knowledge is necessary to understand potential functions of individual salivary compounds in the host.

♦183 Ina Hermann

The role of paxillin in alpha-hemolysin induced reorganisation of focal adhesions in human airway epithelial cells

Authors: *Ina Hermann[1], Susann Räth[1], Sabine Ziesemer[1], Jan-Peter Hildebrandt[1]*
Affiliation: [1]*Ernst Moritz Arndt University of Greifswald, Animal Physiology and Biochemistry*

Because of a thick mucus layer protecting the human airway epithelium against direct contact with bacteria, it is likely that the first interaction between inhaled Staphylococcus aureus and the airway epithelial cells is through soluble bacterial virulence factors. We could recently show that the staphylococcal alpha-hemolysin (Hla) induced the opening of paracellular gaps and changes in cell shape in confluent monolayers of immortalized human airway epithelial cells.

To investigate potential effects of Hla on the stability of cell-matrix-connections we used immune fluorescence and cLSM to study the structure, organisation and distribution of focal adhesions and actin stress fibres in 16HBE14o- cells in the absence or presence of 2.000 ng/ml recombinant Hla (rHla). We also examined the phosphorylation status and changes in subcellular localization of the focal adhesion component paxillin in 16HBE14o- cells under rHla-treatment by quantitative Western blotting.

rHla induced a loss of paxillin- and vinculin-positive focal adhesions in the lamellipodia and a disorganisation of cytosolic stress fibres within the cells resulting in changes in cell shape and reduction in cellular protrusions. These alterations coincided with a higher phosphorylation status of paxillin on Y31 and Y118, a decline in the amount of membrane-bound paxillin, and translocation of paxillin from the membrane to the cytosol.

Our results indicate that rHla alters the signalling in focal adhesions, promotes the disassembly of mature focal adhesions and prevents stabilization of native focal contacts and formation of actin stress fibres. We conclude that such changes may impair epithelial barrier functions in airways in early stages of an infection with Staphylococcus aureus.

♦184 Anne-Katrin Rohlfing

Osmotic stress resistance and cuticle defects: two symptoms, one cause

Authors: *Anne-Katrin Rohlfing[1], Todd Lamitina[1]*
Affliation: [1]*University of Potsdam*

The strain osm-8(n1518) is a well defined example of osmotic stress resistant (osr) mutants, which exhibit a constitutive active osmotic stress response. A mutation in the mucin-like gene osm-8 disrupts osmoregulatory physiological processes and leads to a constant expression of the enzyme gpdh-1. GDPH-1 triggers the synthesis and accumulation of high amounts of the osmolyte glycerol within the hypodermis and intestine, as we were able to demonstrate before. The OSM-8 protein is expressed in the hypodermis and is most likely secreted into the extracellular matrix (ECM). In the ECM, OSM-8 is supposed to act as part of an osmosensory structure and to activate the osmotic stress response via the transmembrane protein PTR-23, similar to the osmosensory mucins Hkr1 and Msb2 in *S. cerevisiea*. However, there is evidence for a second function of osm-8 in cuticle formation. osm-8 expression peaks before each molt and before the final molt in developing *C. elegans*. This cyclic expression pattern correlates strongly with expression pattern seen in genes typically connected to molt, like dpy-7. Unlike in dpy strains the typical surface morphology with regular, cirumferential-oriented furrows and annuli was still visible by scanning electron microscopy, as well as are alae. However, the osm-8(n1518) cuticle appeared thinner and displayed an altered fine structure as determined by transmission electron microscopy. The normal *C. elegans* cuticle is composed of three layers: the cortical layer, middle layer with collagen strut and the basal layer. In osm-8(n1518) the basal layer was reduced to the thickness of wildtype cuticle and the struts appeared smaller and more electron dense. This phenotype was reversible to some extent by a heat shock within in the early L4 state in osm-8(n1518) strains carrying a heat-shock inducible osm-8(+) transgene. This treatment also fully reversed the strong osr phenotype of transgenic osm-8(n1518) animals back to a normal response to hyperosmotic environment. Whether there is a connection between the physiological and the morphological phenotypes of osm-8(n1518) or whether they are caused by two distinct functions of one protein has to be further investigated.

♦185 Daniel Rolke

Expression patterns of serotonin receptor subtypes in the honeybee Apis mellifera

Authors: *Daniel Rolke*[1]*, Markus Thamm*[1]*, Arnd Baumann*[1]*, Wolfgang Blenau*[1]
Affiliation: [1]*Institute for Biology and Biochemistry, University of Potsdam*

The biogenic amine serotonin (5-HT) controls and modulates a great variety of physiological and behavioral processes by interacting with various 5-HT receptor subtypes. The honeybee, *Apis mellifera*, is known to express at least four 5-HT receptor subtypes: Am5-HT1A, Am5-HT2?, Am5-HT2?, and Am5-HT7. Interestingly, Am5-HT2 receptors are expressed both as a full length transcript and as a truncated splice variant, as it is known for certain dopamine receptors in Caenorhabditis elegans and humans. To provide a basis for further investigations and to develop testable hypotheses, e.g. on the physiological and behavioral functions of 5-HT receptors, the tissue specific expression patterns of both Am5-HT2 receptors were investigated using quantitative real-time PCR. Both full length and truncated transcript variants of Am5-HT2? could be detected in all tissues tested. In case of Am5-HT2?, the presence of the full length transcript could be verified in all tissues except the head salivary gland. In the nervous system and in the hypopharyngeal gland the expression of the full length Am5-HT2? transcript was higher than that of the truncated version, whereas the opposite holds true for the Am5-HT2?.The hypopharyngeal gland showed considerably higher expression of Am5-HT2?-full length than any other tissue. This led us to the assumption, that the hypopharyngeal gland activity is modulated by serotonin.

◆186 Cristina Sánchez Gonzalez

ENaC Expression levels in CF and non-CF human airway epithelial cells can be modulated by dexamethason

Authors: *Christina Sánchez, Philipp Lemke , Katja Sobczak, Wolf-Michael Weber*
Affiliation: [1]*Institute of Animal Physiology, WWU Münster*

In cystic fibrosis (CF), the most common genetic disease in the Caucasian population, the mutation of the CFTR (cystic fibrosis transmembrane conductance regulator) implicate a defective Cl- secretion leading to Na+ hyperabsorption mediated by ENaC (epithelial sodium channel).

The disturbance of this membrane transport causes the severe symptoms of the CF. For the research on the molecular causes of this disease and the development of potential drugs and therapies, two established human epithelial cell lines could serve as model system: The CFBE41o- cells, homozygous for the CF mutation ?F508, and 16HBE14o-, acting as model for non-CF epithelia. In functional Ussing chamber analyses both cell lines show Cl- secretion representative for CF or non-CF cells. But they fail to show any amiloride-sensitive ENaC current and hence do not express the CF phenotype correctly. Thus, we tried to induce the functional ENaC expression by the use of the glucocorticoid Dexamethasone (Dex), which is known to have a positive effect on ENaC expression.

We analyzed the time and dose depended influence of Dex in functional Ussing chamber studies. Moreover, we performed Western Blot analyses to proof which ENaC subunit is responsible for this effect.

Thereby we could show that the application of Dex is able to increase the ENaC expression on the functional and, depended on the analyzed ENaC subunit, also on the protein level.

Therefore, we conclude that by the induction of the ENaC expression by Dex these cell lines could represent a good model for CF in the human airway epithelia.

◆187 Rosalie Morisset

Even a locked running wheel affects short-day acclimation in Djungarian hamsters

Authors: *Rosalie Morisset*[1]*, Frank Scherbarth*[1]*, Victoria Diedrich*[1]*, Stephan Steinlechner*[1]
Affiliation: [1]*Institute of Zoology, University of Veterinary Medicine Hannover*

We have previously shown that the photoperiod-driven changes in body and testes weight are affected by wheel-running activity in seasonal Djungarian hamsters (*Phodopus sungorus*). Voluntary exercise prevented the typical short day-induced reduction in body weight and, additionally, decelerated testis regression. Testicular recrudescence, on the other hand, was advanced compared to sedentary controls. In the present study, we not only used hamsters with and without access to a running wheel but also a third group with access to wheels that were locked during the first nine weeks of exposure to artificial short photoperiod. Interestingly, during short-day acclimation the animals of the latter group showed a significantly smaller reduction in body weight compared to sedentary controls. However, there was no difference in testes weights between the two groups after 3, 6 and 9 weeks in short photoperiod. Together with our previous findings, the present results suggest that 1) even locked running wheels might be considered as environmental enrichment that stimulates locomotor activity in captive Djungarian hamsters, 2) already small daily amounts of exercise seem to be sufficient to dampen short-day acclimation of body weight, 3) the gonadal axis needs higher amounts of regular exercise for stimulation resulting in pro-gonadal effects.

♦188 Jaim Sivan

Seasonal variations of the sexual segment of the kidney in the Saharan Sand Viper, Cerastes vipera (Viperidae)

Author: *Jaim Sivan*[1]
Affiliation: [1]*Achva Academic College, Shikmim, Israel*

The reptilian nephric sexual segment of the kidney (SSK) is lying between the distal and the collecting tubules of the nephron. The lumen of SSK tubules are surrounded by one or more layers of elongated cells containing cytoplasmic filaments and with other cytological characteristics of smooth muscle cells. The SSK cycle is related to the cyclic activity of the testes. The pre-terminal and terminal parts of the renal tubules (sexual segment) develop hypertrophy in males when spermatogenetic activity is observed. These segments are not developed in females and in immature males and its morphology varies from species to species. In *Cerastes vipera* testes, an increase in spermatogenesis occurs in spring and autumn with an inactive period in spermatozoa production intercalated in June until the beginning of July. In this study we examine the seasonal variations of the sexual segment of the kidney related to the cyclic activity of the testes in *Cerastes vipera*. For light microscopy observation of tubular diameter and cell height, semi-thick sections were prepared from samples embedded in epoxy resin material and stained with toluidine blue. As expected, hypertrophy in the SSK according to the spermatogenic cycle of the testes was found but they do not precisely coincide with testes values. We have found maximum hypertrophy in the SSK in the fall (October) and minimum hypertrophy in the summer (July) when testes values are at a maximum in spring and a minimum in June. We conclude that SSK secretion have possibly an important role in conservation of sperm mostly during periods of non-reproductive activity, during hibernation until copulation in spring (May).

Keywords: *Cerastes vipera*, reptilian nephric sexual segment of the kidney

♦189 Wolf-Michael Weber

Suppressing sodium hyperabsorption in cystic fibrosis using ENaC specific siRNA

Authors: *Wolf-Michael Weber*[1], *Katja Sobczak*[1], *Ken Clark*[2], *Steven Hughes*[2]
Affiliation: [1]*Institute of Animal Physiology, WWU Münster*; [2]*Therapeutic Oligonucleotide Discovery Performance Unit & Respiratory Therapeutic Area Unit, GlaxoSmithKline; Stevenage, United Kingdom*

The inherited disease cystic fibrosis is characterized by an ion transport imbalance, principally caused by a defective chloride secretion mediated by a mutated cystic fibrosis transmembrane conductance regulator (CFTR) and excessively increased Na+-absorption via the amiloride-sensitive epithelial Na+ channel (ENaC). To circumvent

one of these basic problems of CF we tried to reduce the Na+ hyperabsorpption mediated by ENaC using specific siRNA.
We used primary cultured human nasal epithelia cells that were transfected with siRNA aginst the most likely channel pore-forming ?-ENaC subunit. To prove the functional inhibition of ENaC expression we employed modified Ussing chambers. The Na+ absorption through ENaC was assessed as short-circuit current (ISC) and conductance (Gt) in presence of amiloride after siRNA transfection. Using this method we also analyzed the dose- and time-depended effect of the siRNA used. Furthermore, we carried out biochemical Western blot analyses with a specific ENaC antibody.
Statistical evaluation revealed that the siRNA is able to inhibit the functional ENaC by about 69% compared to the controls. We demonstrated that the siRNA is able to sustain this functional ENaC inhibition over a time period of 72h. Furthermore, we showed a 63% suppression of the ?-ENaC protein by Western blot analyses in siRNA transfected cells compared to the controls. From these data we conclude, that the ENaC specific siRNA could have a benefit for the CF related symptoms of the patients and therefore could turn out to be a potential therapy option.

16. *Zoolocial Systematics TALKS*

Saturday, September 22, 2012

Chair: Sven Bradler

☐125 Anja Golombek A 703 / 16:00

Interstitial annelid taxa: addressing their phylogeny with complete mitochondrial genomes using Next Generation Sequencing

Authors: *Anja Golombek[1], Günter Purschke[1], Sarah Tobergte[1], Torsten Struck[1]*
Affiliation: [1]*Zoological Research Museum Alexander Koenig (ZFMK),* Bonn; University of Osnabrueck, Department Biology/ Chemistry, Division Zoology, Osnabrueck

Several interstitial annelid taxa (i.e, *Dinophilidae, Diurodrilidae, Nerillidae, Polygordiidae, Protodrilidae, Protodriloidae,* and *Saccocirridae*) are characterized by a small size, weak segmentation, few or no appendages, parapodia or chaetae, and ventral ciliary gliding bands. Because of these features some of them have been considered as primitive annelids and as part of the basal grade "Archiannelida". Conversely, these taxa were regarded as polyphyletic assemblage of highly derived but secondarily simplified annelid taxa adapted to their interstitial realm. Due to adaption to the interstitial habitat, these taxa lack several characters, which are typical for larger annelids, and hence cause the problem of differentiation between primary and secondary absence, which so often leads to conflicts between morphological and molecular analyses. We are using Next Generation Sequencing-Methods (Illumina shot gun sequencing) to generate complete mitochondrial genomes of about 15 – 17 kb to address the phylogenetic position of the former archiannelidan taxa. For animals with only limited amounts of tissue material we used whole genome amplification to obtain the required amount of genomic DNA. With this method we are able to generate nearly complete mitochondrial genomes respectively large mitochondrial fragments. Only small gaps have to be filled in with species-specific primers and traditional Sanger sequencing. The preliminary Maximum Likelihood analysis of the mitochondrial sequence data showed the potential of these data to address the phylogenetic position of the former archiannelidan taxa.

☐126 Anne Weigert A 703 / 16:15

A transcriptomic approach using next generation sequencing to reconstruct annelid phylogeny

Authors: *Anne Weigert*[1], *Günter Purschke*[1], *Kenneth M. Halanych*[1], *Scott Santos*[1], *Christoph Bleidorn*[1], *Torsten Struck*[1]
Affiliation: [1]*University of Leipzig - Molecular Evolution and Animal Systematics*

Annelida is a highly diverse animal phylum with over 15,000 described species. Whereas the monophyly of the approximately 80 higher ranked taxa usually classified as families was well established, relationships between those taxa remained controversial. Recent studies have investigated annelid relationships supporting two major groups, Errantia and Sedentaria. Additionally *Chaetopterids*, *myzostomids* and *sipunculids* grouped outside this core Annelida now named *Pleistoannelida*.

☐127 Torsten Struck A 703 / 16:30

Platyzoa - a monophyletic group or a long-branch artifact?

Authors: *Torsten Struck*[1], *Alexandra Wey-Fabrizius*[1], *Lars Hering*[1], *Anne Weigert*[1], *Christoph Bleidorn*[1], *Holger Herlyn*[1], *Thomas Hankeln*[1]
Affiliation: [1]*Zoologisches Forschungsmuseum Alexander Koenig, Bonn*

Lophotrochozoa, one of the three major bilaterian taxa, comprises several worm-like taxa. The relationship of these taxa to each other is still unresolved. One taxon within Lophotrochozoa, which has been proposed based on morphological data, is Platyzoa comprising *Platyhelminthes*, *Gastrotricha*, *Syndermata* and *Gnathostumulida*. Platyzoan taxa are generally direct developers, lack a vascular system and their worm-shaped body is usually ciliated, flat and non-segmented. However, unique morphological autapomorphies supporting the monophyly of Platyzoa are lacking. Recent phylogenomic results showed some progress and generally placed monophyletic Platyzoa as sister to the other lophotrochozoans. However, the inclusiveness and monophyly of Platyzoa as well as the relationships of the platyzoan taxa is still controversial. Moreover, substantial support for platyzoan relationships is still lacking even in these recent phylogenomic studies. This is, among other reasons, due to the facts that all taxa exhibit long branches and that several taxa such as Gnathostomulida and Gastrotricha are only poorly covered with respect to taxa and number of analyzed genes. To address these issues we generated large EST databases using next generation sequencing technologies for four gastrotrichs, one gnathostomulid, three syndermatans and two platyhelminths. We will present the results of our phylogenomic analyses based on a better taxon sampling of platyzoans as well as substantially increased data coverage.

☐128 Jörn von Döhren A 703 / 16:45

Phylogeny and evolution of Nemertea

Author: *Jörn von Döhren*[1]
Affiliation: [1]*University of Bonn*

Nemertea (ribbon worms) is a monophyletic group of unsegmented nocturnal predators that hunt their prey by means of an eversible proboscis. Recently it has been shown that within *Spiralia Nemertea* show affinities to Trochozoa. Presently however, their sister group still remains a matter of debate. Neither target-gene nor genomic approaches have led to a sufficient resolution. Morphological approaches have been hampered by the unknown ground pattern which is due to the unresolved nemertean phylogeny. New molecular data successfully support certain nemertean subgroups, but do not show consistent resolution of a single topology. In the last two years our group expanded the morphological data matrix significantly. This contribution represents a re-assessment of different organ systems regarding their usefulness for a phylogenetic analysis with morphological data and allows for establishing preliminary ancestral states for nemerteans.

☐129 Sabrina Kaul-Strehlow A 703 / 17:00

The smallest solitary deuterostome: a miniaturized acorn worm (Hemichordata: Enteropneusta) from the Western Atlantic

Authors: *Sabrina Kaul-Stehlow*[1]*, Katrine Worsaae*[1]*, Wolfgang Sterrer*[1]*, Anders Hay-Schmidt*[1]*, Gonzalo Giribet*[1]
Affiliation: [1]*Department for molecular Evolution and Development, University of Vienna, Austria*

The interstitial environment of marine sandy bottoms is a nutrient-rich, sheltered habitat whilst at the same time also often a turbulent, space-limited, and ecologically challenging environment dominated by meiofauna. The interstitial fauna is also one of the most diverse on earth and accommodates miniaturized representatives from many macrofaunal groups as well as several exclusively meiofaunal phyla.

Here we describe a new enteropneust species inhabiting the interstices among sand grains in shallow tropical waters. With a maximum body length of 0.6 mm, it is the first microscopic adult enteropneust known, a group otherwise ranging from 2 cm to 250 cm in adult size. Asexual reproduction by paratomy has been observed in this new species, a reproductive mode not previously reported among enteropneusts.

Morphologically, *Meioglossus psammophilus gen. et sp. nov.* shows closest resemblance to an early juvenile stage of the acorn worm family *Harrimaniidae*, by featuring a post-anal tail and one pair of gill pores. Moreover, such a relationship is also supported by a phylogenetic analysis of molecular data. Its position, clearly nested within the larger macrofaunal hemichordates, suggests that this represents an extreme case of miniaturization. The evolutionary pathway to this simple or juvenile appearance, as chiefly demonstrated by its small size, dense ciliation, and reduction of a proboscis skeleton and stomochord, may be explained by progenesis. The finding of *Meioglossus psammophilus gen. et sp. nov.* underscores the notion that meiofauna may constitute a rich source of undiscovered metazoan diversity, possibly disguised as juveniles of other species.

