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ABSTRACT BOOK

116th Annual Meeting of the German Zoological Society

September 9th – 13th, 2024

University of Hohenheim, Natural History Museum Stuttgart

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DZG 2024

Stuttgart, Germany

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DZG

Center for Biodiversity
and Integrative Taxonomy
(KomBioTa)

WELCOME TO THE

116TH ANNUAL MEETING OF THE GERMAN ZOOLOGICAL SOCIETY

DZG 2024

Stuttgart, Germany

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Vote your Talk and Poster!

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Please put your vote in the provided box!

This can be done until Thursday at the end of the poster session in the „Mensa“.

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This can be done until Friday 5:10 pm at the Welcome Desk.

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SCIENTIFIC CORE PROGRAM

Public Lecture

Teamwork in der Natur: Wie bleiben Insektenkolonien gesund?

Sylvia Cremer
Institute of Science and Technology Austria (ISTA), Österreich

Ameisen, Bienen und Termiten bilden große Kolonien von oft tausenden von Einzeltieren, die meist nur von einer oder wenigen Königinnen abstammen. Durch dieses enge Zusammenleben vieler nahverwandter Tiere könnte es zu rascher Krankheitsausbreitung kommen. Dies ist jedoch fast nie der Fall, da die Kolonien sozialer Insekten zweifach vor Pathogenen geschützt sind: zum einen besitzen auch Insekten ein sehr effizientes Immunsystem, das sogar ein Immungedächtnis aufweist, zum anderen wehren die Tiere einer Kolonie Krankheiten gemeinsam ab. Hierzu gehören ausgeprägte Nesthygiene, gegenseitiges Putzverhalten, Wund- und Infektionsbehandlung, und letztlich auch social distancing.

Durch das Zusammenspiel dieser kooperativen Verhaltensweisen in der Gruppe wird die Kolonie vor Krankheitsausbrüchen geschützt, erhält also „Soziale Immunität“. In meinem Vortrag gehe ich vor allem darauf ein, wie die individuellen Immunsysteme und die kooperative Krankheitsabwehr aller Koloniemitglieder zusammenwirken, und wie Pathogene es trotzdem manchmal schaffen, die Abwehrstrategien ihrer sozialen Wirte zu umgehen.

Evolutionary topology of animal genomes: irreversible processes and novelty in macroevolution

Oleg Simakov
University of Vienna, Austria

Recent studies have highlighted the conservation of chromosomal and sub-chromosomal genomic organization that dates back to the last common ancestor of animals over 600 million years ago.

There are several key processes that have shaped animal genomes since, ranging from „algebraic" combinations of ancestral chromosomal units to complete chromosomal reshuffling in some clades. In both cases, newly formed chromosomal elements provided for a fresh landscape to evolve local gene linkages, many of which potentially constituting functional co-regulated units.

In this talk, I will highlight the latest results from our team that describe how such switches in „evolutionary topology" may be instrumental for shaping irreversible macro-evolutionary trends in animal genomes, characterizing the time-frame for the continuing evolution and emergence of local gene regulation.

In particular, I will share our latest results from cephalopod and cnidarian regulatory and structural genomics studies that aim to probe the functional landscape along evolutionarily diverse chromosomal elements.

The nature of adaptive radiation in the cichlid fishes of Lake Tanganyika

Walter Salzburger
University of Basel, Switzerland

Adaptive radiation is probably the source of much of the ecological and morphological diversity of life on Earth.

Because of their spectacular taxonomic, phenotypic, ecological and behavioral diversity and their propensity for explosive speciation, the cichlid populations in the African Great Lakes of Victoria, Malawi and Tanganyika are an excellent example of this evolutionary process. The cichlids of Lake Tanganyika form the most morphologically, ecologically and behaviorally diverse cichlid species groups.

Our in-depth study of almost all of its approximately 250 cichlid species revealed that this spectacular adaptive radiation did not occur gradually, but in the form of three successive and trait-specific pulses of accelerated phenotypic evolution.

Three trait complexes - body shape, mouth morphology and lower jaw bone - are very diverse and show a particularly strong relationship with the environment. Furthermore, there is evidence that diversification in terms of behavior and pigmentation patterns has contributed to the adaptive radiation of cichlids in Lake Tanganyika.

Using high-throughput species discovery with robots and Nanopore sequencing to overcome taxon biases in biodiversity science

Rudolf Meier

Natural History Museum Berlin, Humboldt-Universität Berlin, Germany

Biodiversity science neglects hyperdiverse arthropod clades, although they are species-rich and provide many ecosystem services (‚dark taxa‘).

In my keynote, I highlight that over half of the diversity of flying insects belongs to only 20 family-level clades, a pattern consistent across habitats and continents. I then demonstrate how little is known about most of these clades by comparing the number of described species with the number of species in samples from all over the world. This leads to the conclusion that we need new approaches for such taxa.

One key innovation is a robot (‚DiversityScanner‘) jointly developed with KIT that detects, images, and measures individual specimens prior to placing them into microplates for DNA barcoding with Nanopore sequencers. Morphological data collected for selected specimens can then be used to validate ‚barcode clusters‘ as species, thus readying them for identification or description.

I will show how this approach significantly accelerates the transformation of dark taxa from obscurity to sufficiently well known for biomonitoring. Furthermore, I will illustrate how AI identification tools for a relatively small number of species can eliminate the need to barcode 50 % of all specimens in bulk insect samples. In conclusion, I thus advocate for confronting the darktaxon problem in biodiversity science through high-throughput integrative taxonomy, facilitated by new technologies, and applied to one local sample at a time.

Development as a driver or a brake of morphological diversity?

Anne-Claire Fabre
Natural History Museum of Bern, University of Bern, Switzerland

The majority of animals, including the most successful and speciose groups of insects (over 80 %) and vertebrates (more than one half of their known diversity or ~20,000 species), undergo metamorphosis implying drastic morphological, functional and ecological changes during the life of an organism. Thus, indirect development (i.e. biphasic) with a complex life cycle is a dominant developmental strategy and has resulted in much of the exceptional diversity that is evident today. Metamorphosis is consequently a widespread phenomenon and may be an important driver of biodiversity, a hitherto largely neglected question which I propose to investigate in this keynote. Salamanders are an excellent model to do so, as they are sensitive ecological indicators, highly diverse (~800 species) and show the largest variation in life cycle types among vertebrates. The conceptual framework offered by the presence of a diversity of life cycles allow us to test the ability of an organism to adapt to environmental changes by producing morphological variation (larval and adult stages) from a single genome.

As such, we quantitatively analyse the role of development and function on the evolution of phenotypic diversity on the feeding system over evolutionary timescales, using a comparative approach combining different taxonomic and ontogenetic scales. To do so, we use interdisciplinary approaches combining functional morphology, developmental biology, diversification analyses and statistical modelling to disentangle the factors driving diversity at different ontogenetic stages across space and time. Our results show that life cycle complexity can, depending on the anatomical structure, constrain or alternatively facilitate the evolution of morphological structures and their diversity. As such life cycle complexity can strongly impact the pattern of morphological diversification across species. Furthermore, the changes encountered during life cycle shifts have, in some cases, facilitated divergent evolutionary dynamics between species and the colonization of new habitats.

This presentation will shed light on whether life cycle variation has played a major role in the morphological and functional diversity of salamanders.

Specialized gut microbiota-host interactions in social bees

Philipp Engel

University of Lausanne, Department Fundamental Microbiology, Switzerland

Animals often harbor specialized microbial communities their gut. These communities have significant physiological and metabolic effects on their hosts, and hence impact animal health and disease in many ways.

However, understanding mechanisms underlying gut microbiota-host interactions still represents a formidable challenge due to the complex and often inaccessible biology of gut microbial communities and their animal hosts.

Social bees (i.e. honey bees, stingless bees and bumble bees) offer fantastic opportunities to study gut microbiota-host interactions as they harbor relatively simple yet specialized and experimentally tractable gut bacterial communities. In my talk, I will present recent findings from ecological surveys of wild bee species and gnotobiotic bee experiments with honey bees which advance our understanding of the evolution, ecology, and functioning of microbiota-host interactions and provide new insights into bee health.

Bees, bugs and pollination: how global change can affect population health and disease ecology

Lena Wilfert

University of Ulm, Germany

Global change, such as land use intensification, invasive species and of course of climate change, can disrupt biotic interactions, for example leading to emerging diseases or declines in population health.

We combine studies of wild assemblages of bees and other pollinators with omics approaches and experimental studies to understand how global change affects biotic interactions in these beneficial insects, crucial for the maintenance of biodiversity and human food security.

For example, we study how the anthropogenic de-novo acquisition of vector-borne transmission has led to disease emergence and changes in pathogen ecology in wild and managed bees and how land-use intensification affects pollinator health. This sheds light on fundamental evolutionary ecology, such as what drives the evolution of virulence, but at the same time identifies conservation strategies that can mitigate the effects of climate change on pollinator communities.

Round Table Discussion #IchBinHanna

#IchBinHanna. Prekäre Wissenschaft in Deutschland

Amrei Bahr
University of Stuttgart, Germany

Sven Bradler
German Zoological Society, Germany

Manuela Sann
University of Hohenheim, Germany

Johannes L.M. Steidle
University of Hohenheim, Germany

Jörn von Döhren
University of Bonn, Germany

Peter Warth (Moderation)
Stuttgart State Museum of Natural History, Germany

Mit dem Twitter-Hashtag #IchBinHanna und dem 2022 erschienen Buch “#IchBinHanna: Prekäre Wissenschaft in Deutschland” kritisieren die drei Wissenschaftler:innen Amrei Bahr, Kristin Eichhorn und Sebastian Kubon die Arbeitsbedingungen und Berufsaussichten des akademischen Mittelbaus. Ausgangspunkt war ein 2021 veröffentlichtes Video des Forschungsministeriums, in dem die fiktive Biologin Hanna die Vorteile des seit 2007 eingeführten Wissenschaftszeitvertragsgesetz (WissZeitVG) propagiert.