☐130 Thomas Stach A 703 / 17:15

Prospects of cell lineage data in phylogenetic analyses

Author: *Thomas Stach*[1]

Affiliation: [1]*Humboldt-Universität zu Berlin*

Precise data of cell genealogy and cellular fate restriction are accumulated in an increasing number of model organisms where they are widely used in functional and molecular studies of development. Although there have been attempts to utilize some of the information from such cell lineage studies in evolutionary considerations across animals, a methodological approach to conceptualize cell lineage data into characters for phylogenetic analysis is still lacking. The reason for this might be that the nature of cell lineage data is very diverse ranging from purely numerical data (e.g., number of cell cycles before fate restriction) to qualitative data (e.g., mosaic cleavage versus regulatory cleavage), necessitating a range of character coding strategies. In the current presentation, I show examples of high quality cell lineage data and suggest solutions for character coding, in order to use these data for phylogenetic analyses. I argue that lack of data is currently the main bottleneck that prevents a more meaningful use of the scattered cell lineage data in phylogenetic analyses across higher animal taxa. Data acquisition should therefore be the main priority combined with explicit attempts of homologizations across taxa.

Sunday, September 23, 2012

Invited speaker 1: Chair – Lars Podsiadlowski A 701 / 11:30

Saskia Brix-Elsig (Hamburg)

Highlights in isopod research - news from the deep sea

Author: *Saskia Brix-Elsig*[1]

Affiliation: [1]*Senckenberg am Meer, DZMB, Hamburg*

This talk aims to present highlights in deep-sea isopod research from the DIVA (Latitudinal Gradients of deep-sea BioDIVersity in the Atlantic Ocean) and the IceAGE (Icelandic marine Animals: Genetics and Ecology) projects. While DIVA presently concentrates on the South Atlantic Ocean, IceAGE coveres the subarctic marine environment around Iceland. Asellote isopod examples from the DIVA expeditions 1-3 show results of an integrative taxonomy approach analysing species complexes

from neighbouring South Atlantic deep-sea basins. IceAGE aims to combine classical taxonomic methods with modern aspects of biodiversity research, in particular phylogeography (population genetics and DNA barcoding) and ecological modelling in the climatic sensitive region around Iceland. The sampling area is characterised by several local pecularities like submarine ridges (geographical barriers) and influence of different water masses of different origin. This allows the analysis of factors influencing the distribution and migration of species as well as investigation of the background of biogeographic zonation. The first IceAGE expedition with RV Meteor (M85/3) took place August/September 2011.
To highlight the promising approaches of the IceAGE-project, examples from isopods can demonstrate the complexity of the sampling area and show the first steps in modelling species distribution in Icelandic waters.

Monday, September 24, 2012

Invited speaker 2: Chair – Christoph Bleidorn A 704 / 11:00

Oliver Niehuis (Bonn)

Insect phylogenetics in the era of genomics

Author: *Oliver Niehuis*[1]
Affiliation: [1]*Zoological Research Museum Alexander Koenig Bonn*

The evolutionary history of the extant insect orders has received considerable attention, yet our knowledge of their phylogenetic relationships is far from complete. Next generation sequencing technology provides new opportunities to study the phylogeny of insects by analyzing an unparalleled amount of nucleotide characters as well as new genomic meta-characters. We used whole genome sequencing to infer the evolutionary origin of twisted-wing parasites (order Strepsiptera) whose phylogenetic relationship to other endopterygote insects has proven notoriously difficult to resolve. Using this approach, we were able to study more than 1.7 million codon sites from approximately 4,500 orthologous and inparalogous genes ? the largest dataset ever analyzed to resolve the phylogenetic position of Strepsiptera or any other insect order. We additionally studied near intron pairs and gene order for phylogenetic reconstruction. In second project (1KITE), we are currently applying transcriptome sequencing to reconstruct the phylogenetic relationships of all remaining insect orders by studying transcriptome nucleotide sequence data from about 1,000 insect species. I will discuss the challenges that are associated with studying such a large amount of nucleotide data, with assessing orthology among transcript sequences (and the role of accurately annotated genomes for doing so), and I will provide first glimpses on the obtained results. Finally, I will show how genome and transcriptome nucleotide sequence data can be exploited to aid targeted amplification of genes of interest in research projects with a more narrow phylogenetic scope and/or with a limited budget.

Chair: Torsten H. Struck

☐132 Udo Rempe A 703 / 16:15

Refining evolutionary distances by character weighting

Author: *Udo Rempe*[1]
Affiliation: [1]*Zoologisches Institut, Universität Kiel*

If two species B and C descend from their last common ancestor A an evolutionary track runs from A to B. During evolution shots" may change the states of characters. For instance at position 996 of mt-DNA-coded proteins compiled by MAX TELFORD there occur the three amino acids FLY. The probabilities that one of the three aminoacids is retained after one shot or substituted by another one can be calculated. The probabilities that after a given number of shots (1) the amino acids remain unchanged or differences are lost by succeeding changes or (2) differences are observed can too be calculated. By use of the changing probabilities the number ab of shots between A and B, the number of shots ac between A and c, and the number bc=ab+ac between B and C can be estimated. Position 996 is only one of 1101 homologous protein positions with more than one amino acid. From these we get 17851 regressors x1, x2, ..., x17851. Position 996 contributes regressors x6282 for FL, x6283 for FY, x6284 for LL, x6285 for LY, and x6286 for YY which have the value 1 if the corresponding amino acid pair is found and else have the value 0. For each number of shots we get regression coefficients b1, b2, ..., b17851. These are the values necessary for character weighting. The importance of the resulting evolutionary distances for resolving deep metazoan phylogeny will be discussed.

☐133 Richard Mally A 703 / 16:30

Testing monophyly of megadiverse *Spilomelinae* (Insecta: Lepidoptera: Pyraloidea)

Authors: *Richard Mally*[1]*, Christoph Neinhuis, Matthias Nuss*
Affiliation: [1]*Senckenberg Natural History Collections Dresden, Museum of Zoology*

Spilomelinae represent one quarter of the 16,000 described species of Pyraloidea, making it the most speciose subgroup of the snout moths. *Spilomelinae* have a worldwide distribution with highest diversity in the tropics, and they contain many species of economic importance, including invasive pests like the box tree moth *Cydalima perspectalis*. So far, *Spilomelinae* are exclusively defined by typological means and have repeatedly been claimed to be polyphyletic (Minet 1982, Solis & Maes 2003). A morphology-based cladistic analysis (Solis & Maes 2003) failed to find autapormorphies for the group. As an initial step towards a stable, phylogenetically justified nomenclature, we present first results of our test on the monophyly of *Spilomelinae*.

Our taxon sampling comprises representatives of most of the 15 genus groups defined by Munroe (1995) (though he did not give a diagnosis for any of these groups), 25 of the 29 spilomeline genera occurring in Europe and representatives from the Afrotropical and Oriental regions as well as 11 *Pyraustinae* taxa. We compiled molecular data of mitochondrial COI gene and nuclear genes EF1a, GAPDH, IDH and analyzed them phylogenetically using MrBayes. Our preliminary results indicate a sister-group relationship of *Spilomelinae* and *Pyraustinae*. *Spilomelinae* only form a natural group with the inclusion of *Wurthiinae*, confirming the results of Mitter et al. (in press). None of the investigated genus groups with exception of the Samea group appear monophyletic. The Udea s.l. group (Mally & Nuss 2011) appears to be a key group at the base of the *Spilomelinae-Pyraustinae* clade. However, several enigmatic taxa (e.g. *Euclasta*) and genus group representatives are still missing from the sampling and may provide further insights, once they are included.

Apart from enhancing the taxon sampling, the next major undertaking is the generation of a morphological data matrix based on anatomical characters of the adults. By this, we intend to get insights into character evolution within *Spilomelinae* and *Pyraustinae*, to constitute a phylogenetically well-founded circumscription of *Spilomelinae*, and to establish the groundwork for the further investigation of its 318 genera.

☐134 Sven Bradler A 703 / 16:45

The stick insects of Madagascar: Ancient lineages or recent adaptive radiation?

Authors: *Sven Bradler*[1]*, Kim Stey*[1]*, Julia Goldberg*[1]
Affiliation: [1]*Johann-Friedrich-Blumenbach-Institut für Zoologie und Anthropologie, Georg-August-Universität Göttingen*

Madagascar is one of our planet's leading biodiversity hotspots exhibiting an extraordinarily distinct and diverse biota. Many elements of its fauna are still poorly documented and remain largely unexplored. One example is the Malagasy stick insects (*Phasmatodea*) whose evolutionary history is entirely obscure. Stick insects are large terrestrial arthropods with limited direct-dispersal abilities, forming at least four distinct taxonomic groups on Madagascar, i.e., endemic families and subfamilies. Their phylogenetic affinities to continental lineages are completely unresolved. We present informative sets of molecular and morphometric data to investigate the origin and evolution of Malagasy stick insect lineages. Analysing a representative taxon sampling we demonstrate that the stick insects of Madagascar are more closely related to each other and much younger than previously suggested in traditional classifications, representing a classical example of adaptive radiation in geographic isolation. The application of a comparative morphospace analysis to the obtained phylogeny additionally provides an opportunity to compare unrelated and geographically distant radiations among phasmatodeans, for instance those of Madagascar compared to a diverse lineage of Australasian stick insects (*Lanceocercata*). Thereby, we detect an impressive degree of convergence between these otherwise distinct communities.

☐135 Claus Fischer A 703 / 17:00

Evidence for a mechanism of genetic exchange in an ancient asexual bdelloid rotifer

Authors: *Claus Fischer*[1], *W.H. Ahlrichs*[1], *Olaf R.P. Bininda-Emonds*[1]
Affiliation: [1]*AG Systematics and Evolutionary Biology, IBU Faculty V, Carl von Ossietzky Universität Oldenburg*

Bdelloid rotifers have been labelled as an evolutionary scandal for being ancient asexuals. Indirect evidence of ancient horizontal gene transfer in *bdelloids* provides a partial explanation of how this group might have escaped the progressive accumulation of deleterious mutations associated with asexual reproduction (a phenomenon known as Muller's ratchet). However, rather than being an accidental occurrence, we present the first empirical evidence that DNA is actively taken up at adult stages by the asexual *bdelloid Philodina roseola*. This ability is not present in the facultative asexual monogonont rotifer *Brachionus rubens*.

Three additional results hint that this ability could facilitate the exchange of genetic material as an imperfect analogue of sexual reproduction. First, the amount of DNA apparently retained by P. roseola correlates roughly with the phylogenetic relatedness of its donor species. Second, in agreement with theory, the incorporated DNA results in an increased variance in the reproductive output of the F1 generation, but only if the parental generation has undergone desiccation. Third, these effects are also seen when individuals are desiccated in groups (and can therefore act as DNA donors), but not individually. Taken together, our results indicate a mechanism for regular genetic exchange in *bdelloid rotifers* that favours more closely related individuals / taxa, thereby potentially providing an answer to the riddle as to how the 'asexual' bdelloids have escaped being ground down by Muller's ratchet for over 35 million years.

☐136 Alireza Keikhosrav A 703 / 17:15

Cryptic species in European freshwater crabs revealed by genetic comparison of populations of Potamon ibericum (Brachyura, Potamidae)

Authors: *Alireza Keikhosravi*[1], *Sebastian Klaus*[2], *PD Dr. Christoph D. Schubart*[1]
Affiliations: [1]*Biologie 1, Universität Regensburg;* [2] *Ecology and Evolution, Goethe Universität, Frankfurt a.M., Germany*

Potamon ibericum (Bieberstein, 1808) is a well known freshwater crab species distributing from the southeastern Balkan Peninsula to the tributaries of the Caspian Sea. This study aims to describe the population genetic structure of *P. ibericum*, reconstruct gene flow patterns within and among faunal regions, and investigate the presence of possible cryptic lineages. Specimens for the current study were collected from an introduced population in France and from native populations in Bulgaria, Greece and Iran. A partial fragment of approximately 900 basepairs of the mitochondrial gene cytochrome oxidase 1 was amplified and sequences compared and analysed.

Our results show restricted gene flow and high genetic heterogeneity among faunal regions. The strongest differentiation is observed between the Caspian and the Black-Aegean Sea drainage systems, respectively. Within the latter, populations from southwestern Bulgaria and northern Greece from rivers draining into the northern

Aegean appear distinct from populations of the Black Sea drainage system and thus represent a divergent cryptic lineage and may require further taxonomic attention. The here presented phylogenetic and phylogeographic data show remarkable diversity within the *P. ibericum* complex from a wide distribution area. This, combined with the diverse range in topography and climate, suggests additional uncovered diversity which may be discovered after further sampling efforts (i.e. Turkey, Georgia and Azerbaijan). Morphological and morphometric studies are being carried out in order to determine, if molecular divergence at intraspecific level is accompanied by morphological differentiation and different taxonomic units may be involved.

17. Zoological Systematics POSTERS

♦190 Stephanie Andorfer

Regional endemismsof the stone crayfish *Austropotamobius torrentium* (Decapoda: Astacidae) in central and eastern Europe

Authors: *Stefanie Andorfer*[1], *Alireza Keikhosravi*[1], *Christoph D. Schubart*[1]
Affiliation: [1]*Biologie 1, Universität Regensburg*

Water pollution, habitat destruction, introduction of invasive species, and the lethal crayfish plague *Aphanomyces astaci* (Schikora, 1906) are constantly reducing the number of viable populations in native European crayfish species. *Austropotamobius torrentium* (Schrank, 1803) is the smallest endemic European crayfish species. It is a red list species in Germany, confined to headwaters, and adapted to cold water with high flow-through and rocky environment.

French, Swiss, and German populations of *A. torrentium* are mostly genetically impoverished and dominated by one most common haplotype. However, unique haplotypes can be found in some Alpine drainage systems suggesting local glacial refugia. This needs to be elaborated as it is important for future conservation efforts of stone crayfish populations in Germany and Austria.

Previous studies have shown clearly divergent genetic lineages of *A. torrentium* in the Balkans (Slovenia, Serbia, Bulgaria), whereas populations of the Danube drainage system in Romania and Bulgaria are more similar to the most common haplotype in Central Europe. The present study investigates the haplotype composition of populations in central and eastern Europe to document regional endemisms, to possibly determine glacial refugia, and to reconstruct pathways of postglacial re-colonization.

♦191 Olaf Bininda-Emonds

A dated species-level supertree of fowls (Aves: Galloanserae)

Authors: *Olaf Bininda-Emonds*[1], *Florian Müller*[1]
Affiliation: [1]*Carl von Ossietzky Universität Oldenburg*

Despite their socio-economic and biological importance to humans and the fact that they form the sister group to all remaining 'modern birds' (Neoaves), no complete species-level phylogeny for *Galloanserae* (ducks, chickens and allies) yet exists. The most complete estimate on this level derives from a supertree analysis based on literature trees that contained 376 of approximately 452 species in total and all but one genus. Through data mining of GenBank, we sought to augment the non-molecular portion of this data set and, through supertree analysis, to provide the most complete and up-to-date species-level phylogeny of the group. The new molecular data also enable the estimation of divergence times throughout the tree in combination with fossil calibration data. Altogether, the updated data set comprises nearly 400 species obtained from over 250 trees from the literature in combination with 50 new maximum-likelihood gene trees; the latter together are based on approximately 25000 bp of sequence data. The supertree confirms many traditional hypotheses within the group, such as the monophyly of both *Anseriformes* (waterfowl) and *Galliformes* (landfowl) as well as most of the traditional families and genera. Importantly, our dated supertree provides the first comprehensive set of divergence-time estimates throughout the group and so provides important new information needed to assess macroevolutionary patterns within *Galloanserae* in comparison with other avian taxa.

♦192 Lisa-Marie Eschner

The first mitochondrial genome of a caddisfly

Authors: *Lisa-Marie Eschner*[1], *Lars Dietz*[1], *Ralph Tollrian*[1], *Florian Leese*[1]
Affiliation: [1]*Ruhr-Universität Bochum*

Caddisflies (*Trichoptera*) are holometabolous insects which are of central importance in freshwater ecosystems. They are furthermore important for inferences of holometabolan phylogeny. Interestingly, caddisflies are one of the few insect orders whose mitochondrial genomes have not been sequenced so far. Here, we present the mitochondrial genome of the caddisfly *Sericostoma personatum*, assembled from 454 pyrosequencing data with remaining gaps closed by conventional sequencing. The mitochondrial genome shows the typical insect gene order. Previous phylogenetic analyses of Holometabola based on mitochondrial genomes show relationships strongly contradicting those based on other evidence, especially concerning the phylogenetic position of Lepidoptera. However, they only included derived ditrysian Lepidoptera. Therefore, the inclusion of a mitochondrial genome from *Trichoptera*, which are generally considered the sister group of Lepidoptera, is expected to improve the quality of the phylogeny. We conducted a phylogenetic analysis based on mitochondrial genomes including the new trichopteran mitogenome as well as representatives of all other holometabolan orders, including a large sample of Lepidoptera. Implications for our understanding of holometabolan phylogeny, as well as possible biases influencing the analysis, are discussed.

♦193 Lars Hering

Evolution of colour vision in Panarthropoda: Insights from opsin genes in *Onychophora* and *Tardigrada*

Authors: *Lars Hering*[1], *Christoph Bleidorn*[1], *Georg Mayer*[1]
Affiliation: [1]*Animal Evolution & Development, Institute of Biology, University of Leipzig*

Multiple visual pigments, prerequisites for colour vision, are found in arthropods, but the evolutionary origin of their diversity remains obscure since it is unknown whether multiple pigments are also present in the closest arthropod relatives, the *onychophorans* (velvet worms) and *tardigrades* (water bears). To clarify the evolutionary origin of colour vision in Panarthropoda (*Onychophora* + *Tardigrada* + Arthropoda), we explored the opsin genes in five distantly related species of *Onychophora* and in one species of *Tardigrada*, using deep transcriptome sequencing and screening approaches. Our data revealed the existence of only one functional r-opsin gene in each onychophoran and tardigrade species studied. In our phylogenetic analyses, the onychophoran and the tardigrade r-opsins form a monophyletic clade, which is the sister group to the monophyletic clade of visual r-opsins of arthropods. These results provide evidence for monochromatic vision in velvet worms and tardigrades, and in the last common ancestor of Panarthropoda. We conclude that the diversification of visual pigments and colour vision evolved in arthropods, along with the evolution of compound eyes - one of the most sophisticated visual systems known.

♦194 Hasan Ibrahim

A survey of the prevalence of hard ticks infection on camels in Sebha city, Libya.

Authors: *Hasan M. S. Ibrahim*[1], *Rokayya A. Esmaeil*[1], *Shala S. Ahmed*[1]
Affiliation: [1]*University of Sebha*

The study was conducted on the prevalence of ticks infection on camels in Sebha city, Libya. Collection and identification of the ticks were undertaken from April to July 2002. A hundred samples of animals was randomly selected from 25 sites in Sebha including farms and open grazing lands. The most of these camels imported from Chad and Niger. All the body parts of camels were examined and the visible adult ticks were separately collected from the different parts. The results of the study showed that, 74% of the study camels were infected with species belong to one genus of the hard ticks namely: *Hyalomma sp.* The results also showed there was no significant differences ($P>0.05$) in the prevalence of infection between the male (74.4%) and female (73.7%) camels, and between groups of camels with different ages. No significant difference was observed between the prevalence in males and females, and the infection rate was not increase with the age groups ($P<0.05$). According to the site of infection on animal body, it was found that single infection (36.9%) was found in abdomen (14.9%), udder (14.9%), boss (12.1%), flanks (8.9%), and tail (1.4%). While the mixed infection (37.8%) was found in more than one part of the animal body.

◆195 Carolin Kindler

Molecular phylogeny of African hinge-back tortoises (*Kinixys*): implications for phylogeography and taxonomy (Testudines: Testudinidae)

Authors: *Carolin Kindler*[1]*, William R. Branch, Margaretha D. Hofmeyr, Jérome Maran, Pavel Široký, Miguel Vences, James Harvey, J. Susanne Hauswaldt, Alfred Schleicher, Heiko Stuckas, Uwe Fritz*

Affiliation: [1]*Museum of Zoology, Senckenberg Natural History Collections Dresden*

We examine the phylogeography, phylogeny and taxonomy of hinge-back tortoises using a comprehensive sampling of all currently recognized *Kinixys* species and subspecies and sequence data of three mitochondrial DNA fragments (2273 bp: 12S rRNA, ND4 + adjacent DNA coding for tRNAs, cytb) and three nuclear loci (2569 bp: C-mos, ODC, R35). Combined and individual analyses of the two data sets using Bayesian and Maximum Likelihood methods suggest that the savannah species of *Kinixys* are paraphyletic with respect to the rainforest species *K. homeana* and *K. erosa*, and that the rainforest species may be derived from a savannah-living ancestor. The previously recognized savannah species *K. belliana* was a conglomerate of three deeply divergent clades that we treat here as distinct species. We restrict the name *K. belliana* (Gray, 1830) to hinge-back tortoises ranging from Angola to Burundi, while five-clawed hinge-back tortoises from the northernmost part of the formerly recognized range of *K. belliana*, together with four-clawed tortoises from West Africa, are assigned to the species *K. nogueyi* (Lataste, 1886). These two species are allied to *K. spekii*, whereas Southeast African and Malagasy hinge-back tortoises formerly lumped together with *K. belliana* represent the distinct species *K. zombensis* Hewitt, 1931, which is sister to *K. lobatsiana*. Mitochondrial data suggest that *K. natalensis* has a basal phylogenetic position in a clade embracing K. *belliana sensu stricto*, *K. nogueyi* and *K. spekii*, while nuclear data and the two data sets combined favour a sister group relationship of *K. natalensis* to all other hinge-back tortoises.

◆196 Lars Podsiadlowski

Five new mitochondrial genomes challenge the monophyly of 'Coraciiformes'

Authors: *Lars Podsiadlowski*[1]*, Albrecht Manegold*[1]*, Alexander Suh*[1]*, Gerald* Mayr[1]

Affiliation: [1]*Inst. Evolutionary Biology & Ecology, Universität Bonn*

Several recent studies question the monophyly of ‘Coraciiformes’. Due to a large nuclear gene dataset (Hackett et al. 2008, Nature) core *Coraciiformes* (*Alcedinidae*, *Coraciidae* and *Meropidae*) form the sister-group of (*Piciformes* + *Galbuliformes*). From the remaining ‘Coraciiformes’ the *Bucerotidae*, *Upupidae* and *Phoeniculidae* together form another monophyletic clade (*Bucerotifomes*) closely related to the assemblage mentioned above. The cuckoo roller *Leptosomus discolor* seems not to belong to any of these taxa. To evaluate this phylogenetic hypothesis with a molecular dataset independent from that of Hackett et al, we sequenced complete or almost complete mitochondrial genomes from five bird species. We provide the first mt genome from a member of the *Galbuliformes* (*Malacoptila panamensis*) and enhance the taxon sampling of ?Coraciiformes? from 6 to 10 species with records of *Tockus nasutus* (*Bucerotidae*), *Coracias cyanogaster* (Blue-bellied Roller, Coraciidae), *Upupa epops* (*Hoopoe*, *Upupidae*), and *Phoeniculus purpureus* (Green Wood Hoopoe,

Phoeniculidae). In general mt genome based phylogenetic analysis of birds shows no good resolution of basal branches. *Upupa* and *Phoeniculus* exhibited the longest branches of all Neoaves in our mt genome tree (and as well in the nuclear gene tree presented by Hackett et al.). This probably affects the results of phylogenetic analysis concerning the position of these two species, which do not cluster with the other Coraciiformes/Piciformes.

♦197 Theodor Poettinger

New insights on the history of freshwater crabs from Sulawesi and the colonizationof limnic habitats

Authors: *Theodor Poettinger*[1]*, Christoph Schubart*[1]
Affiliation: [1]*University of Regensburg*

Ancient lakes probably represent the most stable freshwater environment on Earth, with a species richness clearly exceeding that of younger and less stable limnic habitats. The biological colonization of these old lake systems in most cases must have occurred via the surrounding rivers. Reconstructing these colonization events may thus help to better understand evolutionary processes like subsequent adaptive radiations. Furthermore it allows us to depict one or several moments in time in which an ecological transition took place from a riverine ancestor to a lake inhabitant, potentially occupying new ecological niches. If the age of the corresponding ancient lake is known, reconstruction of colonization events can then aid to calibrate molecular clocks for the phylogeny of the respective freshwater-dependent taxa. Two ancient lake systems of Sulawesi (Malili lake system and Lake Poso) have been studied in terms of the taxonomy and phylogeny of freshwater crabs (Decapoda: Brachyura: Gecarcinucidae). Both systems have been colonized twice independently and in both systems we can find three ecological niches which are always occupied by different crab species: molluscivores, omnivores, detritivores. In a recent effort, we have obtained mtDNA sequences from crab populations inhabiting more than twenty river systems in Sulawesi to allow a better reconstruction of lake colonization events. The reconstructed phylogenetic trees confirm two independent colonization events for both ancient lake systems with a subsequent radiation. Furthermore they imply that the species which are today molluscivorous were the first to colonize, whereas omnivores and detritivores are derived from later colonization events and the outcome of radiations due to their monophyletic relationship. The significance of these results will be discussed.

♦198 Thomas Stach

Evolution and development of the coronal organ in tunicates: homology to vertebrate lateral line?

Authors: *T. Stach*[3], *F. Rigon*[1], *S.M. Shimeld*[2], *F. Caicci*[1], *F. Gasparini*[1], *P. Burighel*[1], *G. Zaniolo*[1], *L. Manni*[1]
Affiliations: [1]*Department of Biology, University of Padua, Italy*; [2]*Department of Zoology, University of Oxford, UK*; [3]*Institut für Biologie, AG Vergleichende Zoologie, Humboldt-Universität zu Berlin*

The coronal organ is a sensory system present in the oral region of tunicates, possessing secondary sensory cells supposed to have the same evolutionary origin as vertebrate hair cells. Indeed, coronal sensory cells strictly resemble the latter, because of morphology, location, function and embryonic origin. Vertebrate hair cells are characteristic of the lateral line and inner ear, where they function as mechanoreceptors. We conducted a comparative ultrastructural analysis of the coronal organs in several tunicate species and complimented the study with an examination of molecular developmental aspects in the ascidian *Ciona intestinalis*. We found that several genes that are involved in mechanoreceptor differentiation in vertebrates are expressed around the rudiment of the oral siphon in tadpole larvae of *C. intestinalis*. These findings are in agreement with the hypothesis that the coronal organ in the tunicate *C. intestinalis* might be homologous to the lateral line system in vertebrates.

♦199 Andrea Weis

DNA barcoding of Sea spiders (*Pycnogonida*) from the chilean fjord region, with remarks on *Achelia assimilis* (Haswell, 1885)

Authors: *Andrea Weis*[1], *Roland Melzer*[1]
Affiliation: [1]*Staatssammlung München*

In the present study we report the first attempt to resolve Chilean pycnogonid taxonomy using DNA sequence data in combination with morphology. In a subproject of the Marine Barcode of Life (MarBoL) campaign we analyzed a fragment of the mitochondrial protein-coding gene COI (cytochrome c oxidase subunit 1) from 76 Chilean/Subantarctic pycnogonids based on about 657 base pairs. Since most molecular data on pycnogonids are from the Antarctic area, the new information constitutes a significant extension.

The phylogenetic consensus tree displays 10 distinct, well supported clades corresponding to the studied species, namely *Achelia assimilis* (Haswell, 1884), *Ammothea spinosa* (Hodgson, 1907), *Tanystylum cavidorsum* Stock, 1957, *T. neorhetum Marcus*, 1940, *Colossendeis macerrima Wilson*, 1881, C. megalonyx Hoek, 1881, C. scoresbii Gordon, 1932, Callipallene margarita (Gordon, 1932), *Pallenopsis patagonica* (Hoek, 1881), and *Anoplodactylus californicus Hall*, 1912. These represent four superfamilies, and five of the eleven existing pycnogonid families (Bamber & El Nagar 2011): *Ammotheidae Dohrn*, 1881, *Colossendeidae Hoek*, 1881, *Callipallenidae Hilton*, 1942, *Pallenopsidae Fry*, 1978, and *Phoxichilidiidae Sars*, 1891.

Within *Achelia assimilis*, four distinct subclades correspond to the different geographic regions represented in our samples. While these include a total of 11 distinct haplotypes, the morphological differences among the corresponding specimens lie well within the variation described in the literature for this cosmopolitan species. Therefore, the four clades of *A. assimilis* are interpreted as representing at most possible subspecies.

Standard barcoding sequences are confirmed as a suitable tool in addition to morphology for taxonomic analyses in Pycnogonida. The corresponding haplotype distribution patterns allow inferences on the biogeographical history of the relatively unexplored Chilean fjord region.

◆200 Christina Wesse

Phylogenomics through data mining: comparing promise and pitfalls using Mammalia as a case study

Authors: *Christina Wesse*[1]*, Olaf R.P. Bininda-Emonds*[1]
Affiliation: [1]*Universität Oldenburg*

The archiving of molecular sequence data through databases such as GenBank has helped to democratize phylogenetic analysis by making potentially large amounts of homologous data freely accessible. As a result, phylogenetic analyses are becoming increasingly comprehensive by being able to incorporate more data than could be generated by any single lab group or even consortium, even in the age of next-generation sequencing. However, the potential benefits to phylogenomics of such data are often ameliorated by a variety of problems associated with them. Using Mammalia, one of the most comprehensively sequenced major taxa, as an example, we examine how well we are able to reconstruct the phylogeny of the group using publically available data and where specific problem areas lie. Although the major limitation of insufficient data availability or overlap is becoming less problematic with time (at least for well studied or popular groups like mammals), other problems such as sequencing errors or faulty annotations remain and could even become exacerbated in the future through the automation associated with high-throughput data generation. This latter fact argues strongly against automated phylogenetic analysis, but raises the dilemma as to how ever larger phylogenies can be achieved practically.

◆201 Katharina Wyschetzki

Undescribed diversity in the Perisesarma bidens species complex (Decapoda: Brachyura: Sesarmidae) based on molecular and morphological data

Authors: *Katharina von Wyschetzki*[1]*, Christoph D. Schubart*[1]
Affiliation: [1]*Institut für Zoologie, Universität Regensbug*

Sesarmid crabs are conspicuous and ecologically significant inhabitants of mangrove forests worldwide. Especially the species-rich genera *Peri-* and *Parasesarma De Man*, 1895, form an important part of the mangrove fauna in the Indo-West Pacific. Besides of the squarish carapace, the cuticular structures on the chelipeds used for the production of acoustic signals are characteristic for these genera. Two or three transverse pectinated crests on the upper surface of the palm and a row of well identifiable dactylar tubercles form the stridulation organ. The classification of the

species level was guided so far by the morphology of these characters. However, previous molecular phylogenetic examinations suggested that both genera are not reciprocally monophyletic and that undescribed species exist. This study focused on the biogeography and phylogeny of *Perisesarma bidens De Haan*, 1835 which is believed to have a large distribution, ranging from Japan to Vietnam (even India and Sri Lanka according to Dai & Yang, 1991). Specimens were analysed by mitochondrial and nuclear DNA sequences on the one hand and by scanning electron microscopy, morphometrics and larval morphology on the other hand. The mtDNA and nDNA revealed several independent lineages within *Perisesarma bidens*, of which one corresponds to *Perisesarma cricotus Rahayu & Davie*, 2002, from eastern Indonesia. Further clades are composed of animals from the coast of southern China and two from Taiwan and the Philippines. Since these clades can be furthermore distinguished on the basis of several morphometric features, it is intended to describe them as distinct species.

18. Anthropod Neuroscience Network (ANN)

Thursday, September 20, 2012 | 08:00 – 18:00

Friday, September 21, 2012 | 08:00 – 16:00

Room: M 629

Routed in the traditional “Arthropodenseminare”, the ANN meetings provide an important platform for scientific exchange between the different laboratories working in the wide field of arthropod neurobiology in the German-speaking countries.

Konstanz as venue is a fortunate choice for us given the strong neurobiological groups at Konstanz University that use arthropods as model organisms, as well as the nice surroundings and the vicinity to Austria and Switzerland.

Key Note

Dr. Nicholas J. Strausfeld, University of Arizona
(*http://www.neurobio.arizona.edu/faculty/strausfeld.html*)

Organized by:
Jochen Schachtner, Uni Marburg & Christian Wegener, Uni-Würzburg
Local Coordinators: Christoph Kleineidam & Andreas Thum

19. Daphnia-Symposium

Saturday, September 22, 2012

Key Note Chair: Dominik Martin-Creuzburg R513 / 11:00

Dieter Ebert

Toward the ecological genomics of *Daphnia*

Author: *Dieter Ebert*[1]

Affiliation: [1]*Basel University*

Four-hundred years of Daphnia research resulted in an impressive knowledge about it ecology and natural history. However, only recently we started to explore genetic aspects of Daphnia. Technical breakthroughs resulted in a rapid gain of genetic and genomic tools, which allows us today to explore the genetics underlying phenotypic traits. In my I talk will introduce some of the latest genomic tools developed for Daphnia and give examples how these tools allowed us to gain insight into their ecology and evolution. I will focus on traits with strong phenotypic variance within and among populations, such as resistance to parasitic diseases and induction of sexual reproduction.

Key Note Chair: Dominik Martin-Creuzburg R513 / 11:30

Alexander Wacker

Determining nutritional constraints using *Daphnia* as a model

Author: *Alexander Wacker*[1]

Affiliation: [1]*University of Potsdam*

To understand the transfer of energy and nutrients within food webs it is essential to understand nutritional constraints at the plant-animal interface. The reason lies in the fact that on the one hand plants often exhibit large variations in their mineral (elemental) and biochemical contents. On the other hand, for efficient growth and reproduction herbivorous animals require balanced ratios of minerals and/or macronutrients such as proteins, lipids, and carbohydrates in their diets. Recent stoichiometric approaches consider the balance of minerals such as nitrogen (N) and phosphorus (P) as decisive factors for the nutritional quality of plant species for animals. Furthermore, the dietary balance of more complex molecules, such as proteins, carbohydrates and of essential sterols and polyunsaturated fatty acids (PUFAs) is important. A dietary deficiency in PUFAs and sterols has been shown to impair the performance of the keystone herbivore Daphnia. Just recently we have learned that Daphnia (and probably also other consumers) are not strictly limited by ‚the single nutrient in shortest supply‘ relative to demand. Instead, different resource ratios such as P : C, PUFAs : C and sterols : C can act as multiple limiting factors that simultaneously and interactively affect Daphnia‘s performance. Daphnia may adjust its metabolic pathways, respond in its behaviour, and change its ecological interactions within food webs. I will give a couple of examples for assessing nutritional constraints that involve chemical analyses to reveal consumer-diet imbalances, experimental series with measurements of growth and reproduction, dietary supplementation approaches, and will stimulate a discussion about the potential of new approaches to identify and quantify the intensity of nutritional limitation of animals.

TALKS

S□1 Mathilde Cordellier R513 / 12:00

Tiny European Daphnia, a newcomer in eco- and paleogenomics

Authors: *Mathilde Cordellier*[1]*, Maike Herrmann*[1]*, Pia Kreuzer*[1]*, Klaus Schwenk*[1]
Affiliation: [1]*Biodiversity and Climate Research Centre, Frankfurt*

Daphnia species, among other resting-stage producing organisms, have a unique potential for evolutionary studies. With the ability to obtain resurrected individuals from past populations, it is possible to address basic evolutionary and ecological questions, such as the pace of adaptation and its mechanisms. I will present here the results of a multi-disciplinary approach to evaluate the response of European Daphnia galeata populations to anthropogenically caused environmental changes, such as global warming. Using a combination of neutral (e.g. microsatellites) and temperature related candidate gene regions, we investigated gene frequency changes in space and time. By contrasting population differentiation measured through F-statistics, we could show how geographical distance and environmental differentiation shape genetic diversity across a latitudinal gradient and between different time periods (covering several decades). In a second part, I will report on the progress made with developing resources for genome-wide studies in Daphnia *galeata* (Daphnia Genomics Consortium). First results of a combined analysis using transcriptome data and genetic variation at temperature-related genes (candidate genes) among natural populations revealed highly divergent mutation rates in in exon and intron regions and a strong signature of directional selection. Further studies using paleogenomic approaches will allow us to predict the evolutionary potential and trajectory of this keystone species in European lake ecosystems.

S□2 Barbara Pietrzak R513 / 12:15

Evolutionary demography of ontogenesis and senescence in Daphnia

Author: *Barbara Pietrzak*
Affiliation: [1]*Max Planck Institute for Demographic Research, Rostock*

Survival and reproduction determine fitness of an organism. Understanding evolutionary and ecological processes that shape birth and death of individuals and populations is thus crucial to understanding evolutionary dynamics. Daphnia has often served as a model organism in the study of how ecological context affects survival and fertility trajectories. Here, focus is given to the both ends of life history. First, recent results on how environmental interventions affect the rates of Daphnia aging are discussed. Second, an undergoing project is presented, in which Daphnia is used in experiments aimed at explaining the patterns of developmental mortality via linking age-specific mortality to age-specific transcription.

S☐3 Justyna Wolinska, Sabine Gießler R513 / 13:45

Coevolution between Daphnia and their parasites: a new method to capture genetic changes in parasite population

Authors: *Justyna Wolinska*[1]*, Sabine Gießler*[1]
Affiliation: [1]*Ludwig-Maximilians-Universität München*

Many Daphnia species are infected by tiny microbial parasites, potentially resulting in dynamic host-parasite coevolution between the two players. So far, however, the genetic changes have been followed only for one of the players, the host. It‘s high time to shed light on a so far hidden part of coevolutionary process: the genetic changes within parasite populations. Using recently developed molecular markers, ITS sequence data, we captured the spatial and temporal dynamics in population structure of two different parasite species infecting Daphnia hosts. Furthermore we relate the spatial structure of parasite populations with their most likely dispersal mode and discuss how parasite life cycle variation can shape coevolution. Moreover, we will now be able to use genetic information from both players at the same time. This opens tremendous possibilities for both field and experimental studies.

S☐4 Olivia Hesse R513 / 14:00

The impact of anthropogenetic stressors and simultaneous parasite infection on Daphnia

Authors: *Olivia Hesse*[1]*, Justyna Wolinska*[1]*, Christian Laforsch*[1]
Affiliation: [1]*Ludwig-Maximilians-Universität München*

In most studies evaluating the potential danger of anthropogenetic chemicals, the target animal is exposed to the substance under otherwise ideal conditions. However, in nature, organisms are often exposed to other environmental stressors such as parasites. The impact of anthropogenetic substances might considerably differ when the organism is additionally infected. To test this, we conducted several experiments where we exposed Daphnia magna to environmentally relevant concentrations of pesticides (diazinone, imidacloprid) or the pharmaceutical carbamazepine and additionally infected them with the parasite Metschnikowia sp. The pharmaceutical carbamazepine and the pesticide diazinone significantly increased the susceptibility of Daphnia to the parasite. Moreover, when exposed to the pesticide imidacloprid, the infection rate, but also life span was reduced. Our results show that the effect of anthropogenetic substances on non target organisms can be stronger if these organisms are additionally exposed to parasites. Hence, studies testing the effects of toxic compounds may underestimate the environmental impact of these chemicals.

S☐5 Nina Schlotz R513 / 14:15

A dietary polyunsaturated fatty acid protects Daphnia against pathogenic threats

Authors: *Nina Schlotz*[1], *Dominik Martin-Creuzburg*[1]
Affiliation: [1]*University of Konstanz*

Dietary restrictions, both in quantity and quality, have been proposed to affect the resistance of animals to pathogenic infections. Using an oral infection model consisting of the freshwater herbivore *Daphnia magna* and the opportunistic bacterial pathogen Pseudomonas sp. we explore the hypothesis that a dietary deficiency in C20 polyunsaturated fatty acids (PUFAs) impairs the capability to cope with pathogenic threats, because C20 PUFAs serve as precursors for eicosanoids which in turn act in immunity of invertebrates and vertebrates. Survival, somatic growth and reproduction of the host were recorded under different algal food regimes which contained or were deficient in C20 PUFAs. We show that animals feeding on a diet rich in C20 PUFAs are less affected by pathogen exposure and that this effect is mediated mainly by a single dietary PUFA.