Gemeinsam mit der Philosophin und Initiatorin Amrei Bahr werden wir den Hintergrund der #IchBinHanna Initiative und gegenwärtige Situation Rund um das WissZeitVG besprechen und Lösungsvorschläge und Reformansätze diskutieren.

Wir möchten eine lebendige Podiumsdiskussion gestalten und bitten Sie um aktive Teilnahme an der Vorabumfrage. Im Foyer finden Sie Fragebögen, die Sie ausgefüllt in die zugehörigen Boxen werfen können.

Die Veranstaltung findet auf Deutsch statt.

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INVITED SUBJECT GROUP TALKS

How to „organize“ a spider embryo. Insights into early spider embryogenesis and beyond.

Matthias Pechmann

University of Cologne, Cologne Biocenter, Institute of Zoology, Germany

The establishment of the anteroposterior (AP) and dorsoventral (DV) body axes is a crucial process during the early embryonic development of bilaterally symmetric animals. In many animals, ‘organizers’ are key players to induce the main body axes and to induce gastrulation and germ layer patterning. In spiders, the organizer is known as the ‘cumulus’. The spider cumulus, a cluster of migratory and signalling cells, is formed during early embryogenesis and induces the formation of the dorsoventral (DV) body axis via the activation of the BMP signalling pathway in cumulus adjacent cells. In close association to this process, cumulus migration is crucial to induce dorsal cell fate at the correct position within the embryo. Previous studies indicate that Hedgehog- as well as FGFR-signalling is involved in cumulus migration. Overall, the proper formation and migration of cumulus cells is key to normal spider embryogenesis. While the loss of the cumulus is blocking DV axis formation, duplication of the cumulus can induce embryonic twinning.

Many aspects of the organizing capacities of the spider cumulus are still poorly understood. Especially the gene regulatory networks that are associated with cumulus migration, cumulus cell cohesion and signalling are crucial to understand axes formation in spiders. Our analyses focus on these cumulus specific gene regulatory networks (GNRs) and provide a better understanding of the mechanisms that lead to proper axes formation in spiders and other chelicerate species.

Developmental Biology

Taller or smaller: How feeding controls body plasticity in a sea anemone

Patrick Steinmetz
University of Bergen, Norway

Most animals regulate their growth rates and body sizes to match the amount of nutrients available in the environment. Although this capacity constitutes one of the oldest physiological control processes in animals, it is only poorly understood on a cellular and molecular level.

I will present our current cellular and molecular understanding of how changes in nutrient supply affect body size and growth rates in the sea anemone Nematostella vectensis. On a whole-body level, we found that feeding drives body growth by cell proliferation while starvation leads to whole-body shrinkage and massive cell loss. I will show how food supply affects cell cycle progression, TOR signalling activity and apoptosis levels on a whole-body level and in a specific population of multipotent stem-like cells. In addition, we observed that epithelial cell extrusion occurs during starvation-induced cell loss and is likely evolutionary conserved between cnidarians and bilaterians.

Altogether, our research forms the foundation to start understanding how cell physiology integrates nutritional input to control cell cycle progression and body plasticity in animals with lifelong growth.

Evolutionary Biology

Short time, big impact – host-microbiome interactions in the Anthropocene (stories from honey bees and bark beetles)

Vienna Kowallik
Albert-Ludwigs-Universität Freiburg, Germany

In recent decades our environment has been experiencing drastic, human-made changes. The consequences, especially regarding insects, range from steady declines/extinctions of species on the one hand, to outbreaks/invasions on the other. As most insects live in intimate relationships with microbial symbionts, these biotic interactions are undoubtedly disturbed by anthropogenic change such as chemicals, habitat modification, or climate change. In this talk, I will look at some of these effects on microbial symbioses in honey bees and bark beetles, two systems that show rather contrasting responses to environmental change.

The microbiome of honey bees (*Apis mellifera*) is well defined, socially transmitted and experimentally tractable. Leveraging these facts, we tested whether a chemically perturbed microbiome, as well as associated effects on host phenotypes, are transmitted across adult worker "generations".

In aggressive bark beetles (such as *Ips typographus*), which are known for their increasing mass outbreaks, host-microbiome relationships are much less understood. I will present our current work on protective functions, symbiont mediated effects on beetle behavior, and our plans to investigate how the microbiome may be affected by climate change.

Evolutionary Biology

Evolution in the Anthropocene: Bees and Urbanisation

Panagiotis Theodorou
Martin Luther University Halle-Wittenberg (MLU), Germany

Cities are expanding worldwide, and urbanisation has been identified as a threat to global biodiversity as well as a driver of evolutionary change. The growth of cities results in an increase in impervious surfaces, habitat loss and fragmentation, invasion of non-native species and long-term environmental changes associated with the heat island effect and pollution. The combination of these effects constitutes a challenge to the survival and persistence of many species, including essential ecosystem service providers, such as wild bees, while also imposing altered selective regimes. Only organisms that can cope with and/or adapt to this novel set of challenging urban abiotic and biotic conditions can survive in cities.

Recent reports of bee declines have focused attention on insect pollinators, and urban ecology has provided significant insights into how urban environmental changes affect bee species‘ community structure. However, we know little about how the ecological impacts of urbanisation affect the evolution of wild bee populations living in cities.

In this talk, I will highlight the latest results from our ongoing research, which investigates how consistent and predictable the effects of urbanisation are on the adaptive and non-adaptive evolution of wild bee populations.

Morphology

Egg Morphology at the Nanoscale

Liliana d'Alba
Naturalis Biodiversity Center (NCB), Netherlands

Eggs are multifunctional structures that have enabled animals to colonize terrestrial habitats for millions of years. Egg morphology, particularly eggshell nanostructure, is at the core of animal survival, mediating the interactions between embryos and their environment, and has evolved into a massive diversity of forms and functions in modern taxa. These functions are critical to embryonic survival, have profound effects on animal evolution and may serve as models for new antimicrobial and/or breathable materials.

Nevertheless, we lack essential knowledge on the basic properties of eggs, including their ultrastructure, chemical composition, and material properties. These data are critically needed if we are to understand their effects on evolution and diversification of animal lineages. Here, I showcase our research on the relative contributions of structural constituents and chemistry of eggshells to their biomechanical performance using squamate and stick insects as study systems.

I combine techniques to characterize eggshell structure (i.e. X-ray micro-Computed Tomography (µCT) coupled with scanning electron microscopy), with the analysis of eggshell chemical composition using FTIR. Bridging form to function, I then present our findings on the functional performance (optical, mechanical, interaction with water) of these eggshells and finish by revealing the insights we have gained about the evolution of these remarkable egg structures and their impact on animal fitness.

History, Novelty, and Function: Cases from Beetles and Wasps

Brendon E. Boudinot
Senckenberg Research Institute and Natural History Museum, Frankfurt am Main, Germany

In this talk I will introduce the beetles (Coleoptera) and pincer wasps (Hymenoptera: Dryinidae) as evolutionary morphological systems for understanding the dimensions of history, anatomical identity, and function.

Using the early evolutionary history of the Coleoptera as the first of two case studies, I will contrast the deepest fossil record of this group to the Hymenoptera and use phylogenetic methods to test hypotheses of fossil placement and transformation series. In so doing, I will highlight the evolutionary patterns of Coleoptera that demonstrate the need for deciding criteria for the determination of homology and character polarity. In the second case study, I will define a new system for the study of novelty and function: The grasping mechanism of Dryinidae. I will define the system anatomically and mechanically, which involves the recognition of new biological characters and the modified states of inherited characters. By tracing the derivation of form and function across the phylogeny of the group, I will contrast plesiomorphy and apomorphy of states versus the origin, inheritance, and extinction of characters. Finally, using these two systems, I will reflect on the insights that can be provided by a phylogenetically informed and systematic-phenomic approach to evolutionary developmental biology.

Presenting work done in collaboration with Rolf G. Beutel [Institut für Zoologie und Evolutionsforschung, Jena], Thomas van de Kamp [Institute for Photon Science and Synchrotron Radiation (IPS), Laboratory for Applications of Synchrotron Radiation (LAS), Karlsruhe Institute of Technology (KIT)], and Carly Tribull [Farmingdale State College, USA], among others.

Neurobiology

Neuronal control of flight turns in *Drosophila*

Bettina Schnell
Max Planck Institute for Neurobiology of Behavior – caesar Bonn, Germany

Flies perform rapid turns termed saccades to change direction during flight, which constitute an important aspect of their behavior. However, how these turns are controlled by the brain is still poorly understood. Saccades can be elicited by looming stimuli mimicking an approaching object such as a potential predator, but can also be initiated spontaneously.

We study the neuronal mechanisms underlying the control of saccades during flight with a focus on descending neurons (DNs) that transmit information from the brain to the ventral nerve cord. Using whole-cell patch-clamp recordings during head-fixed flight in *Drosophila*, we have identified DNs whose activity is correlated with flight saccades (measured as changes in wing stroke amplitude in our preparation), some of which receive direct input from looming-sensitive visual projection neurons. To study the actual contribution of these DNs to the control of saccades, we use genetic tools to manipulate their activity during both head-fixed and free flight.