S☐6 Eric von Elert R513 / 14:30

Evidence for inducible tolerance of *Daphnia magna* to cyanobacterial protease inhibitors

Authors: *Eric von Elert*[1], *A. Zitt*[1], *Anke Schwarzenberger*[1]
Affiliation: [1]*University of Köln*

The frequency of toxic cyanobacterial blooms has increased worldwide due to man-made eutrophication. Daphnia has been shown to acquire tolerance to cyanobacterial toxins on the population level and within an animals‘ lifetime, however, the molecular basis of this is unknown. Among the most wide-spread cyanobacterial secondary metabolites are protease inhibitors. Here we investigate if these cyanobacterial inhibitors cause a reduction of food quality and if Daphnia shows inducible tolerance to these inhibitors. We use a strain of the cyanobacterium Microcystis aeruginosa, which contains known chymotrypsin inhibitors, the green alga Scenedesmus obliquus as reference food and a clone of *D. magna*. When grown on the green alga, three chymotrypsins in the mass range from 16 kDa to 22 kDa were distinguished in *D. magna*. Already with 20% *M. aeruginosa* this pattern of chymotrypsins changed. Feeding encapsulated purified cyanobacterial chymotrypsin inhibitor induced the same changes in pattern and reduced the growth of *D. magna* on the green alga. IC50 values for inhibition of chymotrypsins of *D. magna* by the cyanobacterial inhibitors increased significantly when the cyanobacterium was part of the diet in comparison to a pure green algal diet. We conclude that *D. magna* acquires increased tolerance to cyanobacteria protease inhibitors within an animal‘s lifetime by remodelling the digestive chymotrypsins. This mechanism might be relevant for the transfer of tolerance to the next generation through maternal effects.

S□7 Anke Schwarzenberger R513 / 14:45

Local adaptation of *Daphnia magna* to cyanobacterial protease inhibitors?

Authors: *Anke Schwarzenberger*[1], *Eric von Elert*[1]
Affiliation: [1]*University of Köln*

Lakes are well known for having a pattern of seasonal succession of phytoplankton and zooplankton. The succession of different taxa of phytoplankton results in a succession of zooplankton taxa, and within the genus Daphnia, into a succession of different genotypes (clones). One reason for this observed succession of Daphnia clones might be the production of digestive protease inhibitors by cyanobacteria, which usually bloom in early summer. Here, seasonal changes in the frequency and the abundance of *Daphnia magna* haplotypes were observed in a eutrophic lake which developed a chymotrypsin-inhibitor-producing cyanobacterial bloom in May. These seasonal changes were not related to the changes of biotic and abiotic lake parameters. However, a very high amount of chymotrypsin inhibitors was observed in May (but not in other months). This was assumed to have exerted a strong punctual selection pressure on the Daphnia population and on the direct targets of the protease inhibitors, i.e. the digestive chymotrypsins of Daphnia. Actually, D. *magna* from before and during the cyanobacterial bloom showed a different protease pattern on activity stained SDS-PAGE in comparison to clones from the month after the bloom. However, no difference in tolerance, measured as IC50 values, to inhibition by the natural lake seston from May was found between the clones from before and after the bloom. Thus, the hypothesis that a seasonal adaptation of *D. magna* subpopulations from either April/May or June might have occurred could not be proven. This suggests that this Daphnia population is locally adapted to cyanobacterial protease inhibitors. To test this hypothesis we compared this putatively locally adapted Daphnia population with Daphnia from an oligotrophic lake which never have been exposed to cyanobacteria.

S□8 Bettina Zeis R513 / 15:00

How Daphnia copes with changing temperature conditions: The role of metabolic enzymes

Authors: *Bettina Zeis*[1], *Rüdiger J Paul*[1]
Affiliation: [1]*Institut für Zoophysiologie, Universität Münster*

Challenged by variable temperature conditions in its habitat, the poikilothermic planktonic crustaceans of the genus Daphnia can adjust metabolic properties and physiological performance to a broad temperature range. Fast increase of temperature are closely related to reduced oxygen supply to the cells, therefore anaerobic energy metabolism involving glycolysis gains importance under these conditions. The presented studies focus on selected enzymes of this pathway, PGM (phosphoglucomutase), PGI (phosphoglucose isomerase) and LDH (lactate dehydrogenase) in Daphnia, combining laboratory analyses and field studies. Their properties concerning activity and affinity are severely affected by temperature. In response to persisting temperature changes, differential subunit expression supplies individuals with more suitable subsets of isofoms. This phenotypic plasticity can restore enzyme activity to the appropriate level for the new conditions within an individual. Widening the view to the population, the occurrence of different allozymes of glycolytic enzymes offers the chance for microevolutive processes, selecting genotypes optimally suited for the prevailing conditions. Accordingly, the abundance of animals carrying specific variants of these enzymes of interest changes along with the season or along a vertical temperature gradient within the lake. The presentation will aim at an integrative view from biochemical and molecular properties of the three enzymes to resulting shifts in thermo-tolerance and genotype contribution to the Daphnia assemblage.

S☐9 Marcus Lukas R513 / 15:15

Daphnia feels the difference: Stoichiometric regulation at different food conditions

Authors: *Marcus Lukas*[1], *Alexander Wacker*[1]
Affiliation: [1]*Dept. Theoretical Aquatic Ecology, Institute of Biochemistry and Biology, Univerität Potsdam*

The energy, nutrient and biochemicals transfer from autotrophs to herbivores is a key process in all ecosystems, but we know little about how fast herbivorous zooplankton such as Daphnia could adapt carbon stoichiometry to varying food quality and quantity. Thereby the availability of food could decrease quickly (i) if Daphnia migrates into deep water layers to avoid predation or (ii) during clear water phases. During certain time phases also the species composition of the phytoplankton community changes quickly, which strongly affects food quality in terms of the availability of essential biochemical nutrients such as phytosterols. In the present study we investigated the stoichiometric regulation of Daphnia magna acclimatized to different food conditions for different acclimatization times. We measured short time assimilation, excretion and respiration rates by the usage of 14C radio-labeling. While Daphnia immediately adapted the stoichiometric regulation to changing food quantity, their adaptation to changing food quality appears to be more complex. The presented results will deliver further insights in the primary producer - consumers interface at changing environmental conditions.

S☐10 Sarah Oexle R513 / 16:00

Sterol metabolic constraints in *D. magna*

Authors: *Sarah Oexle*[1], *Alexander Wacker*[2], *Dominik Martin-Creuzburg*[1]
Affiliations: [1]*University of Konstanz*; [2]*University of Potsdam*

In Daphnia, as in all arthropods, cholesterol is an essential nutrient, which must be obtained directly from food sources or by bioconversion from other dietary sterols. Eukaryotic phytoplankton contains a great variety of different sterols. However, these sterols differ in their chemical structure and it is not yet known to what extend Daphnia is able to convert them to cholesterol. We investigated the effects of ten different sterols provided as dietary supplements in increasing concentrations along with the sterol-free cyanobacterium Synechococcus elongatus on the growth of Daphnia magna. Somatic growth rates in response to dietary sterol concentrations and thresholds for sterol-limited growth were evaluated comparatively for each supplemented sterol using a modified form of the ‚Von Bertalanffy‘ function.

Furthermore, the sterol composition and the concentrations of individual sterols in the animals were analysed by gas chromatography - mass spectrometry (GC-MS) to obtain information on sterol metabolism and bioconversion capacities of *D. magna*. Our results indicate that dietary phytosterols strongly differ in their suitability to support Daphnia growth and thus highlight the importance of considering sterol-mediated nutritional constraints on Daphnia performance in the field.

S☐11 Piet Spaak R513 / 16:15

Daphnia populations in (ultra) oligotrophic lakes?

Author: *Piet Spaak*

Affiliation: [1]*Eawag Duebendorf*

The successful reoligotrophication of lakes had led to situations where phosphorus concentrations in lakes declined to values below 2 or 3 microgram per litre. This has led to decreased primary production, less zooplankton and declined fish catches. In lake Brienz, Switzerland, Daphnia disappeared during several years and also in other lakes there are indications that the Daphnia population decreases. In this presentation I present data about the historic Daphnia densities in lake Brienz as well as life history data about the two main Daphnia species in large Swiss lakes. With this data I try to answer the question: „is there a threshold for phosphorus in a lake for the support of a Daphnia population?“

S☐12 Markus Möst R513 / 16:30

Assessing the human impact on Daphnia populations in peri-alpine lakes

Authors: *Markus Möst[1/2], Dalia Aidukaite[1], Livia Baumgartner[1], Sarah Oexle[3], Martin Wessels[4], Flavio Anselmetti[1], Hans-Bernd Stich[4], Dominik Martin-Creuzburg[1], Piet Spaak[1/2]*

Affiliations: [1]*Eawag Duebendorf*; [2]*Institute of Integrative Biology, ETH Zürich*; [3]*University of Konstanz*; [4] *Institut für Seenforschung der Landesanstalt für Umwelt, Messungen und Naturschutz Baden-Württemberg, Langenargen*

Anthropogenic activities can affect the evolution of natural populations and species by altering selective forces. Consequently, humans become themselves an important evolutionary force. Pollution, eutrophication, as well as introduction of species are well known examples for such human-induced changes.

Resting eggs preserved in lake sediments together with traces of human activities stored in the sediment record allow to reconstruct human impacts on the evolutionary history of water flea species over the last decades. The egg bank allows for a reconstruction of population structure and dynamics, invasions, and microevolutionary changes for Daphnia species. Lake sediments constitute also a useful record for trophic changes in lakes. During a phase of eutrophication in peri-alpine lakes, several Daphnia species managed to established new populations in several of these lakes often accompanied by hybridization with native members of the same complex.

In an interdisciplinary approach, bringing together evolutionary ecologists and sedimentologists, we are reconstructing population patterns and dynamics in the D. longispina - galeata - cucullata complex south of the Alps as well as in D. pulicaria in Lower Lake Constance. We also aim to identify patterns of pollution and eutrophication across the Alps on the basis of lake sediments, in order to identify factors that drive evolutionary change and invasion patterns in these groups.

S☐13 Nicole Henning R513 / 16:45

The evolutionary adaptation potential of *Daphnia galeata* in time and space

Authors: *Nicole Henning*[1]*, Mathilde Cordellier*[1]*, Bruno Streit*[1]*, Klaus Schwenk*[1]
Affiliation: [1]*Biodiversity and Climate Research Centre, Frankfurt/Main*

In the framework of global change research we aimed at estimating the impact of elevated water temperatures on an aquatic keystone species, the freshwater zooplankter *Daphnia galeata*. We performed two main experiments to measure variation in life-history traits under different temperatures and to assess the evolutionary adaptive potential of daphnids. For both experimental approaches we sampled dormant egg banks of *Daphnia galeata* populations to obtain a representative sample of natural genetic diversity. In addition to superficial sediment layers, sampled along a latitudinal gradient across Europe, we used layers from different depths in a ‚resurrection ecology‘ approach to study responses to variation in water temperatures. We performed common-garden experiments after hatching and establishment of clonal lineages in the laboratory. In flow-through-systems *D. galeata* individuals from different time periods and latitudes were exposed to various temperature regimes. To quantify the evolutionary potential of the resident natural populations we compared their response to changes in temperature by measuring several life history traits. In all experiments elevated water temperatures were shown to result in a reduced body size, a higher reproduction rate, an increased somatic growth rate and accordingly an earlier age at maturity. In addition to observed phenotypic plasticity, significant temperature-age-interactions and temperature-origin-interactions indicate thermal micro-evolution within last decades. We discuss these genetic adjustments regarding the consequences of global warming on the fate of Daphnia populations and the freshwater ecosystems they inhabit.

S☐14 Johanna Griebel R513 / 17:00

Can a hybrid outcompete its parental species? - a competition experiment with a “super clone” (*Daphnia galeata × longispina* hybrid)

Authors: *Johanna Griebel*[1]*, Monika Poxleitner*[1]*, Sabine Gießler*[1]*, Justyna Wolinska*[1]
Affiliation: [1]*Ludwig-Maximilians-Universität München*

Interspecific hybridization is an important force in evolutionary processes, leading to new genotypes and adaptations to new environments. In general, hybrids show lower fitness than their parental species. However, during the last years it has been found that the Daphnia longispina community inhabiting a small quarry lake in Munich (Feldmochinger See) has become dominated by a single hybrid clone. This ‘super clone’ outcompeted the entire population of hybrids and against all expectations their parental species. Thus, we conducted an experiment to test for the ability of 'super clone' to outcompete other hybrids. Different clones, isolated from 10 quarry lakes around Munich have been assigned randomly in five different groups of 15 clones (5 *D. longispina*, 5 *D. galeata*, 4 of their hybrids and one clone of a different Claderoceran species from the same lakes). These experimental communities have been kept for ten weeks to measure the changes in community composition.

We expect that the experimental communities will become dominated by a single clone in the F1 hybrids but not in the parental taxa. This is because most of the hybrids show extreme phenotypes and thus are poorly adapted to local environments. But also a few genotypes might be especially fit and so would be a successful competitor. The studied quarry lakes were created and thus opened for colonization only about 20 years ago, our work might then contribute to a knowledge how hybrid-specific traits may facilitate the colonization of novel habitats.

S□15 Christian Laforsch R513 / 17:15

Stealth mechanism or predator confusion? The exact defensive mechanism of protective helmets in Daphnia

Authors: *Christian Laforsch, Johannes Aman*

Affiliation: [1]*University Bayreuth*

Inducible defences are strategies for coping with predation in heterogeneous environments. In recent years conspicuous and often dramatic morphological plasticity of several waterflea-species of the genus Daphnia has been found. For instance helmets proved to be protective against predatory invertebrates. However, the exact defensive mechanisms of the protective traits remained elusive. We used high-speed camera video analysis to study the exact defensive mechanism of protective helmets. Our study showed that helmet formation in Daphnia cucullata leads to a wrong strike distance estimation in Chaoborus larvae. Chaoborus larvae either completely miss their target or they only could catch a part of their prey item. Given that Chaoborus larvae detect their prey with mechanoreceptors; our results suggest that the protective traits alter the flow field around Daphnia. While our study questions the current paradigm for the defensive mechanism, the 'anti-lock-and-key hypothesis', it does not rule out, that multiple effects, incompatibility with the predator mouthparts, an increased mechanical stability of their armour, and a altered flow field act synergistically.

S□16 Kathrin Otte R513 / 17:30

Proteomic analysis of predator-induced phenotypic plasticity in *Daphnia magna*

Authors: *Kathrin A. Otte*[1]*, Thomas Fröhlich, Georg J.Arnold, Christian Laforsch*

Affiliation: [1]*Department of Biology II, Ludwig-Maximilians-University Munich*

Inducible defences have evolved under specific ecological conditions: spatial or temporal variation in predation risks, availability of reliable cues indicating the threat, possibility to form effective defences within a relatively short time span, and an association of costs that can be saved when defences are not required. Inducible

defences affect predator-prey relationships, competitive interactions, and potentially ecological processes, including population and community structure: this renders them an interesting phenomenon from both an ecological and evolutionary point of view. To fully understand the adaptive value of inducible defences in nature, it is required to investigate the mechanisms underlying these plastic responses. In freshwater ecosystems inducible defences are found in a variety of taxa spanning from bacteria to vertebrates. However, the dominant model system for studying predator-induced formations of protective traits is Daphnia.
We recently discovered an inducible morphological defence in Daphnia magna in response to the tadpole shrimp Triops cancriformis. Using this system, we started to discover candidate proteins linked to predator induced morphological defences in Daphnia magna by applying a proteomic ‚2D Fluorescence Difference Gel Electrophoresis' (DIGE) approach followed by mass spectrometric (MS) analysis. Initially, a crucial step was to adjust the proteomic workflow to the special features of Daphnia, namely the high proteolytic activity found in Daphnia protein extracts. By using different ontogenetic stages we overcame the difficulties arising from high proteolytic activity and were able to find differentially expressed proteins between predator exposed Daphnia and the control group. These results may contribute to the knowledge on molecular pathways involved in the formation of inducible defences in Daphnia.

POSTERS

♦**202** Wolfgang Engelbrecht

Double-stressed *Daphnia longicephala*: Does the encounter with Metschnikowia sp. spores in the presence of predator cues lead to changes in morphological defenses and life history?

Authors: *Wolfgang Engelbrecht*[1]*, Olivia Hesse*[1]*, Justyna Wolinska*[1]*, Christian Laforsch*[1]
Affiliation: [1]*Ludwig-Maximilians-Universität München*

Although both predator-prey and host-parasite interactions have been extensively studied in Daphnia, there is still a lack of information on the effects of parasite exposure on the formation of inducible defenses. We exposed two *Daphnia longicephala* clones to parasites (yeast Metschnikowia sp.) and predator cues (backswimmer) to study how morphological defenses and life history are affected by the combination of both stressors. Albeit the parasite was able to produce spores only in a few hosts, all Daphnia in the parasite exposed treatments still showed effects stemming from an infection. Parasite exposure did not reduce the expression of the morphological defenses. In one clone, however, the body size reduction in the parasite exposed Daphnia was absent in presence of the predator cues. Our data suggests that even without visible signs of infection the parasite can already affect its host.

♦203 Jakub Rusek

Access to poor quality Daphnia samples – a novel SNP based approach

Authors: *Jakub Rusek*[1], *Patrick Turko*[2], *Christoph Tellenbach*[2], *Sabine Gießler*[1],*Piet Spaak*[2], *Justyna Wolinska*[1]
Affiliation: [1]*Department of Biology II, Evolutionsoekologie, Ludwig-Maximilians-University*; [2]*Eawag, Swiss Federal Institute of Aquatic Science and echnology, Duebendorf, Switzerland Munich*

Microsatellite genotyping of natural plankton populations is a well established method for the identification of species and their hybrids in the *Daphnia longispina* complex. However, we found these length-based markers unsuitable when analyzing poor quality samples (such as historical or degraded samples). For example, formaldehyde fixation, which fragments DNA, prevents amplification of longer DNA fragments. SNP genotyping seems to be a good approach to overcome this problem, due to the possibility of shorter fragment amplification. Furthermore, this method allows not only high-throughput genotyping, but the calibration among laboratories is also relatively precise. Therefore, we aim to develop a reliable method to identify species of the *D. longispina* complex and their hybrids by SNP genotyping. After comparing the *D. galeata* transcriptome with the *D. pulex* genome, we are selecting several putatively informative genes and designing corresponding primers. Candidate SNPs are being identified based on sequence information of all three species from the *D. longispina complex*. To confirm the diagnostic value of these candidate SNPs, we are using a set of genetically well-defined clones from species and hybrids originating from diverse locations across Europe. For large-scale screenings we are optimizing SNP detection via the SnaPshot Multiplex kit. By multi-locus SNP genotyping we will be able to assess the population structures in long-term formaldehyde preserved samples of a hybridizing species complex.

♦204 Max Rabus

Uncovering hidden morphological defences in *Daphnia magna* - an interdisciplinary approach to assess the predator-induced fortification of the carapace

Authors: *Max Rabus*[1], *Thomas Söllradl*[1], *Hauke Clausen-Schaumann*[1], *Christian Laforsch*[1]
Affiliation: [1]*Department of Biology II, Ludwig-Maximilians-University Munich*

The cladoceran *Daphnia magna* has been shown to develop a bulky morphotype as an effective inducible morphological defence against the predatory tadpole shrimp Triops cancriformis. Mediated by kairomones, the daphnids express an increased body length, -width and an elongated tail spine. In the present study we examined whether these large scale morphological defences are accompanied by additional ‘hidden’ defences, i.e. a fortification of the exoskeleton. To obtain this goal we employed atomic force microscopy to assess the hardness of the cuticle, we used semi thin sections of the carapace to measure the cuticle thickness and finally, we used fluorescence microscopy to analyse the diameter of the pillars connecting the two carapace layers. We found that *D. magna* indeed expresses hidden morphological defences against Triops predation. Thereby, the cuticle in induced individuals is approximately five times harder and two times thicker than in control daphnids. Moreover, the pillar diameter is significantly increased in induced daphnids. These induced changes in the carapace architecture should provide an effective protection against being crushed by the predator's mouthparts and might thus add to the protective effect of the bulkiness.

♦205 Sebastian Kruppert

Daphnia Carapace: Structure, Form, Function, Plasticity

Authors: *Sebastian Kruppert*[1]*, Linda C. Weiss*[1]*, Hans-Peter Prüfer, Christian Laforsch, Ralph Tollrian*[1]
Affiliation: [1]*Department of Animal Ecology, Evolution & Biodiversity, Ruhr-Universität Bochum*

Phenotypic plasticity describes the ability of an organism with a given genotype to respond to changing environmental conditions by the adaptation of its phenotype. Inducible defenses represent a special form of phenotypic plasticity that has been well studied in the model crustacean Daphnia. Changes of the biotic environment such as an increased predation risk result in a species-specific development of e.g. morphological anti-predator defenses which increase the organism‘s chance of survival. It has been shown, that these distinct morphological structures are accompanied by changes of the Daphnia‘s carapace ultrastructure leading to 2- to 3-fold increased rigidity. Although the morphological defenses and their benefits are well studied the mechanical properties and characteristics leading to the increased rigidity remain unknown. This project aims to analyze the physical properties of the Daphnia‘s carapace, using atomic force microscopy. Based on the empirically determined physical properties of the control and adapted Daphnia digital 3D-Models of the carapace and its ultrastructure will be created. These models will be tested for their mechanical behavior under the impact of a predatory attack to identify characteristics increasing carapace rigidity.

♦206 Philipp Meyer

Does Daphnia equal Daphnia? Genomic challenges working with a phylogenetically diverse model species

Authors: *Philipp Meyer*[1]*, Andrey Kuzmin*[1]*, Linda Weiss*[1]*, Florian Leese, Ralph Tollrian*[1]
Affiliation: [1]*Ruhr-Universität Bochum*

The recently published genome of *Daphnia pulex* is a keystone connecting the vast ecological knowledge accumulated for this species over more than a century with functional evolutionary and developmental biological approaches. The genome of the sequenced Daphnia strain contains several interesting characteristics such as a large number of paralogous genes with highly specific regulation patterns as well as genes of as yet elusive function and a high density of repetitive elements. It is unknown whether these traits are general for phylogenetically different Daphnia species/clones and how well the genomic resources of the sequenced clone can be transferred to other daphnids. We compared the genes involved in the development of inducible defenses using high-throughput RNA sequencing of induced and non-induced phenotypes of Daphnia. Subsequently, we analyzed the transcriptional

profiles in a clone with strong defense response in comparisonto the reference genome clone. Our results underpin the necessity to extend the genomic information available by sequencing the genomes of further ecologically well-characterized clones.

♦208 Patrick Turko

Unlocking the formalin DNA archive: The role of variable environments on hybrid success

Authors: *Patrick Turko, Piet Spaak*
Affiliation: [1]*Eawag*

Hybridization is a common phenomenon in both plant and animal kingdoms. Recent data suggest that hybridization is a creative force forming novel genotypes and allowing rapid adaptation to new environments. Assessing hybrid fitness relative to that of parental species is crucial for understanding the widespread nature of hybridization, but most studies of hybrid fitness focus on snapshots" that are limited in space and time. Using new technologies, we have isolated PCR-amplifiable DNA from formalin-preserved zooplankton samples collected over the last 100 years. By combining this long-term, high resolution genetic data with similarly high resolution environmental and ecological data, and by focusing on lakes that have undergone environmental changes over the same time period, we are investigating the role that environmental variation plays in the relative success of hybrids. "

♦209 Beate Mittmann

Development and staging of *Daphnia magna*

Authors: *Beate Mittmann*[1]*, Petra Ungerer*[2]*, Carsten Wolff*[3]
Affiliation: [1]*Institut für Biologie III, Neurogenetik, Albert-Ludwigs-Universität Freiburg*; [2]*SBCS Queen Mary University, London, UK;* [3]*Institut für Vergleichende Zoologie, Humboldt-Universität zu Berlin*

Over the past years the water flea *Daphnia magna* became an interesting organism for comparative developmental biologists. Due to its easy keeping and breeding under artificial conditions, its high reproductive rate and its short developmental time, *Daphnia magna* became an attractive lab organism. However, a detailed description of its development serving as basis for comparative developmental studies is still missing. We will provide a detailed description of the (direct) development of the subitaneous eggs and a staging system which allows an easy recognition of the individual developmental stages.

♦210 Christoph Tellenbach

Cyanobacteria - a missing link in Daphnia epidemics?

Authors: *Christoph Tellenbach*[1]*, Piet Spaak*[1]
Affiliation: [1]*Eawag*

The composition and abundance of single taxa in plankton communities is fluctuating constantly. These fluctuations are due to several biotic and abiotic factors like temperature, oxygen and nutrient availability, which shape presence or absence of certain taxa, whilst others are little affected. Moreover, the presence of keystone species like parasites and predators, but also strong resource exploiters can significantly affect the taxa composition of a community. Therefore, a complex network of interactions is occurring in lake ecosystems.

The plankton community of Greifensee, a middle-sized pre-alpine eutrophic lake in Switzerland, has been monitored intensely during the last decade, including the Daphnia population and their parasites. There are three major parasite epidemics occurring regularly, with Caullery mesnili, a protist gut parasite, being the most abundant taxon that sometimes reaches a prevalence of over 30%. Initially, Caullerya epidemics seemed to occur annually with high prevalence, but suddenly the epidemic was virtually absent for three years, and attained a high prevalence of 30% in 2011 again. However, factors affecting fluctuations in Caullerya epidemics are not well understood.

At the same time, there occurred an algal bloom of the cyanobacteria species Microcystis aeruginosa. A comparison of Caullerya epidemics with cyanobacterial abundance has shown that these two organisms are closely associated, whereas none of the of the other two parasite epidemics was. Therefore, the question poses how Caullerya epidemics and cyanobacteria blooms are interlinked, and particularly, whether they require the same environmental conditions or whether cyanobacteria create an environment facilitating the outbreak of Caullerya epidemics.

♦211 Anna Bednarska

Intergeneration differences in responses of Daphnia to the presence of cyanobacteria under raised temperature?

Author: *Anna Bednarska*[1]
Affiliation: [1]*Department of Hydrobiology, University of Warsaw, Poland*

Cyanobacteria are considered as poor food source for herbivorous zooplankton (e.g. *Daphnia*), and many arguments indicate that forecasted global warming will intensify the negative influence of Cyanobacteria on *Daphnia* fitness. The increase of mean water temperature can extend the period of Cyanobacteria dominance in phytoplankton, thus exposition of *Daphnia* to Cyanobacteria will last for many generations. The intergenerational differences in responses of *Daphnia* to presence of Cyanobacteria and elevated temperature and the ability of *Daphnia* to survive the long lasting exposition to those two factors was tested in this study. *Daphnia magna* from three clones were fed for five generations with green algae *Scenedesmus obliguus* or Cyanobacteria *Cylindrospermopsis raciborskii* and kept in 20° or 24°C. The key life history parameters were recorded. Detrimental effects of Cyanobacteria increases with lengthening time of exposition of *Daphnia* to Cyanobacteria presence (e.g. production of sexual eggs in later generations). However, even when Cyanobacteria were the only available food, they sustained the growth and reproduction of *Daphnia* for five generations. The elevated temperature can intensify the negative influence of Cyanobacteria on *Daphnia* (e.g. the highest number of individual which did not reproduce in later instars was observed in the presence of Cyanobacteria at higher temperature).

♦212 Quirin Herzog

Reversibility of inducible defenses in *Daphnia barbata*

Authors: *Quirin Herzog*[1]*, Carmen Tittgen*[1]*, Christian Laforsch*[1]
Affiliation: [1]*Dep. Biol. II, Evolutionary Ecology, LMU München*

Predator-Prey interactions are among the most common interspecific interactions in nature. Due to spatial or temporal heterogeneity in predation risks, many prey organisms respond with so-called inducible defenses. To evolutionary favor this type of phenotypic plasticity over permanent defenses, they have to imbue costs, which can be saved in the absence of a predator. Depending on the nature of these costs (i.e. formation or running costs) these inducible defenses themselves are expected to be either persistant or reversible, when not required anymore. Despite intense research on inducible defenses in a variety of organisms the aspect of reversibility has been widely neglected. So far, the same is true for the genus Daphnia, which has been extensively studied in the context of inducible defenses. Here we test *Daphnia barbata*, which displays a wide array of morphological defenses for reversibility of these traits. We used two different invertebrate predators (Triops cancriformis and Notonecta glauca), which cause predator-specific changes in the same traits (i.e. helmet, tail spine, dorsal ridge) in *D. barbata*. By comparing the reversibility and constancy of defensive structures depending on the predator, our results may indicate the relevance of reversibility regarding the evolution of phenotypic plasticity.

♦213 Linda Weiss

Neurophysiology of Inducible Defenses in Daphnia

Authors: *Linda C. Weiss*[1]*, Christian Laforsch*[2]*, Ralph Tollrian*[1]
Affiliation: [1]*Department of Animal Ecology, Evolution and Biodiversity, Ruhr University Bochum*; [2]*Department of Biology II, Ludwig-Maximilians-University Munich*

The immense ability of the model crustacean Daphnia to phenotypically adapt to changing biotic and abiotic environmental conditions has eminent impacts on freshwater ecosystems and their dynamics. Its ecological importance has been intensively described throughout the past century. Progression on genome structure and differential gene expression in unstable environments has been made since the sequencing of the genome in 2007. Nevertheless, information on the underlying cellular and neuronal mechanisms that are responsible for differential gene expression and the resulting phenotypic adaptations is sparse. This study focused to unravel the cellular and neuronal mechanisms underlying phenotypic plasticity in Daphnia.

We here describe the internal physiological functions and determine the neurotransmitters involved in the formation of inducible morphological defenses in Daphnia.

♦**214** Gerd Gäde

Peptide signalling in branchiopod crustaceans: the AKH/RPCH system in *Daphnia pulex*

Authors: *Gerd Gäde[1], Heather G. Marco[1], Lance A. Anders[1]*
Affiliation: [1]*Zoology Department, University of Cape Town, Rondebosch, South Africa*

Neuropeptide and peptide hormones are a well-studied group of signalling molecules involved in regulating a variety of physiological processes in animlas. With the advent of whole organism genome sequencing, it has become possible not only to predict the sequence of such hormones, but also the potential receptor for such a ligand. By using bioinformatic tools available and accessing sequence information in databases, this has become a preferred methodological avenue to the classical chemistry and biochemistry approaches, despite several short-comings to the in silico route. In our study, we accessed the water flea Daphnia pulex genome data base to identify the predicted, putative red pigment-concentrating hormone (Dappu-RPCH) and its receptor (Dappu-RPCHR). We then designed primers to amplify, clone and sequence these predicted products from total RNA extracted from two different D. pulex ecotypes: one originating from Germany, and the other from South Africa. We show distinct, repeatable differences in the preprohormone sequence deduced from the whole genome data base information versus what we cloned from the German and from the South African water fleas. These differences are not in the Dappu-RPCH sequence but in the signal peptide and the precursor-related peptide. These differences are very interesting, considering that the same species is being investigated and surely reflect genomic differences that have arisen between the different water flea clones used in this study. The source and the function of Dappu-RPCH are still unknown. We attempt to address this aspect by reverse transcription polymerase chain reaction with cDNA templates derived from different tissue types in *D. pulex*.

Supported by NRF and URC of UC

♦**215** Faten Gabsi

A modeling approach to characterize population-level effects of sub-lethal exposure to toxicants in *Daphnia magna*

Authors: *Faten Gabsi[1], Thomas Preuss[1]*
Affiliation: [1]*RWTH Aachen University*

In this study, we aim to determine how sub-lethal effects measured on individuals affect population properties in *Daphnia magna*.

Toxicant-induced changes on individuals translate differently at the population level. For instance, population decline may arise from simple affected individual-level endpoints, whereas a significant influence on other endpoints might have negligible impact on population size and/or structure.

Population modeling has been used as a powerful tool to extrapolate measured effects on individuals to the population level. It allows including the variability between individuals in response to chemical‘s exposure and accounting for the different mechanisms of action of a toxicant.
In this work, we use an already developed and validated individual-based model for *D. magna* (IDamP, see Preuss et al, 2009) as a virtual laboratory in order to investigate the sub-lethal effects of a hypothetical toxicant on the population level, and to compare their relative magnitudes of effects.
Different simulation scenarios will be tested: Effects on reproductive performance might be exerted via various mechanisms like reduction in the filtration rate, delay in the time to first reproduction, etc. A slowed or inhibited growth induced by exposure to the toxicants will also be assessed solely or combined to reproductive effects.
Modeling these different responses will be addressed in combination to varying environmental factors like variable food levels.
Using such an approach allows us to explain the interactions between natural factors and toxicity at the level of individuals which ultimately emerge as effects on populations‘ properties.

20. Symposium “Genomics of adaptation and population genomics”

Sunday, September 23, 2012

Key Note: Chair: Axel Meyer R 513 / 11:00

Scott Edwards

The phylogeography-phylogenetics continuum in the genomic era

Author: *Scott V. Edwards*[1]
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As genomics makes available ever-increasing numbers of loci for phylogenetic analysis, the diversity of gene histories due to incomplete lineage sorting and other factors increases as well. Concatenation of multilocus data sets into supermatrices has proven an effective way of increasing phylogenetic signal for the Tree of Life. However, when analyzed by standard methods that ignore gene tree heterogeneity, theory suggests that concatenation yields inconsistent estimates of phylogenetic relationships when gene tree heterogeneity is high. Natural selection is yet another variable that can increase or decrease the degree of gene tree heterogeneity. Here I illustrate these principles with empirical examples from songbird genomes and transcriptomes, and from eutherian mammals. Gene trees from transcripts in the gonads of the promiscuous Australian Fairy Wrens (Maluridae) show less evidence of incomplete lineage sorting relative to neutral markers, presumably due to persistent natural selection on reproductive genes. Among 37 eutherian mammals, analysis of 447 coding regions reveals a remarkably high level of gene tree heterogeneity, much of which can be explained by the multispecies coalescent model, and which results in inconsistent results when analyzed by standard concatenation methods. These results suggest that so-called “species tree” methods – a family of phylogenetic methods that accommodates gene tree heterogeneity through the multispecies coalescent model – provide a robust way forward for phylogenomic data sets and exploration of genomic heterogeneity. With large multilocus data sets the line between phylogeography and phylogenetics becomes increasingly blurred, and the statistical models by which population genomic and phylogenomic data are analyzed are predicted to converge.

Key Note: Chair: Axel Meyer R 513 / 11:30

Felicity Jones

The genomics of adaptive divergence and reproductive isolation in sticklebacks

Authors: *Felicity C. Jones*[1], *Yingguang Frank Chan*[1/2], *Manfred G Grabherr*[3/4], *Pamela Russell*[3], *Evan Mauceli*[3], *Jeremy Johnson*[3], *Ross Swofford*[3], *Mono Pirun*[3], *Michael C. Zody*[3], *Simon White*[5], *Ewan Birney*[6], *Stephen Searle*[5], *Jeremy Schmutz*[7], *Jane Grimwood*[7], *Mark C. Dickson*[7], *Richard M. Myers*[7], *Craig T. Miller*[1,8], *Brian R. Summers*[1], *Anne K. Knecht*[1], *Shannon D. Brady*[1], *Haili Zhang*[1], *Alex A. Pollen*[1], *TimothyHowes*[1], *Craig Lowe*[1], *Nicellio Sanchez-Luege*[1], *Chris Amemiya*[9], *Tom Reimchen*[10], *Bruce Deagle*[10/11], *Dolph Schluter*[12], *Eric S. Lander*[3], *Federica Di Palma*[3], *Kerstin Lindblad-Toh*[3/4], *David M. Kingsley*[1/13]

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The adaptive radiation of sticklebacks, coupled with rapidly increasing genetic and genomic tools, provides an outstanding opportunity to characterize evolutionary processes underlying phenotypic diversity, adaptation, and speciation. Previous studies have shown that parallel evolution of lateral plate morphology occurred on a global scale via the repeated reuse of genetic variation at the *EDA* locus (Colosimo *et al.,* 2005). To search for other loci contributing to repeated adaptation, we sequenced 21 marine and freshwater sticklebacks from globally diverse populations (Jones *et al.,* 2012). We identified with high resolution a set of 81 shared adaptive loci, including chromosomal inversions that are consistently associated with marine–freshwater divergence.

Our results indicate that reuse of globally shared standing genetic variation, including chromosomal inversions, has an important role in repeated evolution of distinct marine and freshwater sticklebacks, and in the maintenance of divergent ecotypes during early stages of reproductive isolation. We used this genome-wide set of loci to address a long-standing debate about the relative contribution of coding and regulatory changes underlying adaptive evolution in natural populations. We find that both coding and regulatory changes occur, but regulatory changes predominate in this classic example of repeated adaptive evolution in nature.

We have previously shown that adaptation does not always proceed by reuse of globally shared genetic variation: for example, parallel evolution of pelvic reduction occurs via population-specific mutations at the *Pitx1* locus (Chan *et al.,* 2010). Ongoing analyses of additional benthic–limnetic and marine–freshwater populations should make it possible to estimate the relative proportion of both shared and locally-restricted adaptive variants contributing to recent diversification and reproductive isolation of sticklebacks.

Key Note: Chair: Axel Meyer R 513 / 12:00

Philine Feulner

Genome-wide structural variations and adaptation in parapatric lake-stream populations of the three-spined stickleback Gasterosteus aculeatus

Author: *Philine Feulner*[1]
Affiliation: [1]*Westfälische Wilhelms University, Münster*

Recent advances in technology have enabled the characterization of various types of genome architectural variation and their prevalence in populations. It has been revealed that many such structural differences have significant functional impacts. The three-spined stickleback has been established as a supermodel for evolutionary ecological genomics. However, genome-wide structural variation data from natural populations remain scarce. Here we present whole genome data from 66 three-spined stickleback individuals representing three ecotypes from a broad geographic range, a marine population and multiple lake-stream population pairs. For each population, the sequencing of six individuals per population allows an in-depth evaluation of genome-wide polymorphism. Population diversity is contrasted between parapatric and geographically distant (allopatric) population pairs undergoing parallel ecological adaptation. Large structural variations such as deletions, insertions, copy number variations, inversions, and translocation are accessed exploiting different signatures apparent in short-read sequencing data. Utilizing paired-end mapping, depth of coverage, and split read analysis, we are constructing a structural variation discovery set for the three-spined stickleback. First results analyzing the marine population highlight the relevance of structural variation. About 7% of the genome varies in structural organization within our samples, encompassing over 10% of genes. In addition, we find first indications for population-specific structural variation in the lake-stream comparisons, many of which interfere with known protein coding regions. Evaluating structural variation of the stickleback genome within and between natural populations will contribute towards a better understanding of the evolution of genomes. In addition, our nested experimental setup allows us to gain insights into the importance of structural variations underlying adaptive responses in the wild.