For this, we have developed a setup that allows us to track the flies' behavior during free flight while presenting visual stimuli or optogenetically activating DNs. This work provides an entry point into understanding how sensory information is transmitted to the motor system to control an important behavior of the fly.

Neurobiology

Songbird brain circuits for skilled vocal and non-vocal behaviors

Felix Moll
University of Tübingen, Animal Physiology, Germany

From typing an email to swinging a tennis racket, learned motor sequences are commonplace in our everyday lives. In humans, these complex behaviors are often associated with the use of tools, but how tool use is controlled at the level of the neural circuit remains virtually unexplored.

To gain traction on this issue, we first consider our previous work on the neuronal mechanisms underlying a different complex learned behavior: the courtship song of the zebra finch (*Taeniopygia guttata*). Next, we demonstrate that the zebra finch shares its songbird-typical brain structures dedicated to vocal control (i.e., the "song system") with the carrion crow (*Corvus corone*) – another songbird species that readily learns to use tools in the laboratory.

In the crow brain, the well-characterized song system is anatomically paralleled by identified areas involved in voluntary head movement control, which we have mapped out using tract-tracing methods. These premotor areas are likely involved in controlling our crows' behavior in a task that requires them to employ a stick tool to reach for food pellets in a fully automated behavioral setup. By tracking their movements with high-speed video cameras, we demonstrate both the reproducibility and the sensory feedback-driven adaptability of the crows' tool use. This new behavioral paradigm and an anatomical atlas of the crow's premotor system will enable us to identify the neuronal underpinnings of tool use control in the crow brain, uncovering network coding principles underlying skilled action sequences.

Ecology

The role of environmental features in shaping insect traits

Sabine Nooten
University of Würzburg, Biocenter, Department of Animal Ecology and Tropical Biology, Germany

Insects are an essential part of global biodiversity. They stand at the relative base of the food chain and play important roles in ecological processes. They are also sensitive to environmental change.

I am using social Hymenoptera (ants and wild bees) as model organisms to tackle questions related to global patterns, species traits, and key ecological processes. On the global scale, my research shows that there is a huge variety of the sheer numbers and densities across biomes, regions and habitats. On smaller scales, regional communities are related to land use types and habitat features. In climatically challenging environments, only species with a specific suite of traits persevere.

Given the current loss of insect biodiversity in terms of species richness and abundances, it is paramount to understand relationships between insect species, their traits and the environment. In other words – why are insects where they are and which key features are important to persist in the future?

Ecology

The influence of environmental stressors and associated landscapes on diet diversity, body traits, and reproduction in wild bees

Samuel Vieira Boff
Ulm University, Germany

Wild bees are crucial pollinators, guaranteeing the reproduction of many flowering plants and their production of diverse nuts, fruits and seeds. Despite their vital ecosystem service of pollination which is tightly linked to food production, generating billions of dollars every year, wild bee populations are declining in response to anthropogenic stressors. Deforestation and the depletion of floral resources are key challenges, reducing nesting opportunities and food availability for wild bees. Sublethal doses of pesticide disrupt the behaviour and physiology of solitary bees, including their chemical communication, in the case of the latter, affecting their own reproduction.

In this talk, I will present two case studies: one in the Neotropical region and another in the Temperate region, addressing these stressors and how they impact wild bees. The first study focuses on the primitively eusocial orchid bee, *Euglossa cordata* (Apidae: Euglossini), for which I examine diet diversity and brood production in Neotropical areas. First, we assess the impact of deforestation on pollen diversity in *E. cordata* nests, finding that forested areas in São Paulo (Brazil) support higher pollen diversity and greater brood production. Moreover, published studies across the Neotropical region corroborate the idea that forest cover predicts higher pollen diversity in *Euglossa* bees. The second study investigates the influence of conventional and organic farming systems on the nesting occupancy rate and body traits of *Osmia bicornis* (Megachilidae: Osmiini), an essential crop pollinator in Germany. Our findings reveal that sustainable agriculture enhances nesting and brood cell production, and local farming practices affect body size and cuticular hydrocarbons. These cuticular hydrocarbons are sex pheromones that influence mating behavior, potentially mediating the effect of pesticide on bee populations.

Our results highlight the need for collaboration among scientists, farmers, and policymakers to protect wild bees, emphasizing that landscape and resource management, along with greater attention to sustainable pest management, are key to wild bee conservation.

Funding: Aurelia Stiftung and SAGST

Physiology

Metabolic Adaptation to Nutrient Limitation in Vertebrates

Nicolas Rohner
University of Münster, Germany

Adaptation to food deprivation is widespread among animal species, reflecting the intimate connection between genotype, phenotype, and the environment. However, the genetic basis of physiological adaptations to nutrient availability remains an unresolved challenge of both organismal biology and modern evolutionary genetics.

We are using the cavefish Astyanax mexicanus as a promising research organism to unravel the genetic basis of starvation resistance. A. mexicanus exists in two forms: a river-dwelling surface fish and a blind, depigmented cavefish. Whereas the surface forms live in a rich ecological environment, multiple distinct cave populations have evolved metabolic adaptations to nutrient limitations in caves. Importantly, the surface and cave morphs remain interfertile and can be bred in the laboratory.

Using recently developed genetic and genomic tools, we have shown that cavefish evolved a massive capacity for fat storage due to increased appetite, adipogenesis, and lipogenesis. In addition, we found that cavefish display elevated blood sugar levels and insulin resistance caused by a mutation in their insulin receptor. Unlike humans with the same mutation, cavefish do not display diabetes markers and live long and healthy lives. Furthermore, cavefish develop hypertrophic visceral adipocytes without obvious signs of inflammation due to reduced amounts of pro-inflammatory cytokines.

In a more recent series of studies, we showed that cavefish are thriftier due to decreased muscle mass, improved glycogen production, and efficient recycling of amino acids. As all these extreme adaptations have no negative consequences on the metabolic health, immune response, and lifespan in these fish, it suggests that cavefish develop these phenotypes as part of their starvation resistance and have evolved resilience phenotypes that allow them to tolerate deviations from normal vertebrate physiology. This positions cavefish as a promising model to gain mechanistic insights into disease phenotypes from an evolutionary and adaptive perspective.

High voltage immunity in strongly electric fish

Stefan Schuster
University of Bayreuth, Germany

Strongly electric fish are renowned for shocking prey and foes, but it is not known what protects them from being shocked themselves. I will report evidence for two strongly electric fish, the African electric catfish, and the South American electric eel. In both species, the operation of muscles, nervous systems, and of the heart is immune not only against their own but also against external high voltage discharges. Surprisingly, both species do not simply insulate their body but allow low-frequency currents to pass, so that it is possible to pick up electrocardiograms from their surfaces.

By studying explanted organs, we show that heart and muscles of the electric eel are intrinsically tolerant against high voltages. However, in the electric catfish the explanted organs are not immune but are efficiently protected in vivo by a thin layer with remarkable cellular properties.

How the fairy tube-worm got its dance, and other evolutionary tales of form and function in marine annelids

Jenna Moore

Museum of Nature Hamburg, Zoology, Leibniz Institute for the Analysis of Biodiversity Change (LIB), Germany

Marine annelids are amazingly morphologically diverse, reflecting both the flexibility of their segmented body plan, which has allowed them to radiate into every marine habitat, and their diverse feeding strategies – including suspension feeding, detritivory, herbivory, and predation. Tagmatization is the functional specialization of groups of body segments and a defining feature of arthropods. However, functional body regionalization is not as well understood in annelids, another major lineage of segmented animals.

This talk will explore functional morphological evolution in two distantly related clades of marine annelids. I will present results on the evolution of tagmatization in Chaetopteridae, a small group of tube-dwelling annelids. Their diverse and flexible feeding modes provide a unique natural experiment to explore body region specialization in annelids in phylogenomic context. I will discuss how a complete organismal view, linking phylogeny, form, function, ecology, and oceanography, can inform systematics and taxonomy.

I will also present ongoing research on the evolution of complex jaw structures in Eunicida, a diverse lineage of marine annelids with a rich fossil record from the late Cambrian to the Recent. Eunicidans have diverse, complex, articulated jaw structures, and lifestyles ranging from tiny microphagous worms to the giant “sand-striker” worm, an ambush predator of fish.

Both examples will illustrate how museum collections can be used to investigate functional morphological evolution, generate new character information for systematics and taxonomy, and provide context for global biogeographic patterns by revealing evolutionary constraints and opportunities.

Diversity of the germline-restricted chromosome in passerines birds

Francisco J. Ruiz-Ruano
Leibniz Institute for the Analysis of Biodiversity Change (LIB), Museum Koenig (ZFMK), Bonn, Germany

The genomics field has significantly advanced our understanding of avian chromosome evolution. However, a special chromosome consistently found across all studied songbird species has been scarcely considered in the genomic research. This is a germline-restricted chromosome (GRC) which is absent in the somatic line and only present in the germline.

The recent works in the zebra finch, two nightingales and the blue tit have suggested a shared ancestral origin for songbird GRCs. These chromosomes exhibit an exceptional rate of content turnover compared to the rest of the genome. Here, we aim to explore the biodiversity of GRCs across the passerine phylogeny. Using linked-read libraries from 10x Genomics Chromium, we sequenced draft genomes from both germline and soma tissues of 25 species within the Estrildidae family and other Passeriformes families, including two suboscines as well. Also, we went deep in two species by performing testis long-read assemblies. Our comparative analysis revealed that the GRC was present in a common ancestor of all passerines, so two thirds of all bird species would carry it.