Key Note: Chair: Axel Meyer R 513 / 12:30

Frank Chan

Complex inter-subspecific hybridization and adaptation in an island population of house mice

Authors: *Yingguang Frank Chan* [1], *Eleanor P Jones*[2], *Sabrina Renaud*[3], *Floyd A Reed*[4/5], *Diethard Tautz*[4]

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Island biology has a special place in evolutionary biology, with islands acting as natural laboratories in which theories about evolution, ecological turnover, speciation and adaptation can be formulated and tested. Here we investigate the role of hybridisation in adaptation and differentiation in the context of the Faroe house mouse. Originally described as a distinct subspecies, *Mus musculus faeroensis*, the Faroe house mouse has long attracted attention as being unusually large and possessing unique morphological characters. Using high-density genotyping, we have identified >73,000 ancestry informative SNP markers and show that the Faroese house mice arose through a *M. m.musculus* introgression into a largely *M. m.domesticus* background, confirming our previous findings from a small number of nuclear markers. Having identified areas of *M. m.musculus* introgression within the genome, we estimated a likely demographic scenario of this hybridization. Our molecular data supports a modest number of *M. m.musculus* immigrants since Danish colonization of the Faroes. We have found also multiple selective sweeps arising from these introgressions. A geometric morphometric analysis revealed that the Faroese house mice exhibit greatly divergent skull morphology compared to continental populations, as was described in the early literature. Taken together, our results suggest that the Faroese house mouse genome has undergone extensive hybridization and the molecular data support an adaptive trajectory. Therefore, despite founder effects and small effective population sizes, rapid adaptation is clearly possible among island populations, and we hypothesize that hybridization may promote such adaptation.

Key Note: Chair: Axel Meyer R 513 / 17:30

Chris Jiggins

Genome-wide patterns of introgression between hybridizing Heliconius species

Author: *Chris Jiggins*[1]

Affiliation: [1]*University of Cambridge, UK*

During speciation in the face of ongoing hybridization, genes under divergent selection are expected to experience reduced gene flow, potentially accumulating within genomic islands of divergence. However, it is difficult to objectively quantify levels of divergence and gene-flow across the genome, and so it remains unclear how well the islands metaphor applies in nature. The neotropical butterfly species Heliconius melpomene and Heliconius cydno offer a useful system in which to investigate speciation with gene flow. These species have diverged ecologically over the past two million years, most notably in their mimetic colour patterns, but continue to hybridize in the wild. In this study we investigate genome-wide patterns of introgression between H. melpomene and H. cydno by comparing genetic differentiation in sympatry and allopatry, and applying various different tests for introgression. We find a strong signal of introgression throughout the genome, and estimate that at least 25% of the genome has been shared between the Panamanian sub-populations of the two species. Furthermore, we detect patterns divergence and linkage disequalibrium that are consistent with recent or ongoing gene flow in sympatry. Introgression appears to be significantly reduced Z chromosome, which is consistent with the observed female hybrid sterility between these populations. We also observe numerous narrow islands of divergence, which include wing patterning loci known to be under divergent selection. Overall these results show that these species have diverged and persisted despite pervasive genome sharing.

TALKS

S□17 Christian Sturmbauer R 513 / 14:00

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

Authors: *Christian Sturmbauer*[1], *Christian Gülly*[1], *Christian Schlötterer*[1], *Slave Trajanoski*[1], *Christoph Fischer*[1], *Gerhard Thallinger*[1]

Affiliation: [1]*Department of Zoology, University of Graz, Austria*

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 currently decipher 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 use 454 sequencing technology in combination with shotgun approaches to successfully score the two genomes in reasonably complete coverage. The project is carried out as cooperation between four research groups from three Universities, The Karl-Franzens University of Graz, the Medical University of Graz, the Graz University of Technology and the University of Veterinary Medicine Vienna, whereby each group contributes crucial expertise and resources. We utilize two eco-morphologically diverse species as "natural mutants", to understand the common pattern of cichlid adaptive evolution and its connection to speciation processes at various stages of adaptive radiation, to find correlates to divergent eco-morphologies, as recently demonstrated e.g. for Lake Malawi rock cichlids. The key characteristic and complementary potential of the Lake Tanganyika system is its significantly older evolutionary age and the fact of more complete genomic separation, even among morphologically similar species. We present first results.

S□18 Shaohua Fan R 513 / 14:15

Copy number variation in the adaptive radiation of African cichlid fish

Authors: *Shaohua Fan*[1], *Axel Meyer*[1]
Affiliations: [1]*Lehrstuhl für Zoologie und Evolutionsbiologie, Department of Biology, University of Konstanz*

Cichlid fishes are famous for being spectacularly species-rich and phenotypically diverse. More than 2000 species evolved and formed adaptive radiations in the great lakes of East Africa within last few million years. However, little is known about their genomic diversification and the genomics of species differences. The advent of next generation sequencing technology, facilitated the determination of five African cichlid genomic sequences that include *Oreochromis niloticus* the Nile Tilapia as the basal riverine species, and the genomes of four lacustrine cichlid genomes, *Astatotilapia burtoni*, *Metriaclima zebra*, *Pundamila nyererei* and *Neolamprologus brichardi* from the adaptive radiations of Lakes Victoria, Malawi and Tanganyika. Copy number variation (CNV) in genes is generally known as an important evolutionary force. However, little is known so far about the role of CNV during the fast evolution and speciation of African cichlid fishes. By using the Tilapia genome as reference, we investigated copy number variation in relation to the four lacustrine cichlid genomes. Preliminary results show that within the relatively short evolutionary time that separates the African cichlid fishes, a large number of recently duplicated genes in genome of these cichlid species accumulated compared to the more basal Tilapia genome. This indicates that CNVs might have been an important mechanism during the adaptive radiation of African cichlid fishes.

S□19 Helen Gunter R 513 / 14:30

The way you use it is what counts: basis of phenotypic plasticity in the lower pharyngeal jaw of the cichlid fish, *Astatoreochromis alluaudi*

Authors: *Helen Gunter*[1/2]*, Fan Xiong*[1]*, Shaohua Fan*[1]*, Paolo Franchini*[1]*, Carmelo Fruciano*[1]*, Axel Meyer*[1]

Affiliations: [1]*Lehrstuhl für Zoologie und Evolutionsbiologie, Department of Biology, University of Konstanz*; [2]*Zukunftskolleg, University of Konstanz*

Adaptations are predominantly encoded by the genome, yet it is clear that the environment can also alter the shape of adaptations during an individuals' ontogeny. Evaluating the importance of adaptive phenotypic plasticity for evolution remains a challenge as the interactions between environmental signals and developmental pathways are generally not well characterised. We utilised next generation sequencing to examine the molecular basis of phenotypic plasticity in the lower pharyngeal jaw (LPJ) of an East African cichlid fish, Astatoreochromis alluaudi. Two morphs are recognised in the wild, one with an enlarged, robust 'molariform' LPJ and one with a smaller, more gracile 'papilliform' LPJ. Previous research showed that these morphs arise through phenotypic plasticity, induced by differences in the mechanical properties of their diets. We performed a common garden experiment where siblings were fed either whole snails (hard diet), or finely minced snails (soft diet) and analysed the resulting morphological and transcriptional phenotypes. The hard diet induced a molariform phenotype, with increased LPJ and tooth size and altered LPJ shape compared to the papilliform fish. Through exploring patterns of co-variation between jaw size and shape, and genome-wide transcriptional profiles we identified gene expression networks that underlie these diet-responsive adaptive phenotypes. Genes overexpressed in molariform LPJs include markers for both osteoblasts and osteoclasts (which secrete and resorb bone respectively), suggesting that active bone remodelling underlies phenotypic plasticity in the LPJ of *A. alluaudi*. We detected dramatically lower expression of markers for hematopoiesis in the molariform LPJs, suggesting a potential cost of plasticity.

S□20 Jan Oettler R 513 / 14:45

Signatures of divergence and selection in *Cardiocondyla obscurior*

Authors: *Jan Oettler*[1]*, Lukas Schrader*[1]*, Jürgen Heinze*[1]*, Jürgen Gadau*[2]

Affiliations: [1]*Universität Regensburg*; [2]*Arizona State University*

The tramp ant species *Cardiocondyla obscurior* is distributed across the tropics and subtropics. For introduced species, colonization events are associated with genetic bottlenecks drastically reducing allele diversity in the population, a phenomenon referred to as founder effect.

Studies comparing two introduced populations of *C. obscurior* from Brazil and Japan revealed significant phenotypic differences (e.g. in CHC profiles), indicating an early stage of divergence. Furthermore, crossing experiments between the two populations showed fitness defects in outbred queens. This susceptibility to outbreeding depression might be related to the evolutionary history of *C. obscurior*, in which inbreeding in the maternal nest is favoured.

The founder effect of low genetic diversity together with the susceptibility for outbreeding depression in *C. obscurior* provides a framework for studying the evolution of genetic incompatibility and of the very early steps of speciation processes.

By comparing the sequenced genomes from the two different populations we aim to identify genetic differences and signatures of selection potentially accounting for the emerging incompatibility.

S□21 Andreas Kautt R 513 / 15:15

Genome-wide patterns of adaptation and speciation in repeated radiations of Midas cichlid fish

Authors: *Andreas F. Kautt*[1], *Kathryn R. Elmer*[1], *Gonzalo Machado-Schiaffino*[1], *Axel Meyer*[1]
Affiliation: [1]*University of Konstanz*

Even more than 150 years after the publication of Darwin's 'Origin of species', elucidating the processes that drive population divergence and speciation remains a key objective in evolutionary biology. Advances in sequencing technologies allow researchers now to investigate these mechanisms at the genomic level and driven by a renewed recognition of the importance of divergent selection in this (i.e. ecological speciation) recent studies have substantially contributed to our understanding of the genomic basis of adaptation and speciation. Yet, more empirical studies are needed for generalities to emerge. The Midas cichlid fish species complex (Amphilophus cf. citrinellus) in Nicaragua is a powerful model system for studying evolutionary processes. Here recent independent colonizations of several isolated crater lakes have been followed by partly repeated intralacustrine adaptive radiations. In this study we used amplified fragment length polymorphisms (AFLPs) and restriction-site-associated-DNA sequencing (RAD-seq) to investigate genome-wide signatures of adaptation and divergence in different populations / species of Midas cichlids. We detected regions under divergent selection potentially associated with sympatric diversification, but found no evidence that the same genomic regions are involved in the parallel phenotypic evolution across different crater lake adaptive radiations. Yet, comparisons between some crater lake flocks and their source population suggest that there is some genetic parallelism involved in the allopatric divergence of crater lake flocks. The investigation of wild populations within an ecologically relevant and known phylogenetic context will help to further our understanding of the processes driving population divergence and speciation in general.

S□22 Manfred Schartl R 513 / 16:00

The genome of the platyfish, *Xiphophorus maculates*

Authors: *Manfred Schartl*[1], *Ronald B. Walter*[2], *Yingjia Shen*[2], *Tzintzuni Garcia*[2], *Julian Catchen*[3], *Angel Amores*[3], *Ingo Braasch*[1/3], *Domitille Chalopin*[4], *Jean-Nicolas Volff*[4], *Klaus-Peter Lesch*[5], *Angelo Bisazza*[6], *Pat Minx*[7], *Richard K. Wilson*[7], *Susan Fuerstenberg*[8], *Jeffrey Boore*[8], *John H. Postlethwait*[3], *Wesley C. Warren*[7]

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Poeciliid fishes of the genus Xiphophorus have long served as an experimental model for spontaneous and induced melanomagenesis, complex behavior, pigment pattern inheritance, and the variety of different sex determination mechanisms. Use of Xiphophorus fishes is enhanced from the ability to produce fertile interspecies hybrids. To further promote use of Xiphophorus for genetic studies we have sequenced and assembled the female genome of X. maculatus strain Jp 163 A in its 109th inbred generation. The X. maculatus draft genome assembly comprises 669 Mb with a contiguity of N50 contig and supercontig length of 21 kb and 1.1 Mb, respectively. A high-density meiotic map of over 16,000 was produced using RAD-tags. This allowed more than 90% of the sequenced contigs to be ordered and assigned to chromosomal location. Annotation of transposable elements revealed a surprisingly low (6%) overall level compared to other fish genomes. The genome assembly was used to produce a set of 17,783 gene models. Using these gene models we examined molecular signatures of evolution for several traits. Among fishes, viviparity has evolved independently several times and has reached within Poeciliids a highest degree of maternal-embryo relationships. Using a PAML branch-site model and maximum likelihood test we asked if genes associated with viviparity were under evolutionary selection pressure. We determined that several genes reach significance, such as vitellogenin and IGF2. Poeciliid fish display elaborate behavioral traits. Analyses of the platyfish genome for genes considered to be involved in cognition we find a remarkably high representation of such genes in the genome. The Xiphophorus genome assembly will now allow initiation of many new studies aimed at determination of the molecular mechanisms underlying many unique complex biological traits.

S☐23 Julia Jones R 513 / 16:15

Hybridizaiton and speciation in Xiphophorus fish: a genome wide approach using RAD sequencing

Authors: *Julia C Jones*[1/2], *Shaohua Fan*[1], *Paolo Franchini*[1], *Manfred Schartl*[3], *Axel Meyer*[1]
Affiliations: [1]*Lehrstuhl für Zoologie und Evolutionsbiologie, Department of Biology, University of Konstanz*; [2]*Zukunftskolleg, University of Konstanz*; [3]*Physiological Chemistry I, Biozentrum, University of Würzburg*

Next generation sequencing (NGS) techniques are now key tools in the detection of population genomic and gene expression differences in a large array of organisms. However, so far few studies have implemented such data for phylogenetic estimations. Here we use NGS data obtained from genome wide restriction site associated DNA (RAD) to estimate the phylogenetic relationships among all species of swordtail and platyfish (genus Xiphophorus) from Central America. Past studies, both sequence-based and morphological, have differed in their inferences of the evolutionary relationships between members of this genus, particularly at the species level and among monophyletic groupings. We show that by using an increased number of markers throughout the genome we are able to infer phylogenetic trees with unparalleled resolution for this genus. The relationship between all clades and derived nodes are highly supported under both maximum likelihood and Bayesian inference. In addition, we are able to infer the paternal lineage of two putative hybrid species at an exceptional resolution. Using the RAD-marker based tree generated here we also reconstruct the evolutionary history of the sexually selected sword trait born by many swordtail members of this genus. Together our results highlight the outstanding capacity that RAD sequencing data has for resolving previously problematic phylogenetic relationships among species of an entire genus.

S☐24 Arne Nolte R 513 / 16:30

Finding genes that count in a hybrid fish

Author: *Arne Nolte*[1]
Affiliation: [1]*Max-Planck Institute for Evolutionary Biology*

The idea that hybridization may play an important evolutionary role is gaining more and more popularity. We are analyzing a recently emerged lineage of fish (Cottus) to test hypothesis about hybrid speciation. A central idea is that hybridization leads to mixtures of genotypes, which have the potential for rapid adaptation to new environmental conditions. However, that an admixed genome is essential for an increase in fitness remains difficult to prove. We are currently combining analyses of gene expression and whole genome sequencing approaches to assess the impacts of hybridization at a genome wide scale. Sequencing data was used to test for ancestry variation across the hybrid genome. Between 1500 and 3000 ancestry informative SNP loci mapped to each of the stickleback chromosomes which can be used as a reference for Cottus. While our estimates of ancestry are crude, this screen permits to pinpoint genomic regions that may be subject to genotypic selection. A combination of extreme ancestries suggests that genetic material from both parental Cottus species interacts to give a fitness advantage to invasive Cottus. Likewise, a

microarray based transciptome analysis revealed unique patterns of gene expression that may explain the fitness properties of invasive Cottus. We have used whole genome sequencing data to study segmental mutations in the hybrid lineage after initial hybridization. We find evidence that the genome size has increased by approximately 10% through multiple small scale increases of copy number. Importantly, this inflation is particularly pronounced in genes that we have identified as candidate genes in adaptive evolution based on increased levels of gene expression. Our study provides first evidence that mutational mechanisms that are specifically enhanced in hybrid genomes contribute to adaptive evolution in an emerging hybrid species.

S□25 Tereza Manousaki R 513 / 16:45

Parsing parallel evolution: ecology and transcriptomics of hyperthrophic lips in Midas cichlid fishes

Authors: *Tereza Manousaki*[1]*, Pincelli Hull*[2]*, Henrik Kusche*[1]*, Gonzalo Machado-Schiaffino*[1]*, Paolo Franchini*[1]*, Chris Harrod*[3]*, Kathryn Elmer*[1]*, Axel Meyer*[1]

Affiliations: [1]*Lehrstuhl für Zoologie und Evolutionsbiologie, Department of Biology, University of Konstanz*; [2]*Department of Geology and Geophysics, Yale University, New Haven, Connecticut;* [3]*Department of Evolutionary Genetics, Max Planck Institute for Limnology, Plön*

Cichlid fishes are widely known for their explosive rates of speciation and their huge phenotypic diversity. In the great and also the crater lakes of Nicaragua, geographically isolated populations of Midas cichlid fishes have repeatedly evolved similar phenotypic changes in parallel. Here, we examined the repeated evolution of hypertrophic (thick)-lips in Midas cichlid fishes to assess whether similar changes in gene expression accompany the evolution of this parallel trait allowing them to occupy similar, but often, not identical ecological niches. Using next-generation sequencing technology we characterized transcriptome-wide differential gene expression in the lips of wild-caught sympatric thick- and thin-lipped cichlids from two great and two crater lakes. Six genes showed similar expression pattern between the thick and thin-lipped morphs across these comparisons in all four lakes. Much fewer genes are differentially expressed among endemic species in the younger crater lakes than in those from the older great lakes. From a phenotypic perspective, several traits evolved in parallel (those related to foraging ecology; e.g., lip size, body and head shape) but others, somewhat surprisingly, do not (those related to diet and its processing; e.g., jaw size and shape, stable isotopes). The synthesis of our multifaceted approach reveals a somewhat unexpected mosaic pattern of parallel and non-parallel evolution of traits. We conclude that there are multiple evolutionary trajectories that can lead to the repeated evolution of a type of (lipped) fish that characterizes an ecological guild.

S□26 Andrey Rozenberg R 513 / 17:00

Next-generation sequencing data analysis for non-model organisms: a workflow

Authors: *Andrey Rozenberg*[1], *Philipp Brand*[1], *Christoph Mayer*[2], Chester Sands[3], *Ralph Tollrian*[1], *Florian Leese*[1]
Affiliations: [1]*Ruhr Universität Bochum;* [2] *Zoologisches Forschungsmuseum Alexander Koenig;* [3]*British Antarctic Survey, Ecosystems Group*

With next-generation sequencing approaches huge amounts sequence data can be produced in short time and with low costs. This allows addressing biological questions on genomic level even in non-modal organisms. The amount of information inherent in such low-coverage datasets, in particular for genetic marker development, is exceptionally great, yet shotgun low-coverage genomic sequence libraries produced for a species without a reference genome require special treatment since several factors such as contamination from non-target organisms and interspersed repetitive elements may interfere with down-stream analyses. Here we present a workflow for the analysis of low-coverage next-generation sequencing data. First, we found it necessary to perform a de novo assembly of the reads due to the presence of repetitive regions and accidental cases of multiple reads coming from a unique genomic location. Second, we used BLAST routines to search for bacterial, viral and symbiotic contamintants in the contigs and unassembled reads. Then, we searched for mitochondrial and nuclear genes in the libraries. Finally, we searched for tandem repeats with the aid of the software Phobos with a strict filtering settings. The core component of our bioinformatic implementation was a MySQL database, which served as a central storage and analytical environment. All analyses were performed in a pipeline style using a custom web-interface. The workflow was developed and tested on a sample of 454 pyrosequencing libraries representing 16 non-model animal species.

S□27 Hans Hofmann R 513 / 17:15

Deep homology in gene modules that underlie convergent evolution in mating systems

Author: *Hans Hofmann*[1]
Affiliation: [1]*Section of Integrative Biology, University of Texas*

Monogamous mating systems have evolved repeatedly and independently in a wide range of animals, yet little is known about the underlying neural and molecular substrates and their evolution. We test the hypothesis that the convergent evolution of monogamy across wide evolutionary distances involved in part the recruitment of homologous gene modules. We sequenced the brain transcriptomes of mated males from closely related species (one monogamous, one non-monogamous) of *Microtus* voles, *Peromyscus* mice, Ectodini cichlids, Parid songbirds, as well as paired and non-paired *Nicrophorus* burying beetles to compare expression profiles of orthologous genes within and across lineages. We found several gene modules that are similarly regulated in monogamous males, such as neuroendocrine genes and transcription factors, as well as a different set of gene modules that are similarly regulated in non-monogamous males. More detailed analyses as well as transcriptome sequencing of monogamous and non-monogamous sister species of new world primates and poison dart frogs are ongoing. We are currently also using RNA Pol II ChIP-seq on all species in this study to investigate to what extent similarities in gene expression patterns are associated with shared regulatory motifs across the genome. Our results provide insight as to whether common molecular substrates likely underlie the repeated evolution of complex social behavior patterns.

POSTERS

♦216 Geraldine Kavembe

Population genetics and phylogeography of Lake Magadi Tilapia - are extreme environments a barrier to gene flow in the soda lakes?

Authors: *Geraldine Dorcas Kavembe*[1]*, Gonzalo Machado-Schiaffino*[1]*, Axel Meyer*[1]
Affiliation: [1]*University of Konstanz*

The cichlid fish species *Alcolapia grahami* is endemic to Lake Magadi and its satellite lake Little lake Magadi. Those lakes are among the extreme environments that vertebrates can be found in - the pH is ~10, alkalinity ~ 300 mequiv L-1, the temperatures in this lake reach up to 42ºC and the water typically is hypo- or even hyper-oxic.. The Magadi tilapia is restricted to small isolated water pools (lagoons) separated by kilometers of solid sodium carbonate (trona) crusts that could act as a physical barrier preventing movement of fish between the individual pools. Although the populations are considered to be separate, periodic floods and movement of fish by birds are thought to contribute to mixing of the fish populations. Currently, allelic diversity and genetic relationships between the populations remain largely unknown. Given the extreme conditions at the lake and the obvious selective pressures on these populations, population genetic studies to understand genetic connectivity between the populations are crucial in understanding the survival mechanisms of these remarkable fish in this extreme environment. In the current study, we examined five populations drawn from different lagoons (n>200) across the lake basin using two mitochondrial markers (ND2 and control region) and 11 microsatellite markers. Preliminary results from the mtDNA markers indicate some genetic differentiation between some populations, while other comparisons show very little differentiation indicative of gene flow among certain lagoons. In contrast, microsatellite markers indicate differentiation among most of the population comparisons. Our study aims to provide a comprehensive genetic characterization of the Magadi tilapia populations.

♦**217** Hans Recknagel

Linkage mapping of two ecologically and morphologically divergent Midas cichlids (Amphilophus spp.)

Authors: *Hans Recknagel*[1]*, Kathryn R. Elmer*[1]*, Axel Meyer*[1]
Affiliation: [1]*University of Konstanz*

Cichlid fishes are an excellent model system for studying speciation and adaptive radiations due to their tremendous species richness and phenotypic variability. Research, so far, has mostly focused on African rift lake cichlids, but the Neotropical Midas cichlid species flock (*Amphilophus spp.*) also offers a tractable model system with a variety of rather distinct phenotypes. Here we apply double-digest restriction-site associated DNA sequencing (ddRADSeq) in order to obtain a high-density linkage map of an interspecific cross between the benthic A. astorquii and the limnetic A. zaliosus, both endemic to Lake Apoyo, Nicaragua. 343 F2-hybrids were genotyped for a total of 755 RAD markers. 25 linkage groups span over a distance of 1427 cM with an average marker spacing distance of 1.95 cM, almost matching the total number of chromosomes (n=24). Regions of segregation distortion were identified in five linkage groups. The genetic map will facilitate the detection of eco-morphologically relevant adaptive traits in Midas cichlids. We performed comparative genomic analyses in teleosts and found highly conserved synteny between African cichlids and Neotropical cichlids, and less conserved synteny between cichlids and other teleosts. These results suggest that the cichlid’s phenotypic variability does not correlate with a high degree of chromosomal rearrangements, neither do Midas cichlids exhibit a higher mutation rate compared to other teleosts. Our linkage mapping analysis shows that ddRADSeq is an appropriate method to develop hundreds of markers and to construct high-density linkage maps even in genetically very young populations.

21. IMPRS Symposium “Grand challenges in sexual selection and eco-evolutionary processes”

Monday, September 24, 2012

Key Note: Chair: Students of the IMPRS for Organismal Biology M 629 /11:30

Hanna Kokko

Were all interesting predictions in sexual selection theory made in the 1970s, and do they hold in 2012?

Author: *Hanna Kokko*[1]

Affiliation: [1]*Australian National University, Evolution and Genetics, Division of Ecology*

In the 1970s, three extremely important papers saw the light of day: Trivers (1972) explained why parental investment often differs between males and females, and Emlen and Oring (1977) coined the term ‘operational sex ratio’ (OSR), which has been used to explain sexual differences in competitive mate-acquisition traits. In this talk I will show how our current thinking has evolved to be somewhat different from these original contributions, and how parental investment theory, OSR, and Bateman gradients can all be understood within a single framework.

TALKS

S☐28 Mark van Kleunen M 629 / 14:00

Friends and enemies of green aliens

Author: *Mark van Kleunen*[1]

Affiliation: [1]*University of Konstanz, Ecology*

Biotic interactions are likely to play key roles in the establishment and spread of alien organisms. It is widely believed that many alien plant species can invade new regions because they have been released from their natural enemies, such as herbivores. Alien plants may, however, also be released from their mutualists, such as pollinators, and as a consequence alien plants that rely on pollinators for reproduction might not become invasive. Although previous studies have looked at interactions between highly invasive plant species and herbivores or pollinators, few, if any, studies have tested whether such biotic interactions differ between invasive and non-invasive alien plant species. I will present results of several multi-species studies showing that there is little evidence that enemy release drives invasiveness, but that release from pollinators might prevent some alien plants from becoming invasive.

S☐29 Davide Dominoni M 629 / 14:30

Effects of artificial light at night on daily cycles of songbirds

Author: *Davide Dominoni*[1]
Affiliation: [1]*Max Planck Institute for Ornithology, Migration and Immuno-Ecology*

We live in the urban millennium, the age of cities and urbanization. Animals which attempt to settle in such man-made ecosystems must cope with novel environmental conditions. One of the most apparent environmental factors in cities is artificial light at night. The goal of our research was to investigate how urban sprawl has change the temporal life of European blackbirds (Turdus merula), and to correlate this change with light pollution. We quantified daily activity patterns of blackbirds along an urban/rural gradient in Munich, Germany, with the use of an automated telemetry system. Simultaneously we tagged the same individuals with micro light loggers to measure light irradiance to which the birds were exposed to. Diurnal and nocturnal noise levels were also recorded in the territory of each individual. In my contribution I will discuss the relative role of light at night, noise and weather conditions on the daily cycles of European blackbirds and discuss fundamental questions about the fitness consequences of light pollution.

S☐30 Malika Ihle M 629 / 14:45

Does hatching failure breed infidelity?

Author: *Malika Ihle*[1]
Affiliation: [1]*Max Planck Institute for Ornithology Seewiesen*

In socially monogamous species, the reasons for female infidelity are still controversial. It has been suggested that females could seek extra-pair copulations as an insurance against hatching failure caused by male infertility or incompatibility. In species where couples breed repeatedly, females could use previous hatching success as a cue to assess their partner's infertility (or incompatibility). Hence, it has been predicted that females should increase their infidelity after experiencing hatching failures, but to our knowledge this hypothesis has never been tested experimentally. We manipulated hatching success of pairs in a captive population of zebra finches (*Taeniopygia guttata*), a species that forms lifelong pair-bonds, and measured female willingness to engage in extra-pair copulation. By experimentally cross-fostering fertile and infertile eggs, couples either experienced 100% or about 35% hatching success in each of three consecutive clutches. Contrary to our prediction, females that experienced repeated hatching failure did not increase their responsiveness towards extra-pair males relative to those females with 100% hatching success. Moreover, there was no difference in female calling rate for the partner after male removal and no occurrence of divorce when the opportunity was given. These findings seem to contradict the common view that reproductive failure weakens the pair bond. Furthermore, a critical review of the literature suggests that there is no convincing evidence supporting this hypothesis in other species either. We therefore highlight that this fundamental area of behavioural ecology research is still much in need of specific experimental work that controls for confounding factors.

S□31 Henrik Kusche M 629 / 15:0

Mouth asymmetry in scale-eating cichlid fish is not a discrete dimorphism after all

Authors: *Henrik Kusche*[1/2], *Hyuk Je Lee*[1/3], *Axel Meyer*[1]
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Many individuals of the scale-eating cichlid fish, *Perissodus microlepis*, from Lake Tanganyika have remarkably asymmetric heads that are either left-bending or right-bending. The 'left' morph opens its mouth markedly towards the left and preferentially feeds on the scales from the right side of its victim fish and an equally abundant 'right' morph bites scales almost exclusively from its victims' left sides. This striking dimorphism made these fish a textbook example for their astonishing degree of ecological specialization and as one of the few known incidences of negative frequency-dependent selection acting on an asymmetric morphological trait, where right and left forms are equally frequent within a species. We investigated the degree and the shape of the frequency distribution of head asymmetry in *P. microlepis* to test whether the variation conforms to a discrete dimorphism, as generally assumed. In both, adult and juvenile fish mouth asymmetry appeared to be unimodally distributed with no evidence for a discrete dimorphism. Mixture analyses did not reveal evidence of a discrete or even strong dimorphism. The results raise doubts about the veracity of previous claims that head variation in *P. microlepis* represents a discrete dimorphism of right- and left-bending forms. Based on extensive collections of field samples we determined laterality and found that both morphs occur in equal abundance in five populations and that pair formation of wild caught pairs was random with regard to head laterality. The latter finding questions the previously suggested genetic mechanism that assumes disassortative mating.

S□32 Erica Stuber M 629 / 15:15

Intraspecific variation in sensitivity towards novel objects: a problem of sampling bias in ecological studies

Author: *Erica Stuber*[1]
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Sampling bias is a key issue to consider when designing studies to address ecological questions and its importance has been widely discussed in the literature. However, some forms of bias remain underestimated. Inferences about ecological traits and their evolution are often made utilizing within-species sampling, where accuracy (the amount of bias) depends on how well the sample reflects the total population. True population-average values of traits may be mis-estimated when behavior-related sampling bias is neglected, and certain types of individuals are measured more or less often due to the behaviors they express. We describe a new behavior-related bias, sensitivity to novel objects, which has largely been overlooked in sampling design, illustrated by field data from passerine birds.

We show that ‘bold’ individuals that are ‘fast’ explorers are more likely to accept and approach novel objects used in certain sampling techniques. We demonstrate potential pitfalls of neglecting behavior-related sampling bias in ecological studies.

S□33 Jesko Partecke M 629 / 16:00

Partial migration: The ecology and evolution of alternative phenotypes

S□34 Camila P. Villavicencio M 629 / 16:30

Testosterone concentration of male Black Redstarts does not increase during times of social instability

Authors: *Camila P. Villavicencio*[1], *Beate Apfelbeck*[1], *Wolfgang Goymann*[1]
Affiliation: [1]*Max Planck Institute for Ornithology, Seewiesen*

Testosterone has been suggested to play a major role in mating and territorial behavior during breeding. For socially monogamous bird species, The Challenge Hypothesis (Wingfield et al. 1990) predicts that testosterone should increase during male-male interactions, but remains at the breeding baseline to avoid potential costs of prolonged elevated levels of this hormone. During the last two decades simulated territorial intrusion (STI) experiments have been conducted to test the Challenge Hypothesis. Indeed, about half of the species of birds investigated show the expected rise in testosterone during breeding, but many other species do not respond to STIs with an increase in testosterone. Several hypotheses have been proposed to explain this lack of testosterone modulation. Previous studies from our group show that male black redstarts (*Phoenicurus ochruros*) do not increase testosterone levels during single or multiple STIs. The aim of this study was to evaluate whether black redstarts modulate testosterone in a natural situation of social instability. We created a social unstable environment by removing a male from his territory. We then compared testosterone levels of replacement males with those of neighbors and males from a control area. In addition, we compared the behavior of replacement males with that of control males. We found no differences in testosterone levels between replacements, neighbors and control males, as well as no difference in behavior between control and replacement males. Hence, in this species males do not modulate testosterone levels during male-male interactions. In combination with other data from our group this suggests that testosterone plays only a minor role in the control of territorial behavior of the black redstart. We suggest that the control of territorial behavior in species that are territorial throughout most of their annual cycle can be decoupled from testosterone.

S□35 Martin Bulla M 629 / 16:45

Unequal division of incubation in a High Arctic shorebird

Authors: *Martin Bulla*[1]*, Mihai Valcu, Alexander Girg, Anne L. Rutten, Bart Kempenaers*
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Parental conflict arises because the costs of care are specific to each parent whereas the benefits are shared by both. Parents negotiate over the amount of parental care in order to minimize the costs of propagating their genes. Breeding in the harsh conditions of the High Arctic is extremely energetically demanding. Despite the continuous daylight during the Arctic summer, the weather conditions and prey availability fluctuate during the day. This makes some parts of the day more advantageous for foraging or incubation than others. As a consequence, uniparental incubators concentrate their off-nest (foraging) activity around the warmest part of a day (noon). Regardless of the fluctuating conditions, biparentally incubating High Arctic shorebirds incubate the eggs nearly 100% of the time. As a result, only one parent is off-nest during the favorable foraging conditions. We have used the Semipalmated Sandpiper *Calidris pusilla* to investigate the outcome of this parental conflict and found great between-nest differences in the way sexes divide the incubation duties. On average, females tended to be off-nest a) during windier conditions (usually during the day), and b) during warmer periods of the day, that is when foraging is most efficient. This may allow females to replenish their reserves after egg-laying. However, females had also longer incubation bouts than males. It remains to be tested whether female biased incubation is driven by incubating females or by males that forage under less favorable weather conditions and might therefore need longer periods to replenish their energetic reserves.

S□36 Nathalie Feiner M 629 / 17:00

Molecular phylogenetic, comparative genomic and expression analyses of *Pax10*, a novel sister gene of *Pax4* and *Pax6*

Authors: *Nathalie Feiner*[1], *Axel Meyer*[1], *Shigehiro Kuraku*[1/2]
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The prerequisite for comparative molecular biological analyses is an accurate orthology/paralogy assignment. However, this is often obscured by incomplete sequence identification, secondary gene loss or difficulties in reconstructing molecular phylogenies. While Pax6 is present in all vertebrates analyzed to date, Pax4 and Pax10 show mosaic phylogenetic distributions: Pax4 has been found so far only in mammals and teleosts, while a careful survey of publicly available databases revealed the presence of Pax10 only in a few non-mammalian vertebrates. Pax10 is characterized by a paired-type homeodomain, but lacks the paired domain that is present in all other Pax genes (Pax1-9). Despite the lack of the paired domain, a molecular phylogenetic analysis unambiguously placed Pax10 genes within the Pax4/6 subgroup. To tackle the question about the origin of Pax10 we established both intra- and inter-genomic comparisons of chromosomal regions containing Pax4,

-6 and -10 in vertebrate model organisms. We found conserved synteny indicating that the origin of Pax10 was part of a large-scale duplication event. Thus, Pax10 is presumably the third identified member of the original gene quartet generated by the two rounds of whole-genome duplication that occurred in the ancestral vertebrate genome. An analysis of the expression patterns of Pax10 genes in zebrafish, Xenopus and anole lizard using in situ hybridizations and quantitative RT-PCR showed that Pax10 expression patterns differed between three different vertebrate classes and revealed secondary changes in developmental roles between the three sister genes Pax4, -6 and -10.

Award IMPRS Best Student Paper Award M 629 / 17:15

POSTERS

♦218 Andrea Gehrold

Seasonal flexibility in a European migrant, the Gadwall (*Anas strepera*)

Authors: *Andrea Gehrold*[1], *Hans-Günther Bauer*[1], *Wolfgang Fiedler*[1], *Martin Wikelski*[1]
Affiliation: [1]*Max Planck Institute for Ornithology*

During the last decades, the number of Gadwalls (*Anas strepera*) has been continuously increasing in western Europe, supposedly in response to the eutrophication of wetlands and the creation of water impoundments. The potential of migratory birds to discover habitats of suitable quality may, however, depend on the narrowness of migratory routes.

To measure movement behaviour and range, 17 adult Gadwalls were equipped with backpack satellite transmitters and continuously tracked during different stages of their annual cycle. Furthermore, we analyzed direct autumn and winter recoveries of 327 Gadwalls ringed during summer in Germany, western Russia, and England - therefore representing birds from the three known European flyway populations. The migration of tracked individuals was target-oriented and short in time, although bearings differed remarkably. Birds spent some months at the breeding and moulting site, but stopover times significantly decreased in autumn and early winter. During the latter period, Gadwalls also tended to visit multiple sites and to perform reverse migrations. Similarly, ring recoveries revealed that movement directions were highly variable from August to October. Some individuals even travelled hundreds of kilometres in northern directions, obviously moving away from subsequent wintering sites. Our results indicate that Gadwalls may perform complex movements during autumn, the time of the year when they are to some extent released from environmental and fitness-relevant constraints. Flexible migration strategies may enable birds to find, evaluate, and adopt habitats of improved quality which holds important implications for the conservation and management of wetlands and duck populations.

22. Symposium „Olfaction across species and systems"

Monday, September 24, 2012

Key Note: Chair: Giovanni Galizia A 600 / 14:00

Andreas Keller

The combinatorial logic of human olfaction

Author(s): *Andreas Keller[1], Hiro Matsunami[2], Joel Mainland[3], Leslie Vosshall[1]*
Affiliation: *[1]Rockefeller University; [2] Duke University; [3] Monell Chemical Senses Center*

Humans have around 400 different odorant receptors and each odor activates a unique combination of these odorant receptors. The genes encoding the human odorant receptors are genetically extremely variable and it is therefore possible to identify human subjects that lack a specific odorant receptor and then investigate odor perception in those subjects. The results of experiments like this reveal the combinatorial logic of olfactory coding in humans.

We have tested the perception of dozens of odors in several hundred subjects. Our collaborators have sequenced hundreds of odorant receptor genes in these subjects. They also determined in cell culture assays which odorant receptor variants are functional and which variants are non-functional. The combination of this data allowed us to show that lacking an odorant receptor changes the perceived intensity and pleasantness of its ligands. We are now investigating the influence of specific odorant receptors on the ability to distinguish between similar odors.

In another experiment we have tested physiological and psychological responses to an odor that is structurally similar to the sex hormone testosterone in women who are ovulating. We have identified an odorant receptor that influences physiological responses to the odor, but not the conscious perception of it. Together these results provide a fascinating insight into how hundreds of human odorant receptors interact to ensure adaptive behavioral responses to our olfactory environment.

Key Note: Chair: Giovanni Galizia A 600 / 14:45

Leslie Kay

Strategy and plasticity in early olfactory processing of the rat olfactory system

Author(s): *Prof. Leslie Kay[1]*
Affiliation: *[1]The University of Chicago*

It is common for neuroscientists to use behavior as an assay to determine that a subject (rat, mouse, honeybee, moth, fly, human) has recognized or identified the odor stimulus. However, the task that one chooses can affect the functional circuits by which stimuli are processed, even at the very first level of olfactory processing.

Our data show that when rats use a 2-alternative choice (2AC) task to identify odors there is a significant increase in olfactory bulb gamma oscillations (65-90 Hz) during odor sampling. In the GNG task gamma oscillations are absent during odor sampling, but there is an increase in beta oscillation (~20 Hz) power associated with the end of odor sampling and coincident with criterion performance levels. These differences represent differences in the way that underlying principle neurons cooperate in representing the odor stimulus. The effects are modulated by the odorants being discriminated and the level of reward that the rat receives. Behavioral analysis shows that rats use somewhat different strategies for the two tasks after they have learned the first odor set.