Additionally, we found a remarkable diversity in the GRC led by expansion and contraction of repeats as well as events of gene acquisition and loss. Actually, only a few genes are ancient and widespread like elavl4, cpeb1, bicc1 and pim1, raising the possibility that they are important for the function of this mysterious chromosome.

Social relationships in farmed animals and its impact on welfare

Borbala Foris
Veterinärmedizinische Universität Wien, Austria

Social environments in agricultural settings often differ from what animals evolved to live in. Many farm animal species are kept in artificially created groups and have limited agency in avoiding others or maintaining meaningful social bonds over longer time.

Despite these considerable differences from wild counterparts, farm animals live in complex social environments and management practices that prioritize the social needs of animals are needed to ensure a high level of welfare. Technological advances in automated behavioral monitoring open new frontiers in the analysis of social interactions in farm animals and allow us to better understand how the life of individuals is modulated by their social environment.

This talk will highlight key examples of adverse welfare effects of suboptimal social settings through competition and agonistic interactions and outline current research on the potential benefits of facilitating the formation and maintenance of socio-positive bonds. The promises and pitfalls of technology use in routinely monitoring and managing the social environment will also be discussed.

Evaluating the Evolutionary Roots of Cooperation and Conflict through the lens of Pan

Liran Samuni
German Primate Center, Leibniz Institute for Primate Research, Germany

More than any other species, humans exhibit an extraordinary capacity for cooperation that transcends social boundaries and is often considered the secret to our success. However, the same capacity for cooperation can also fuel intergroup conflict and violence, resulting in discriminatory and prejudicial behavior. Studying the evolutionary roots of the interplay between cooperation and competition through the lens of Pan is key to the reconstruction of ancestral hominin conditions that continue to influence the social dynamics of present-day human societies.

In this talk I will discuss the mechanisms underlying violence and cooperation among our closest living relatives, chimpanzees and bonobos. These two species share similar life-histories and social environments but exhibit significant differences in patterns of dominance, social relationships, and out-group attitudes. By leveraging and evaluating the similarities and differences between them, I will present some work on how in-group/out-group identity is manifested in the two species and its potential link to hostile or peaceful out-group attitudes. I will evaluate the contexts underlying out-group competition or cooperation in the two species and the role of differentiated social relationships in shaping their societies.

DZG 2024
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SUBJECT GROUP TALKS

Molecular interplay of conserved and novel genes shapes the neurogenesis of *Hydra*

02

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The neuron is considered to be an evolutionarily ancient cell type, and the first neurons likely emerged in the last common ancestor of Cnidaria and Bilateria. The molecular programme of mature neurons is composed of ancient, highly conserved functional modules. Moreover, neurogenesis - the process of neuronal emergence and differentiation from committed progenitors - is also controlled by a set of conserved transcription factors. However, our observations (Klimovich et al., PNAS 2020) revealed a substantial contribution of non-conserved lineage-restricted genes to the molecular programme of neurons in the freshwater polyp *Hydra*.

Here, we explore the role of lineage-restricted genes in *Hydra* neurogenesis using phylogenomic analysis, single-cell transcriptomics, machine learning tools, functional genetics approaches and behavioural assays. We demonstrate that novel Medusozoa- and Hydrozoa-restricted genes encoding transcription factors and effector proteins play a critical role in the maturation and individuation of *Hydra* neurons. We show that the emergence of novel transcription factors complemented the conserved neurogenesis programme and enabled the assembly of molecular signatures specific to particular neuronal types, such as pacemaker neurons, in Medusozoa.

Our findings provide novel insights into the evolutionary assembly of the neuronal machinery in Cnidaria. They highlight the role of non-conserved genes in the evolution of the nervous systems and suggest an independent maturation of the neuronal machinery in the major metazoan lineages. Our study not only contributes to resolving the evolutionary history of nervous systems, but also provides a paradigm for the joint role of conserved and novel genes in major evolutionary transitions.

The work is supported by grants from the German Research Foundation (DFG) - project KL 3475/2-1 and CRC1461: "Neurotronics: Bio-Inspired Information Pathways", project-ID 434434223.

Cranial neural tube closure and embryonic head formation require differential regulation of tissue tension mediated by the endocytic receptor Lrp2

03

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During embryonic development of the vertebrate head, closure of the cranial neural tube and formation of the skull and face are intimately connected, as highlighted by the frequent co-occurrence of congenital craniofacial dysmorphologies and brain defects. In human patients with Donnai-Barrow-Syndrome, these defects are caused by pathogenic variants of Lrp2, an endocytic receptor of the LDL receptor family.

We functionally analyzed neurulation in the African Clawed Frog Xenopus laevis to decipher the mechanisms of endocytic receptor-mediated embryonic head development. While loss of Lrp2 delayed or entirely inhibited neurulation, CRISPR / Cas9-mediated editing of Lrp2's C-terminal PDZ-binding domain strikingly accelerated neural tube closure - a rarely reported neural tube closure phenotype. Both delayed and premature neural tube closure were associated with head malformations. On the cellular level, Lrp2 controlled apical constriction, a cell shape change essential for cranial neurulation movements. Via its PDZ-binding domain, Lrp2 orchestrated the velocity and spatial distribution of apical constriction. Since constriction of the apical cell surface is mediated by actomyosin contraction, we asked whether Lrp2 influenced the activation of actomyosin. Deletion of the PDZ-binding domain led to aberrant actomyosin activation, disrupting the not only the temporal but also the spatial pattern of apical constriction in the neuroepithelium. Our functional analysis strongly suggests that via its PDZ-binding domain, Lrp2 interacts with intracellular adaptors to regulate the cascade of actomyosin activation. This temporospatial control of tensile forces by Lrp2 is essential to orchestrate the mechanics of neural morphogenesis as a prerequisite for head development during vertebrate embryogenesis.

The making of a pest – Sense organ diversification on the female *Drosophila* ovipositor

04

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In contrast to most other *Drosophila* species, the spotted wing *Drosophila*, *D. suzukii* is able to pierce the skin of ripening fruits. While other *Drosophila* species usually prefer soft egg-laying substrates like rotten fruits, *D. suzukii* evolved an enlarged egg laying apparatus and a preference for harder substrates. In line with this ecological diversification not only the overall ovipositor size and trichomes on the ovipositor show variation between species but also the sense organs on the ovipositor have undergone several evolutionary transitions. These include diversification in number, density, and positions as well as morphological changes between. A strong diversification of ovipositor sense organs is also observed in other Drosophilid species and is in stark contrast to thoracic or leg sense organs showing less variation. While only little is known about sense organ formation on the ovipositor the overall organization and number of cells of the ovipositor is largely comparable among *Drosophila* species therefore it is unlikely that the observed variations are solely a side-effect caused by expansion of the entire tissue. To understand how *D. suzukii* could evolve to a crop pest species we performed differential gene expression analysis in developing genital tissues of closely related *Drosophila* species. Genes with different expression levels in *D. suzukii* were tested for their function during sense organ development using RNAi mediated tissue specific knockdown in *D. melanogaster*. This reveaed several insteresting candidates which we now further study using a variety of bioinformatic and developmental approaches.

Elevated temperature fatally disrupts nuclear divisions in the early *Drosophila* embryo

05

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Temperature variations can challenge animal survival. Elevated temperatures present distinct vulnerabilities at different stages of animal life cycle. Embryonic development is known to be especially vulnerable, though the molecular mechanisms remain unclear. Here we investigate how elevated temperature affects embryogenesis in *Drosophila melanogaster*, a model whose genetic makeup and developmental processes have been thoroughly characterized. We identify the first three hours as a critical window in which *Drosophila* embryos are particularly vulnerable to elevated temperature. This period includes the formation of a syncytial blastoderm, which involves 4 rounds of meta-synchronous nuclear divisions at the embryonic cortex, and cellularization that leads to the formation of the cellular blastoderm. Embryos exposed to elevated temperature during this period subsequently exhibited developmental defects at the gastrulation stage, leading to increased lethality. We observed an increase in mitotic failures causing a loss of cortical nuclei, both, during syncytial blastoderm and cellularization stages, in embryos developing at elevated temperature. There is also a local crowding of nuclei and an increase in asynchrony between the nuclear cycles in the center vs. the poles. Interestingly, these features cooperatively amplify the frequency of mitotic failures, leading to holes in the blastoderm epithelium. We performed functional tests to determine whether known regulators of mitosis could rescue these developmental defects and improve embryo survival, and analyzed genomic datasets from wild populations to determine whether they carry signatures of adaptation in these regulators of mitosis. Our genetic rescue experiments show that in *Drosophila* embryos, the interaction between cortical F-actin and microtubules is vulnerable to disruption at elevated temperatures, leading to mitotic failures that can be potentially rescued by modulating the expression of just a few factors. We propose that levels of expression of corresponding genes could be used as indicators to predict the effects of increasing temperature variations on insect populations.

From Hormones to Armor: Ecdysteroidogenesis-related Halloween Genes in the Development of the Spider *Parasteatoda tepidariorum*

06

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In Ecdysozoa, an external skeletal structure protects internal organs against environmental stressors, thereby contributing to their evolutionary success and diversity. However, to accommodate both exterior and interior stimuli such as growth, this rigid chitinous "amour" necessitates periodic renewal. Consequently, molting is a key process in the lifecycle of Ecdysozoa.

Molting is triggered by ecdysteroid hormones, which are synthesized through sequential hydroxylation of dietary cholesterol by a group of catalyzing enzymes. The enzyme-encoding genes, collectively known as the Halloween genes, play a fundamental role in the ecdysteroid biosynthesis pathway. While the Halloween genes and the corresponding pathway are well-characterized in insect model organisms, the understanding in non-model organisms such as chelicerates remains limited. Identified ecdysteroidogenesis-related genes in chelicerates include neverland, shroud, spook, disembodied, shadow, and shade.