Key Note: Chair: Giovanni Galizia A 600 / 16:00

Heather Eisthen

Tainted Love: Olfactory Detection of Tetrodotoxin In Rough-Skinned Newts (*Taricha granulosa*)

Author: *Heather Eisthen*[1]
Affiliation: [1]*Michigan State University*

Tetrodotoxin (TTX) is a potent and selective blocker of voltage-gated sodium channels. As such it is used as a chemical defense against predation by a variety of organisms, including pufferfish and many species of newts. Given its often lethal effects, it is surprising that some of the organisms that produce TTX have also co-opted it for use in intraspecific communication. The mechanisms by which TTX serves as an odorant are unknown. We are examining the behavioral significance and neural mechanisms of TTX detection in male adult rough-skinned newts, *Taricha granulosa*. Immunohistochemical assays demonstrate that TTX is abundantly present in skin glands in all male newts in the population we are examining. Our preliminary behavioral data suggest that newts can detect concentrations of at least 100 nM - 1 µM TTX. Using electro-olfactogram (EOG) recordings, which measure summed generator potentials, we find that TTX evokes robust responses from the olfactory epithelium in concentrations ranging from 1 nM to 1 µM. These responses are similar in shape and time course to those evoked by other odorants, such as mixtures of amino acids. Experiments using ionic substitutions and pharmacological manipulations indicate that TTX does not activate the canonical odorant transduction pathway, and that a sodium channel seems to be involved. This research has the potential to lead to novel insights concerning the evolution of species-specific chemical communication, as well as the evolution of ion channels.

Key Note: Chair: Giovanni Galizia A 600 / 16:45

Tristram Wyatt

Chemical communication in invertebrates and vertebrates: resolving pheromones (species-wide signals) and signature mixtures (variable cues learned for identity)

Author: *Tristram D Wyatt*
Affiliation: [1]*Department of Zoology, University of Oxford, UK*

Pheromones are not a myth but the highly complex chemical profiles of mammals have caused doubts for some researchers. Part of the problem may be a confusion between pheromones and signature mixtures (variable subsets of molecules of an animal's chemical profile which are learnt as a template by other animals, allowing them to distinguish individuals or social insect colonies. Pheromones are species-wide signals which elicit innate responses (though responses can be conditional on development as well as context, experience, and internal state). The proposed definitions for pheromone and signature mixture are based on the heuristic value of separating these kinds of chemical information. In contrast to a species-wide pheromone, as signature mixtures are a receiver-side phenomenon and it is the differences in signature mixtures which allow animals to distinguish each other, there is no single signature mixture to find. Almost all pheromones and all signature mixtures, whatever the size of molecules, are detected by olfaction (as defined by receptor families and glomerular processing), in mammals by the main olfactory system or vomeronasal system or both. There is convergence on a glomerular organization of olfaction in almost all animals. The processing of pheromones and signature mixtures is usually combinatorial across a number of glomeruli, even for sex pheromones which appear to have 'labeled lines'. Narrowly specific pheromone receptors are not a prerequisite for a molecule to be a pheromone. A small minority of pheromones act directly on target tissues (allohormone pheromones) or are detected by non-glomerular chemoreceptors such as taste (gustation).

TALKS

Chair: Giovanni Galizia

S□37 Jacob Stierle M 627 / 11:00

Honeybees use millisecond time-differences in stimulus coherence for odor-background segregation

Authors: *Jacob S. Stierle*[1]*, Stephanie Biergans*[1]*, Giovanni Galizia*[1]*, Paul Szyszka*[1]
Affiliation: [1]*University of Konstanz*

Airborne odorants rarely occur alone but they intermingle with odorants from multiple sources. Odor mixtures are known to elicit interactions in both behavioral and physiological responses, changing the perceptive quality of mixtures as compared to the components. However, relevant odors need to be segregated from a background. This problem is analogous to effects from different modalities, e.g.

auditory streaming and the visual figure-ground segregation. Both the auditory and the visual system use millisecond temporal differences in stimulus coherence to segregate individual objects from background. It is not known, whether and how the olfactory system uses temporal differences in stimulus coherence for odor-background segregation.

We addressed this issue by combining behavioral and physiological experiments in honeybees. We asked whether honeybees can use short temporal differences between two components of a binary odorant mixture to extract information about its components. We first trained honeybees to respond to an odorant A by pairing it with a sugar reward. Then, we tested memory retrieval with a mixture of A and a novel odorant B. We found that a 6 ms delay between the onset of A and B is sufficient to improve the detection of odor A, and that it is not necessary that odorant A was presented alone at any time during the stimulus. We then searched for a neuronal mechanism of odor-background segregation and asked whether projection neurons in the antennal lobe (the insect analog of the olfactory bulb) are influenced by short time delays in the onsets of individual components in odor mixtures. Using in vivo calcium imaging in honeybees, we found that the processing of temporally incoherent mixtures involved more inhibitory interactions than the processing of coherent mixtures. Moreover, the spatiotemporal responses of antennal lobe output neurons to incoherent mixtures are more complex and contain more information about the components than coherent mixtures. These differences appear to be mediated by a global rather than a glomerulus-specific circuit.

S☐38 Sarah Koch M 627 / 11:15

Pheromone receptor genes in leaf-cutting ants (*Atta vollenweideri*)

Authors: *Sarah Koch*[1]*, Ewald Grosse-Wilde*[1]*, Bill Hansson*[1]*, Christoph Kleineidam*[1]
Affiliation: [1]*University of Konstanz and MPI for Chemical Ecology, Jena*

Living in huge colonies, leaf-cutting ants are the evolutionarily most derived social insects with a sophisticated division of labor. Their social organization is mainly based on olfactory communication with a multitude of pheromones and promoted by a pronounced size-polymorphism within the worker caste. Distinct antennal lobe (AL) phenotypes have been described (Kuebler et al. 2010, Kelber et al. 2010) for all castes and even within the worker subcastes. Two worker phenotypes differ in number of olfactory glomeruli in the AL and the presence or absence of an extremely large glomerulus (macroglomerulus; MG) that is involved in trail pheromone reception. The males' AL contains three MG, presumably involved in detection of sex-pheromone components.

We investigated the antennal transcripts of all castes and of two worker-subcastes, and using microarrays, we analyzed differential expression. A number of genes involved in metabolism, immune defense and reproduction are differentially expressed in the three different castes, and some genes even between the two worker-subcastes.

In order to identify putative odorant receptor genes (OR-genes) for pheromone reception, we searched for differentially expressed OR-genes. In total we found 185 putative OR-genes, and one differs in relative expression by a factor of >3 between the two worker-subcastes. Thus, we now have a very promising candidate gene for trail pheromone reception. With the same strategy, we identified candidates for sex-pheromone receptor genes in males. In addition, we identified genes from all other olfactory related gene families (GRs, IRs, OBPs, CSPs and SNMPs) and we found ant-specific expansions (e.g. CSPs).

Kelber C, Rössler W, Kleineidam CJ (2010) Phenotypic plasticity in number of glomeruli and sensory innervation of the antennal lobe in leaf-cutting ant workers (A. vollenweideri). Developmental Neurobiology 70: 222-234.
Kuebler LS, Kelber C, Kleineidam CJ (2010) Distinct antennal lobe phenotypes in the leaf-cutting ant (Atta vollenweideri). Journal of Comparative Neurology 518: 352-365.

S□39 Christine Nowack M 627 / 11:30

Entering the current discussion on the vomeronasal organ of lungfish (*Dipnoi*): Data from scanning electron microscopy

Author: *Christine Nowack*[1]
Affiliation: [1]*Department of Zoology/Developmental Biology, University of Kassel*

The nasal cavity of most tetrapod vertebrates contains two different organs of smell, the main olfactory organ and the vomeronasal organ. The evolutionary steps leading to this subdivided olfactory system are still obscure. In fish, the olfactory organ is generally classified as an undivided, singular structure, homologue with the main olfactory organ of tetrapods. Nevertheless, several authors in past and present have postulated the presence of a vomeronasal organ in *Dipnoi* (lungfish, Teleostei). In this regard a variety of intranasal structures of embryonic and adult animals were interpreted as parts of a vomeronasal system. Still, the question if a vomeronasal organ actually does exist in *Dipnoi* has not finally been resolved. Recently, small crypt-like structures between the olfactory lamellae of lungfish of the genus *Protopterus* were reinterpreted as groups of sensory cells, and are believed to represent a primordial, segmented vomeronasal organ.
In the present investigation, these epithelial crypts - seen as mere glandular structures in earlier studies - were analysed with the aid of scanning electron microscopy. The resulting images of the surface structure are presented and discussed in the light of the fragmentary data available from the literature.

S□40 Sabrina Jordan M 627 / 11:45

The olfactory organs of the frogs *Bombina orientalis* (Discoglossidae) and *Xenopus borealis* (Pipidae) compared by lectin histochemistry

Authors: *Sabrina Jordan*[1], *Christine Nowack*[1]
Affiliation: [1]*Department of Zoology/Developmental Biology, University of Kassel*

The focus of interest in the presented study is the comparison of two special olfactory systems. Generally, frogs posses different olfactory organs, covering distinct areas within their more or less complicated shaped nasal cavities. For Bombina orientalis, like for most frogs, this includes a main olfactory organ, a vomeronasal organ and a so called recessus olfactorius. For tongue-less frogs (Pipidae) such as Xenopus borealis, the situation differs. These animals are equipped with a main olfactory organ and a vomeronasal organ, too. Instead of the recessus olfactorius, they developed the so called middle chamber epithelium as a third olfactory system. The middle chamber epithelium of Pipidae is relatively well examined, due to the fact that frogs of the Genus Xenopus are used as model organisms. On the contrary, the recessus olfactorius has been only scarcely investigated, and many features like its function or its phylogenetic relation to the middle chamber epithelium remain unknown.

Lectin histochemistry was applied as one part of an extensive investigation of the recessus olfactorius. With this technique, sugar residues of transverse sectioned tissue of both frogs' noses were visualised. Analyses of resulting staining patterns of Bombina orientalis' recessus olfactorius took place by comparison especially to patterns of the middle chamber epithelium of Xenopus borealis, as well as to the main olfactory and vomeronsal organs of both species. One aim is to discuss the obtained results with respect to the possible homology of the recessus olfactorius and the middle chamber epithelium. Further, the recessus olfactorius' nervous connection to the brain is examined.

S□41 Philipp Brand M 627 / 12:00

The evolution of Odorant Receptors (ORs) in sibling species of orchid bees, as revealed by RNA-Sequencing.

Authors: *Philipp Brand*[1], *Santiago Ramírez*[2], *Florian Leese*[1], *Ralph Tollrian*[1], *Thomas Eltz*[1]

Affiliation: [1]*Department for Animal Ecology, Evolution, and Biodiversity, Ruhr-Universität Bochum*; [2]*University of California-Berkeley, Berkeley*

The insect Odorant Receptor (OR) gene-family encodes the ligand-gated ion channels that mediate the perception of volatile chemicals, and therefore constitute the main basis of odorant perception in the insect antennae. ORs are therefore crucially important for foraging and mate detection in insects. In male orchid bees (*Apidae: Euglossini*) olfaction is also used to locate sources of odoriferous chemicals, which are harvested to concoct a complex, species-specific male perfume. This perfume is later displayed at mating territories, presumably to attract conspecific females.

Recent electroantennographic comparisons of orchid bee antennae revealed species-specific responses to certain perfume components. Therefore the detection or attraction elicited by different odorants may be mediated via a species-specific set of OR genes or differential expression of ORs in the antennae. In a first step to test this hypothesis, we examined the antennal transcriptomes of males of two recently diverged sibling species of orchid bees, *Euglossa dilemma* and *Euglossa viridissima*, from southern Mexico. Non-normalized antennal mRNA from male bees was sequenced on a single lane of an Illumina HiSeq 2000 sequencer. The de novo assemblies of the transcriptomes revealed various ORs, most of which had orthologs in both *Euglossa* species and in *Apis mellifera*. Ongoing analyses aim at identifying candidate ORs for detailed expression studies and to identify genomic signatures of diversifying selection. The results are important for a better understanding of orchid bee OR evolution and the role of ORs in orchid bee speciation.

S☐42 Matthias Schott M 627 / 12:15

Insect antennae-based biosensors for *in-situ* measurements

Authors: *Matthias Schott*[1]*, Christoph Wehrenfennig*[1]*, Tina Gasch*[1]*, Rolf-Alexander Düring*[1]*, Andreas Vilcinskas*[1]

Affiliation: [1]*IPAZ Universität Gießen*

Insect antennae represent some of the most sensitive organs for the detection of odors in nature. Amputated antennae, which can operate for hours, can be coupled with an electronic amplifier to monitor the transmitted nerve impulses. This so-called electro-antennography (EAG) can be combined with a parallel trace analysis system such as gas chromatography coupled with mass spectrometry (GC-MS-EAG) which can be used as a biosensor based on insect olfaction. Our project aimed at the development of a portable GC-MS-EAG for in-situ application.

In order to develop a transportable biosensor device for field applications in plant protection we used metal-oxide semiconductor gas sensors for the identification and measurement of the pheromone produced by the grapevine moth *Lobesia botrana*, a major pest insect in viticulture. The selective odorant measurement of a multi-sensor array (SOMMSA) approach was used with metal-oxide semiconductor gas sensors to specify sensors for the pheromone measurement. The combination of SOMMSA with the portable GC-MS-EAG allowed the calibration of the sensors. In addition, we combined the gas chromatograph with a needle-trap sampling device (NTD) which serves as a fast solvent-free extraction and enrichment method that gives the opportunity for a direct quantification of volatiles.

We provided a proof of principle for the applicability of the SOMMSA approach for the calibration of the developed biosensor based on insect antennae. The SnO2 sensor can be used in arrays to increase the selectivity towards various background gases and to develop identification patterns for pheromones and interfering gases. The coupling of the NTD with the portable GC-MS-EAG resulted in a biosensor device with an unprecedented sensitivity for in-situ volatile detection. For example, the detection threshold of the new instrument for the pheromone of the grapevine moth *Lobesia botrana* (7,9-dodecadienyl acetate) was 1,2 ppt and 11 ng/m3 after 15 min enrichment. The developed highly sensitive biosensor for in-situ measurement of odorants can be adapted to many other applications.

POSTERS

♦219 Stefanie Bublak

All good things come in fours? Description of a prospective fourth olfactory organ in Clawed Frogs (Genus Xenopus)

Authors: *Stefanie Bublak*[1]*, Christine Nowack*[1]
Affiliation: [1]*Department of Zoology/Developmental Biology, University of Kassel*

Frogs of the Genus Xenopus (Family Pipidae, tongue-less frogs) ordinarily possess three different olfactory systems: the main olfactory organ and the vomeronasal organ of most tetrapods, as well as a so called middle chamber epithelium (or water-nose), a structure specific for pipid frogs. These three systems differ in terms of their position within the nasal cavity, their ultrastructure, expression of olfactory receptor molecules, and very probable also their functional background.

In the present study the morphology of the nasal cavity of *Xenopus borealis* (Marsabit Clawed Frog), a species that is closely related to the well examined model organism *Xenopus laevis*, was investigated for the first time. Histological cross sections of the nasal region were analysed by light microscopy, as well as additional series sections in horizontal and sagittal plane. In general, the nasal structures of *X. borealis* resemble the situation found in *X. laevis*, including the distribution of the sensory epithelia of the three common olfactory organs.

Surprisingly in sections of the palatal orientation we were able to observe a presumably sensory structure within the main nasal cavity, which has not been described so far.

A vertically oriented groove of sensory epithelium, separated from the main olfactory epithelium by connective tissue, is located in the caudolateral area of the main cavity.

The cytoarchitecture within this groove as well as the presence of subepithelial pigmented cells strongly indicate an olfactory function of this structure.

Further investigations of the ultrastructure, the neuronal connections and the occurrence of olfactory receptor molecules are needed to confirm our histological results. Another important step will be to find out if this is a species-specific finding, or if the structure is also developed in other frogs.

♦220 Annekathrin Junk

Deviant anatomy of the olfactory system in Madagascan mantellid frogs

Authors: *Annekathrin Junk*[1]*, Miguel Vences*[1]*, Christine Nowack*[1]
Affiliation: [1]*Department of Zoology/Developmental Biology, University of Kassel*

Members of the family *Mantellidae* (Anura, Amphibia) inhabit one of the largest islands of the Indian Ocean, Madagascar. Up to now, the anatomy of the nasal cavities of these frogs has not been investigated. In the present study, the intranasal structures of selected members of the *Mantellidae* were examined histologically. Commonly the paired nasal cavity (cavum nasi) of anuran amphibians consists of a main nasal cavity, and a complex structured set of paranasal sinuses. Within the main cavity, the sensory epithelium of the main olfactory organ is located, while the inferior chamber of the accessory cavity encloses a second olfactory system, the vomeronasal organ. Main cavity and accessory cavity are usually connected via a slit-like longitudinal opening, which is called infundibulum in the anterior part of the nose and in caudal direction becomes the so called isthmus.

Surprisingly, in the mantellids we have investigated so far, most parts of this slit no longer form an opening, but are grown together. Only a small rostral area of the infundibulum maintains the spatial connection between the two parts of the nasal cavity.

The functional background of this anatomical exception may be associated with the transfer of olfactory stimuli into the vomeronasal organ; previous studies indicated that the isthmus of other frogs can be occluded temporarily by a vascular pumping mechanism. The deviant anatomy of the nasal cavity observed in mantellids might be related to the presence in many of these frogs of so-called femoral glands that are assumed to produce volatile pheromones.

♦221 Carolin Wittmer

Tales from the crypt: Lectin histochemical study of a potential vomeronasal organ in lungfish

Authors: *Carolin Wittmer*[1]*, Christine Nowack*[1]
Affiliation: [1]*WG Functional Vertebrate AnatomyDepartment of Zoology/ Developmental Biology, University of Kassel*

Lungfish represent the closest living relatives of tetrapods within the group of fish, thus they play an important role in the reconstruction of land vertebrate evolution. Also with regard to their olfactory organ they have a special position within the group of fish: Several authors have observed components of a vomeronasal organ which in addition to the main olfactory organ may be present within their olfactory system. The descriptions of these potential vomeronasal organs, however, differ greatly from each other, regarding their structures and locations.

In the lungfish Protopterus epithelial crypts, located between the olfactory lamellae, were proclaimed as a primordial segmented vomeronasal organ. On the contrary, such crypts were previously interpreted as Bowman's glands. Therefore, an unambiguous classification of these structures is still missing.

In the present approach, lectin histochemistry was used to investigate the mentioned epithelial crypts in the olfactory organ of the lungfish species Protopterus annectens and Lepidosiren paradoxa in order to gain additional information about these potential vomeronasal structures.

♦221 Sigrid Kress

The Correlation of Immediate Early Gene (egr1/c-fos) expression and tyrosine hydroxylase expression in zebrafish brains

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♦189a Gustavo R. Makert

An immunization strategy to combat the poultry red mite (*Dermanyssus gallinae*)

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The blood sucking ectoparasite *Dermanyssus gallinae* causes high economic losses in poultry industry, and different strategies try to control the expansion of poultry red mite (PRM) world wide. However, a solution to this problem still has highest priority. For that reason, we started the development of a strategy to vaccinate chicken against poultry mites. The first step for the development of this vaccine for *Gallus gallus f. domesticus* consisted in the isolation of proteins from PRM. The complete PRM extract, but also individual proteins identified and isolated through 2D-Gel analysis and protein fractionation through HPLC were used for immunization of chickens. Sera and eggs were collected before each immunization and boosts, but also 4 weeks after second boost. Analysis through ELISA and Western blots showed a high specific antibody production against PRM extracts. IgY extracted from eggs after immunization were mixed with fresh chicken blood and applied to an in vitro feeding assay. Through this in vitro feeding assay it was possible to recognize IgY fractions responsible for higher PRM mortality after feeding. The first results show the high potential of this strategy for the development of a vaccine against the poultry mite *Dermanyssus gallinae*. Key words: chicken, ectoparasite, immunity, poultry red mite, vaccine development

Authors Index