As of present, the tissue-specific gene expression and protein localization remain unidentified in spiders. Therefore, mRNA and protein expression of the Halloween genes are currently investigated in embryos of the spider Parasteatoda tepidariorum. The post-embryonic role of these molting-related genes was studied via RNAi knockdowns. The findings are anticipated to offer valuable insights into the intricate processes underlying the ecdysteroid biosynthesis and contribute to our understanding of the evolutionary dynamics within Ecdysozoa.

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Differentiation dynamics for extraembryonic epithelial cell types

07

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During animal embryogenesis, one of the earliest specification events distinguishes extraembryonic (EE) from embryonic tissue fates: the serosa in the case of the insects. While it is well established that the homeodomain transcription factor Zen1 is the critical determinant of the serosa, subsequent realization of the tissue's identity has not been investigated. Here, we examine serosal differentiation in the beetle Tribolium castaneum, comparing embryos from a Tc-zen1 RNAi dilution series, where complete knockdown results in amnion-only EE tissue identity. While some tissue features exhibit an all-or-nothing RNAi outcome, other key features show dose-dependent phenotypic responses, with trait-specific thresholds. Our approach reveals transient hybrid cell states, illustrating how quantitative analysis of tissue maturation dynamics from live imaging extends but also challenges interpretations based on gene expression data. We embed these morphogenetic findings within the known genetic regulatory network of early axial/anterior patterning, providing nuance beyond the known status of Tc-Zen1 as a selector gene.

Relative timing of hemocyte and extraembryonic tissue dynamics after wounding in the red flour beetle

08

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Extraembryonic (EE) tissues and inflammatory responses are two systems that protect developing embryos against wounding and infection. However, the relative timing of when these two systems are functionally competent is not well elucidated. In species without protective EE tissues, such as zebrafish and *Drosophila*, the onset of macrophage (hemocyte) competence is critical for embryonic protection. Yet most insects, such as the flour beetle *Tribolium* castaneum, are fully enclosed by the serosa as an EE tissue with innate immune competence for an extended period of embryogenesis. Are there heterochronic shifts in the onset of hemocyte competence in species with protective EE tissues?

Here we characterize hemocyte response behaviors through live imaging after laser-induced wounding in the *Tribolium* embryo. We demonstrate the strength of hemocyte response in late development and methods for visualizing resident (non-responding) hemocyte behaviors. Ongoing analyses encompass how hemocyte cell protrusion dynamics change as the wound response progresses and quantitative features such as rate and cell number for hemocyte recruitment. In the future, we will examine wound response dynamics at earlier stages and additional tissues to assess serosal repair competence and when hemocytes take over from the EE tissue in conferring protection to the embryo.

Cell lineages in development and evolution of the face

33

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Enormous facial shape diversity evolved in vertebrates, enabling adaptation to the environment, effective food acquisition, and development of specialized functions. In humans, facial shape is important for mutual recognition. The development of the face and its specific geometry occurs during embryogenesis, in a multi-step process controlled by a combination of genetic and molecular factors. Individual events of craniofacial development are tightly coordinated in time and space to achieve precise shape, and divergence in any of the consecutive events can have minor to major impacts on the final shape and function.

Our group employs the development of the face as a model to study cell lineages, their dynamics and underlying molecular drivers. With this knowledge, we aim to reconstruct and compare the developmental history of the face in different species and identify evolutionary mechanisms altering development (such as heterochrony and heterotopy) to understand how morphological variation arises. We focus on the neural crest cells (NCCs), multipotent progenitors arising from the borders of forming neural tube, that give rise to an array of cell types and are essential contributors to facial morphogenesis. We are specifically interested in how the multipotent cells make decisions, how cell positional programs and cell fate acquisition are balanced, and what transcriptional programs orchestrate these decisions.

Here, we utilize single-cell transcriptomics and HCR RNA-FISH in mouse model to explore the coordination of NCC-derived lineage progression along facial development. We reveal the timing of positional and cell fate programs and the unexpected heterogeneity of cells forming the developing face. Furthermore, we predict cell-cell communication throughout development and identify cell populations (known as signalling centres or developmental organizers) that generate signals to instruct facial morphogenesis.

Cell lineages and developmental trajectories of the embryonic olfactory epithelium

34

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In vertebrates, the olfactory epithelium develops from the olfactory placodes, ectodermal thickenings on either side of the early embryonic face. It is composed of neuronal and non-neuronal cell lineages that are present before birth. While the fate of the neuronal lineage giving rise to olfactory sensory neurons is well understood, the developmental trajectories of the non-neuronal lineage, particularly during the prenatal period, remain largely unexplored.

Here, we focus on the development of sustentacular cells, non-neuronal support cells essential for olfactory function, which have recently come into the spotlight as the primary target of SARS-CoV-2. We integrate single-cell RNA sequencing with lineage tracing to generate a 4D map of the mouse embryonic olfactory epithelium. We describe for the first time the progenitors and developmental trajectory of the sustentacular cells. We support these findings with various computational approaches (e.g. RNA velocity) and extensive experimental validation using specific marker genes. To understand the interlineage relationships and interactions, we also investigate in silico the molecular communication between the cell types present in the developing olfactory epithelium.

Our dataset provides new insights into the developmental dynamics of the olfactory epithelium at early embryonic stages. Genetic lineage tracing, which is currently underway, will provide further evidence of cell type origin and differentiation. Our study is instrumental for understanding the ontogeny of the olfactory epithelium, the emergence of its cellular dynamics and functional complexity. Furthermore, given the proposed role of the olfactory epithelium as a critical signalling center for face morphogenesis (Kaucka et al., eLife 2018), identifying the cell types and molecular signals produced by the olfactory epithelium is essential for a holistic understanding of craniofacial development.

Foetal adaptations to matrotrophic viviparity in the Nimba toad revealed by grating-base phase contrast

63

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Viviparity, the retention of eggs and/or foetus within the female genital tract, has evolved numerous times in vertebrates. In amphibians, approximately 25 % of the 220+ caecilian and around 3 % of the 815+ caudate species are known or assumed to be viviparous. In anurans, showing the highest diversity of reproductive modes among amphibians, only 17 (0,0022 %) of the 7.700+ species are known or assumed to be viviparous. A crucial prerequisite for the evolution of viviparity is the provision of the foetus with enough energy until the start of exogenous feeding. Endotrophism, the reliance on internal nutrition mostly in the form of yolk reserves, is widespread among many amphibian species showing a derived reproductive mode such as terrestrial indirect development, direct development and ovovivipary. Direct nutritional provision by the female in form of specialized secretions or tissues (matrotrophy) is less abundant among amphibians and especially rare in anurans. The 'critically endangered' West African Nimba toad, *Nimbaphrynoides occidentalis*, is the only known anuran species showing matrotrophic viviparity. We used the newly established grating-based phase contrast technique implemented at the P-05 beam line at the Deutsches Elektronen-Synchrotron (DESY) to investigate museum specimens at different developmental stages and reconstruct the peculiar intra-uterine development of *N. occidentalis*. Grating-based phase contrast provides high-resolution image stacks of soft and hard tissues within short scan times and without the use of contrasting agents. Total 3D-reconstructions of developing foetus revealed a mosaic of heterochronic shifts, reductions and morphological novelties that are interpreted as adaptations to the intrauterine development of this biologically unique species.

A Burden to be a fish? - Riedl’s Burden tested using Anatomical Networks and heterochrony analyses of the actinopterygian cranium

64

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Is the evolvability of an anatomical structure limited by the number of interactions with neighboring structures? In 1975 Rupert Riedl hypothesized that structures with a high degree of connectivity exhibit limited evolvability and thereby introduced the concept of Burden. As a structure evolves, additional interactions with neighboring structures or with “new” structures may be established. However, “old” interactions often need to be maintained throughout the evolution of the whole system, limiting potential changes. We test Riedl’s concept of Burden using Anatomical Network Analysis in combination with an analysis of the cranial skeletogenic pattern of actinopterygian taxa including Polypteriformes, Acipenseriformes, Lepisosteiformes, Amiiformes and Teleostei. Anatomical Network Analysis investigates structural complexes based on the connections of its structures. We use this technique to quantify the degree of connectivity for each skeletal structure as a proxy for its Burden. Additionally, data on the cranial skeletogenic sequences are used to determine the occurrence of sequence heterochrony during the evolution of the investigated taxa. Sequence heterochrony refers to evolutionary changes in the order of developmental events such as the sequential occurrence of homologous chondrification and ossification centers in different taxa. The combined datasets allows us to test if structures experiencing heterochronic shifts also exhibit lower degrees of Burden quantified by their anatomical connectivity and thereby test Riedl’s Burden from the viewpoint of heterochrony.

* Student (eligible for the Student Awards)

Natural variation in apoptosis control underlies intraspecific eye size differences in *Drosophila melanogaster*

74

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To understand the evolutionary forces shaping morphological diversity, we must link genetic variation to phenotypic differences, as an organism's appearance is encoded in its genome. Advances in sequencing technologies have significantly enhanced our ability to identify the genetic architecture of variable traits. However, a mechanistic understanding of biological processes affected by these genetic variants remains elusive. To identify genes and processes driving morphological divergence, we studied natural variation in compound eye size in a population of *Drosophila melanogaster*. We quantified eye size differences among 162 fly lines from the *Drosophila* Genetics Reference Panel (DGRP) by assessing the number of facets, which ranged from fewer than 600 to more than 800. A genome-wide association study revealed 28 variants (26 SNPs and 2 deletions) related to 13 candidate genes. Loss of function of the candidate gene trim9 during eye development resulted in a significant reduction in eye size. In situ hybridization and single-cell RNA sequencing confirmed that trim9 is expressed in the larval tissue developing into compound eyes. As trim9 encodes a RING domain E3 ubiquitin ligase, known to regulate apoptosis, we confirmed that loss of trim9 function increased apoptosis levels during eye development. To link apoptosis to natural variation in eye size, we compared the number of apoptotic cells in developing eyes of DGRP fly lines with small and large eyes. Lines with smaller eyes exhibited more apoptotic cells in the pool of proliferative progenitor cells. Our data suggest a novel role for Trim9 in regulating apoptosis during *D. melanogaster* eye development. Additionally, we identified genetic variants in the regulatory region of this gene, indicating that variation in apoptosis control contribute to intraspecific eye size differences in *D. melanogaster*.

Looking for love: Genomics of visual mating preference evolution in *Heliconius* butterflies

09

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Visual preferences are an important driver of mate choice and sexual selection, but little is known about the underlying genes, or how they evolve. Heliconius butterflies are well known for their diversity of bright warning patterns, which are also used as mating cues. Closely related taxa often (but not always) display divergent wing patterns, and because males almost invariably prefer to court females that share their own colour pattern, this can contribute an important premating reproductive barrier between species. While the genetics and evolutionary history of Heliconius colour pattern variation is well understood, we know very little of the specific genetic mechanisms contributing to the evolution of the corresponding visual preference behaviours. Combining behavioural, population genomic, and expression analyses, we show that two 'red' Heliconius species, *H. timareta* and *H. melpomene*, have evolved strong preferences for red wing patterns by exchanging genetic material through hybridization, as compared to their close relative *H. cydno*, which has white wings. This corresponds to a visual preference locus tightly linked to a major gene for red patterns, optix, which has also been shared through adaptive introgression in these species. Neural expression of regucalcin1 correlates with visual preference across populations, and disruption of regucalcin1 with CRISPR-Cas9 impairs courtship toward conspecific females, providing a direct link between gene and behaviour. Our emerging results are beginning to place these findings within a broader context of visual evolution, including the nature of the specific cues involved. Together our results support a role for hybridization during behavioural evolution, and show how visual mate choice behaviours contributing to adaptation and speciation are encoded within the genome.

Habitat-associated visual system adaptations in *Heliconius* butterflies

10

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When populations experience different sensory conditions, natural selection may favor complete sensory system divergence, from the peripheral structures to downstream neural pathways. To date, most examples of sensory adaption involve only single aspects of sensory perception (e.g., colour vision), whereas few studies consider the multifaceted nature of sensory perception. Here, we examine the evidence for habitat-associated sensory system adaptation across different levels of the visual pathway and assess the behavioural implications on different components of visual perception. *Heliconius erato cyrbia* and *H. himera* are two closely related butterflies distributed across an environmental gradient in western Ecuador: H. e. cyrbia occurs in low-elevation wet forests, whereas *H. himera* is found in higher semi-arid forests. Prior neuroanatomical reports suggest habitat-associated neural adaptation in these species; the brain regions associated with visual processing are larger in *H. e. cyrbia*, and in choice assays, visual stimuli are preferred over olfactory stimuli. To examine the evidence for visual system adaptation more broadly, we reared both species under common garden conditions and report more ommatidia in the eyes of H. e. cyrbia compared to *H. himera*, and more ommatidia in males of both species. We also performed the first tests of behavioural visual acuity in *Heliconius*: *H. e. cyrbia* has higher acuity than *H. himera*, and males have higher acuity than females. Visual modeling suggests that acuity may differentially influence the perception of wing pattern vs. colours elements, and from eyeshine experiments, we report species- and sex-specific differences in colour sensitivity. Finally, we tested if sensory adaptions in different species converge under similar environmental conditions by including H. e. lativitta, another low-elevation species from wet forests (but allopatric to *H. e. cyrbia*). We find that *H. e. lativitta* is behaviorally and morphologically like *H. e. cyrbia*, suggesting convergent, habitat-associated visual system adaptation.

Evolutionary dynamics of wing shape in dragonflies and damselflies

11

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One of the key innovations in insects is the evolution of flight. The wings of Odonata (dragonflies and damselflies) show an indirect-direct flight system and they are capable of moving all four wings independently. Odonate wings show an enormous shape diversity but the evolutionary causes underlying and regulating this div45ersity remained unclear. Here, I present a geometric morphometric dataset of 1387 specimens (420 female, 967 male) covering 625 species from all families (~10 % of known taxa) together with an extensive set of life-history data. Odonata wing shape shows the classical distinction between dragonflies (Anisoptera) and damselflies (Zygoptera) with Epiophlebioptera nested within Anisoptera. Zygoptera occupy an approximately four times larger shape space compared to Anisoptera although taxon sampling is the same. Some damselfly taxa even overlap with the extremes of the shape space of Anisoptera, thus indicating similar flight regimes. Indeed, there is also limited overlap in the theoretically attainable flight agility in these species based on an analysis of the second moment of wing area. Analysis of phylogenetic signal indicates a significant but weak phylogenetic signal and a low proportion of the shape variation explained by common ancestry. Flight agility shows significant, albeit weak correlations to the type of preferred habitat, wing colouration, and behavioural aspects while wing shape appears to correlate with habitat openness and the type of water body within the habitat. Together, the results indicate that the wing shape of dragonflies and damselflies is not regulated by one dominant factor but rather by an intricate interplay of functional and ecological aspects.

The early evolution of moles (Mammalia, Talpidae): a humerus story

12

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Moles (Mammalia, Talpidae) are often referred to as the archetypical subterranean mammals. But the family also includes subclades with other lifestyles, including ambulatory (shrew-like moles), semi-fossorial (e.g., shrew-moles), and amphibious taxa (desmans and star-nosed mole). These lifestyles are associated with several degrees of specialization of the appendicular skeleton (the forelimb in particular). The first moles are mostly known from isolated teeth. Little is therefore known about the lifestyle of the first members of the family. The history of talpids' lifestyle transitions is also poorly understood, with both the subterranean and amphibious lifestyle so far reconstructed as diphyletic.

Here we revisit the systematics of several key extinct talpids of which postcranial elements – the humerus in particular – are known. We also CT-scanned at high resolution the humerus of most extant talpids as well as these fossils and other terrestrial mammals to quantify their bone microanatomy. Bone compactness (proportion of space occupied by bone tissue) was measured along the whole diaphysis.

The humeral diaphysis of extant, amphibious talpids is more compact (osteosclerotic) than that of the rest of the family and other terrestrial eulipotyphlans. This most likely corresponds to bone mass increase (BMI), an adaptation well known in secondarily aquatic tetrapods who dive at shallow depth. Among mammals, it is hitherto mostly documented in large-bodied, marine taxa.

The humeral microanatomy of several fossil talpids is particularly compact, suggesting that these taxa were amphibious, too. Given their newly estimated phylogenetic position, this result contradicts the hypothesis according to which talpids went through an aquatic phase during their early evolution. Our results also support the notion that BMI can also affect small-sized, amphibious mammals. The body mass of mammals with BMI hence spans 7 to 8 orders of magnitude.

Pleiotropic roles of Alx genes and the repeated origin of anterior fin spines

13

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Morphological diversity shows biases that are only partially explained by their adaptive significance but also results from directional variation caused by underlying developmental genetic mechanisms. Spines are hyper mineralized defensive rays that emerged repeatedly in anterior fin domains during fish evolution. Fin spine development is characterized by expression of alx genes, which also more generally define the anterior appendages across jawed vertebrates. Alx genes have an independent pleiotropic role in skull formation as well as a strong link with biomineralization. Genetic analysis in mutant cichlids identifies alx genes as determinants of spine mineralization, in addition to canonical roles in skull formation and anterior fin patterning. Mutants show downregulation of spine specific mineralization pathway genes. Comparative analysis indicates a deep evolutionary origin of the anterior alx domain in fish coinciding with the heavily mineralized elements. Therefore, horizontal pleiotropy of alx genes in anterior fin patterning and biomineralization may provide a genetic factor that biases the direction of evolution towards the anterior emergence of heavily mineralized fin elements.

Evolutionary Flexibility and Diversification of Daddy-long-leg Spiders (Araneae: Pholcidae)

14

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Understanding the mechanisms of how morphological traits drive speciation and biodiversity is pivotal in evolutionary biology. In this regard, also the evolutionary flexibility of morphological traits may play a significant role. Using the diverse daddy-long-leg spiders, Pholcidae, which currently includes almost 2,000 described species, we explore the interplay between speciation rate, species richness, and interspecific variability of body size, leg length and relative leg length and body size. We apply a combination of large-scale genomic and taxonomic sampling, phylogenetic analysis, and comparative analysis to assess how increased evolutionary flexibility (measured as either the standard variance or disparity of the traits) enhances the organisms' ability to exploit new resources and habitats, leading to increased speciation rates and biodiversity. We argue that the allometric development may facilitate the evolution of flexibility in pholcids. On the other hand, our study suggests that lack of evolutionary flexibility could be an evolutionary dead end, and it supports the idea that taxa may not always follow Cope's rule which postulates that body size increases with lineage age. This study enhances our understanding of the mechanisms of diversification, demonstrating that evolutionary flexibility of morphological traits is likely to have contributed to the uneven distribution of biodiversity in the tree of life.

* Student (eligible for the Student Awards)

The genetic basis of exploratory behavior and its role in diversification in African cichlid fishes

15

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Behavior plays a pivotal role in survival and reproduction of animals, and potentially drives diversification and evolutionary radiations. Despite its importance, the genetic mechanisms behind adaptive behavioral variation are still largely unknown. Our study delves into the exploratory behavior of the cichlid fishes of Lake Tanganyika, one of the most extensive adaptive radiations worldwide. By examining the exploratory behavior of 57 cichlid species (702 wild-caught individuals), we found highly consistent species-specific exploratory tendencies. The integration of the quantitative behavioral data with eco-morphological and genomic information showed exploratory behavior to be part of a niche-adaptation syndrome in Tanganyikan cichlids. Furthermore, we uncovered an outstanding association between a single nucleotide polymorphism (SNP) upstream the AMPA glutamate-receptor regulatory gene cacng5b and differences in exploratory behavior. This relationship was further validated using neural network behavioral predictions and CRISPR-Cas9 genome editing. Located in the putative promoter region of cacng5b, this SNP is implicated in synaptic plasticity, bridging the gap between behavioral tendencies in cichlids and personality disorder-related psychiatric diseases in humans.

The genetics of phenotypic differentiation: Lessons from East African mountain honey bees

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Understanding the evolutionary processes leading to species differentiation and speciation is a central goal in population biology. Phenotypic differentiation can result from phenotypic plasticity or local adaptation. *Apis mellifera* is characterized by its very large native range, living from high mountains to low tropics, thus being well adapted to various climatic conditions worldwide. In East Africa, populations of *A. mellifera* living in montane forest areas exhibit morphological distinctiveness from savannah honey bees. It has been proposed that mountain and savannah bees belong to separate ancestral lineages. A previous studyidentified two loci on two chromosomes exhibiting near fixation for different haplotypes between highland and lowland populations (r7 and r9),Both span several hundred kilobases in length, and were identified as inversions, which are rearrangements frequently associated with adaptation. This study provides insights into the genetics of phenotypic differentiation of East African mountain bees with whole genome and transcriptome sequencing data of honey bees from other African mountain systems. We obtained new datasets from honey bees inside the Rwenzori National Park in Uganda and from translocation experiments in Kenya, for which lowland bees were moved to highland and vice-versa. We identified a remarkable number of genes differentially expressed between highland and lowland bees. Additionally, GO enrichment analysis following genome-wide selection scans revealed that different pathways involved in adaptation to high elevation are significantly enriched. The existence of r7 and r9 inversions in these mountain bees was confirmed. Comparing these two genomic regions to earlier data we found a significant genomic differentiation between geographic regions. Preliminary data of functional analyses of candidate genes involved in cuticular pigmentation using CRISPR/Cas9 provide further insights into the regulatory network underlying *A. mellifera* adaptation to high elevation habitats. Our study willcontribute to better understandthe evolutionary processes which affect honey bee populations in their adaptation to environmental conditions.

* Student (eligible for the Student Awards)

Does learned bird song drive reproductive isolation in the willow tit?

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Cultural traits are learned and can drive prezygotic reproductive isolation and thus may lead to genetic differentiation and speciation. The willow tit (Poecile montanus) forms several subspecies across its Palearctic distribution range that differ phenotypically almost exclusively in their learned song – a cultural trait with three distinct and geographically separated song types that do not induce heterospecific male responses in playback trials. The same song types occur in allopatric subspecies at opposite ends of the distribution range, and we discriminate between song types using artificial neural networks. We hypothesise that subspecies that share the same song type will also cluster genetically. To test this idea, we assemble a high-quality reference genome and perform whole-genome sequencing of 93 individuals sampled across the willow tit's distribution range to elucidate the phylogenetic relationships, admixture and genetic differentiation between subspecies with the same and different song types. We find evidence for five deep and well-supported genetic clusters: (1) Chinese, (2) Central Asian, (3) Central European, (4) Japanese (Honshu), and (5) a panmictic North and East Palearctic cluster. The distribution of song types across these clusters suggests an ancestral origin of all three song types, because all three song types were likely present in the common ancestor of the entire willow tit species group. Thus, all song types have been constant over periods of time, even in isolation, and may constitute reproductive barriers in contemporary contact zones.

* Student (eligible for the Student Awards)

Prezygotic reproductive isolation and phenotypic variation across the willow tit song contact zone in southern Germany

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Cultural traits are learned, can drive reproductive isolation and can lead to genetic differentiation and speciation. Willow tits (*Poecile montanus*) have a simple song, which is most likely culturally transmitted from tutors (genetic fathers) to offspring. Central European willow tits are sedentary and have two song types: the "normal" syllable, found over most of Central Europe, and the "alpine" syllable, found in the Alps and surrounding mountains. These song types are thus allopatric over most of the Central European distribution range of the willow tit, but meet in narrow contact zones in southern Germany and Switzerland. The width of these contact zones suggests that they are maintained by selection rather than being the result of neutral diffusion, and playback experiments confirm that heterospecific male responses are rare. However, oblique transmission from tutors unrelated to offspring is possible, which could lead to a dissociation between genetic ancestry and song type. Here we use our own and citizen science data collected in Germany between 2022 and 2024 via the ornitho.de website to (1) fit species distribution models and map the location of the contact zone between both song types, and (2) use this information to perform geographic cline analyses to see if differences in song covary with subtle differences in morphology. Covariation of song with other phenotypes suggests genetic differentiation and that reproductive isolation is driven by song, which will need to be confirmed by genomic analyses.

How parasitism shapes spiralians: the story of Orthonectida

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Orthonectida are parasitic invertebrates that infect nemerteans, mollusks, turbellarians, ophiuroids, annelids, and tunicates of the northern seas. Their life cycle includes an asexual endoparasitic plasmodium and sexual individuals that develop inside the plasmodium cytoplasm. Mature individuals egress the host, copulate in the external environment, and produce dispersal larvae infecting new hosts. Orthonectids are identified as spiralians, with multiple evidence suggesting their affinity to annelids, although their exact phylogenetic placement has yet to be resolved.

The divergence of Orthonectida from other animal groups is evident at both genomic and morphological levels, marking them as one of the most extreme cases of secondary reduction in spiralian evolution. Using a combination of morphological and molecular methods, we explored the parasitic and free-living stages of four orthonectid species to delineate the primary trajectories of their adaptation to a parasitic lifestyle.

Miniature sexual individuals are characterized by a gradual reduction in morphological complexity among the studied species and comprise only four types of cells. The nervous system of Intoshia linei, reconstructed cell-by-cell, consists of only 61 cells (34 neurons and 27 receptors). The reduction of orthonectid nervous system is also supported genomically. The parasitic stage of orthonectids demonstrates a complete loss of cell organization, forming a shapeless multinuclear organism — a unique trait among Bilateria. Despite its primitive structure, the parasitic stage demonstrates convergence with other endoparasites on morphological and genomic levels. It has intensive endocytotic abilities and interacts with surrounding host cells through extracellular vesicles and excretory-secretory proteins.

Overall, orthonectids are an example of extreme specialization to parasitism at every level, illustrating the trend towards reduction in parasitic evolution.

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* Student (eligible for the Student Awards)

Host-dependent variations in Spiroplasma-induced CI expression in the *Lariophagus distinguendus* species complex

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Many arthropods are infected with bacterial endosymbionts which can manipulate their reproduction. The most widespread manipulation is cytoplasmic incompatibility (CI), which consists in the incompatibility between sperm of infected males and the eggs of uninfected females, leading to the absence of diploid offspring. However, the presence of reproductive manipulation phenotypes can vary even between closely related endosymbiont and host strains.

The species complex of the parasitoid wasp *Lariophagus distinguendus* encompasses at least three different species, provisionally termed clades A, B, and C. They are separated by different reproductive barriers, including CI caused by the Spiroplasma strain sDis infecting clade A. Several strains of the other two species also carry sDis, but the phenotypes of these infections had not been investigated so far. We studied the relatedness of the Spiroplasma infecting the three host species, the occurrence of CI in selected host strains, and the influence of host strain and host sex on the phenotype.

The infections in all three host species were found to be identical, suggesting a single infection even in a common ancestor followed by the subsequent loss of sDis in the strains which are currently uninfected. In crossing experiments with infected and uninfected males and females of strains from clades B and C, we detected no indication of CI despite the infection with sDis. Cross-transfers of sDis between host strains from clades A and B revealed a host-related absence of the phenotype in clade B, which was found to be male-dependent. Therefore, strains of clade B, and possibly also clade C, seem to have evolved a mechanism to suppress CI.

Occasional paternal inheritance of the germline-restricted chromosome in songbirds

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Songbirds have one special accessory chromosome, the so-called germline-restricted chromosome (GRC), which is only present in germline cells and absent from somatic tissues. Earlier work on the zebra finch (*Taeniopygia guttata castanotis*) showed that the GRC is inherited only through the matriline - like the mitochondria - and is eliminated from the sperm during spermatogenesis. Here, we show that the GRC can also be paternally inherited. Confocal microscopy using GRC-specific FISH probes indicated that a considerable fraction of sperm heads (1-19 %) in zebra finch ejaculates still contained the GRC. In line with these cytogenetic data, sequencing of ejaculates revealed that males from two families differed strongly and consistently in the number of GRCs in their ejaculates. Examining a captive-bred male hybrid of the two zebra finch subspecies (*T. g. guttata* & *T. g. castanotis*) revealed that the mitochondria originated from a castanotis mother, whereas the GRC likely came from a guttata father. Moreover, analyzing GRC haplotypes across nine castanotis matrilines (estimated to have diverged for up to 250,000y) showed surprisingly little variability among GRCs. This suggests that a single GRC haplotype has spread relatively recently across all examined matrilines. A few diagnostic GRC mutations that arose since this inferred spreading suggest that the GRC has continued to jump across matriline boundaries. Our findings raise the possibility that certain GRC haplotypes could selfishly spread through the population via occasional paternal transmission, thereby outcompeting other GRC haplotypes that were limited to strict maternal inheritance, even if this was partly detrimental to organismal fitness.

Evolutionary transcriptomics of sociality in carrion beetles

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Social behavior in insects is a phenomenon that ranges from simple social interactions to complex societies. Understanding the genetic basis of sociality is crucial for unraveling its evolutionary origins and mechanisms. Within my PhD project I aim to discover the genomic patterns linked to social evolution, focusing on wood boring weevils and carrion beetles. These beetles exhibit varying levels of social behavior, providing an excellent opportunity to study the genomic changes associated with the transitions from solitary to subsocial and eusocial behavior.

My aim is to uncover the role of changes in transcriptional regulation and gene pathway rewiring in the emergence of subsociality, the increase in regulatory complexity with higher sociality, the association between evolutionary changes in gene regulation and protein sequences with parental and alloparental care behavior, and to identify precursor conditions and general mechanisms involved in the origin of eusociality.

I used transcriptomic analysis to link gene expression to various aspects of parental and alloparental care in five carrion beetle species. Using comparative transcriptomics and co-expression analyses I identify expression patterns, specific genes and regulatory mechanisms associated with social behavior.

The findings of this project contribute to a better understanding of the genomic mechanisms underlying social evolution in insects. By comparing the results with previous studies on sociality in Hymenoptera and termites, the project sheds light on the question whether social evolution across insect taxa is driven by similar or different genomic mechanisms and provides insights into the evolutionary transitions from solitary to social behavior.

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What makes him care? Unraveling male care behavioral syndromes in a simple family system

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Parental care is a driver of social evolution, providing a foundation for the consolidation of family life and advanced animal societies by conveying key benefits to offspring. The costs of care are often paid by the female but sometimes shared with a male via biparental care. Since parents' evolutionary interests differ, sexual conflict needs to be resolved for cooperation to occur. This conflict is well-studied in evolutionarily derived family systems like birds, but why biparental care initially emerged, and how the conflict is resolved when neither parent must remain with the young – a state which likely prevailed during the evolution of parental care - remains poorly understood. We investigated male investment into biparental post-hatching care in *Nicrophorus vespilloides* burying beetles which exhibit facultative biparental care on small vertebrate carrion with components such as offspring feeding and nest maintenance. Females exhibit most of these behaviors while males feed on and guard the carcass, but males also provide direct care to young. However, the mechanisms behind their varying investment into biparental care remain unknown. In our study, we investigated whether male care is repeatable between bouts (depending on personality) or depends more on the investment of the accompanying female. While some behaviors were driven by male personality, others depended on female investment, indicating a mix of negotiation, matching, and sealed-bid conflict resolutions. Overall, our findings show that different male care behaviors during biparental care likely derive from different selective pressures, highlighting that conflict resolution occurs repeatedly for different components of care.

Scent-sational drama: Larval chemical signals and their effect on maternal behavior

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Family life involves conflicts between parents and offspring regarding optimal parental investment and resource allocation. These conflicts can be mediated by offspring signals reflecting their nutritional needs, eliciting parents to adjust their care behavior. Insects primarily use chemical signals to regulate social interactions, but research has focused more on adult chemistry, examining the effects of biotic and abiotic factors, while largely neglecting offspring chemical signals. Using *Nicrophorus vespilloides*, a beetle species with elaborate biparental care, we investigated changes in volatile organic compounds (VOCs) and cuticular hydrocarbon (CHC) profiles during larval development to determine if larval chemistry reflects their nutritional needs. Our findings show that larval CHC and VOC profiles change with developmental and nutritional states, indicating that larvae can communicate their conditions to parents, influencing care decisions. Notably, second instar larvae, which receive the highest feeding rates, produce the highest levels of specific volatiles. Additionally, food-deprived larvae express higher levels of specific volatiles compared to fed larvae. Using electroantennography (EAG) and a novel bioassay, we demonstrated that female antennae respond to larval odor, altering maternal behavior. This suggests that larval odor mediates mother-offspring interactions and plays a significant role in resolving parent-offspring conflict. Our study identified promising candidates for a begging pheromone that impact these interactions. Future research should explore if males also respond to offspring odors and identify specific pheromones that shape family life in burying beetles.

Exploring the condition-dependence of chemical alarm cues in a freshwater gastropod

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Predation-related chemical cues are a crucial element of predator-prey interactions, as they allow prey organisms to estimate predation risk and respond with antipredator phenotypic plasticity, such as induced defenses. For this purpose, freshwater snails, such as the classic plasticity model system *Physella acuta*, use chemical alarm cues released by injured conspecifics. However, the chemical composition and properties of *P. acuta* alarm cues remain poorly understood. We focus on the condition-dependence of alarm cues in *P. acuta* to address this issue and employ a combination of analytical and behavioral trials. Previous research suggests that damage-released chemical alarm cues from high-condition donors are qualitatively and quantitatively greater than those from low-condition donors. Hence, prey organisms may respond differently to alarm cues depending on the donor's condition, with potential implications for their ability to estimate predation risk and induce defensive behaviours. First, we extract alarm cues from high and low-condition donor snails. We then profiled the specific chemical compounds present in these cues using gas chromatography-mass spectrometry (GC-MS). Second, we tested the efficacy of these cues by studying crawl-out behaviour in *P. acuta* before and after exposure to the profiled high-condition alarm cues, low-condition alarm cues or a water control treatment. Our findings may allow us to determine whether alarm cue production is condition-dependent. Additionally, compound-behaviour correlations may allow us first insights into potential key compounds within *P. acuta* alarm cues. Altogether, our study may provide valuable insights into the chemical communication system of gastropods as well as the mechanisms underlying their estimation of predation risk

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Evolutionary Biology

Beyond mammals: The surprising complexity of chewing and other oropharyngeal processing mechanisms

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Oropharyngeal processing behaviours exhibit remarkable diversity and complexity, coordinated by various processing centres linked to the mandibular, hyoid, and branchial arches. Teleost fishes present a unique evolutionary case, having evolved specialised anatomical adaptations for each processing centre. These adaptations appear to compensate for reduced mandibular processing, balancing the trade-off of kinetic skulls that permit enhanced suction feeding – often via jaw protrusion – while frequently limiting the generation of strong bite forces. This evolutionary shift has given rise to numerous novel food processing methods. Conversely, certain teleosts have adopted post-oropharyngeal strategies such as gastric milling and highly acidic chemical digestion, obviating the need for oropharyngeal processing entirely. Most other vertebrates predominantly employ their mandibles for mechanical food processing. These mandibular behaviours may include non-cyclic bites and cyclic activities such as gulping or chewing. Chewing, characterised by rhythmic and cyclic mandibular processing actions, necessitates highly coordinated tongue movements for food transport and is observed across aquatic and terrestrial species. Recent research indicates that complex chewing behaviours, akin to mammalian mastication, are widespread among vertebrates. Intricate jaw movements, once thought unique to mammals, are evident across various taxa, including stingrays, pacus, certain lungfish, salamanders, turtles, canaries, and the tuatara. These movements often incorporate arcuate, longitudinal, and transverse jaw motions, supported by specialised anatomical features such as unique intra- and intermandibular joints, jaw joints and suspensions, or certain forms of cranial kinesis. Comparative analyses revealed that complex chewing mechanisms evolved independently in different gnathostome lineages, and that various combinations of these traits facilitate intricate jaw movements and chewing behaviours. Hence, challenging the notion that such complexity is exclusive to mammals, while underscoring the importance of examining the form and function of oropharyngeal structures to advance our understanding of the evolution of vertebrate oropharyngeal processing.

The impact of niche construction on the adaptation to bacterial pathogens in flour beetles

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Niche construction plays a pivotal role in eco-evolutionary dynamics, enabling organisms to adapt by altering their environment's chemical, physical, or biological characteristics. Niche construction can facilitate adaptation to changing environments, by increasing the phenotype-environment match. In group-living animals this process might be of special relevance, because conspecifics, sharing the same niche might also flourish in the reshaped environment. Despite its theoretical importance, empirical evidence supporting the evolutionary advantages of niche construction is sparse. Our study addresses this gap by using the red flour beetle (*Tribolium castaneum*) and its natural microparasite, *Bacillus thuringiensis tenebrionis* (Btt), in an experimental evolution setting. We manipulated the beetles' ability to modify their environment through quinone-rich stink gland secretions and provided the selection line beetles with differentially conditioned flour niches. Over nine generations, we compared the evolutionary outcomes of populations that grew up in these differently constructed niches under Btt selection pressure. Our results demonstrate that niche construction significantly enhances survival of Btt infection, with noticeable benefits observed as early as the third generation. Interestingly, while niche construction with secretions conferred these survival advantages, it also imposed certain costs, such as slower development and slightly lower offspring production. Transcriptomic analyses further elucidated the genetic underpinnings of these adaptations, revealing selection-induced divergences in genes related to cuticle formation, serine protease activity, DNA repair, endocytosis, and transcription regulation. Thus, our study provides compelling empirical evidence of niche construction's critical role in mediating evolutionary adaptation, underscoring its significance in eco-evolutionary theory.

Past, present, and future of wear analyses of feeding structures in insecta, sauropsida and mammalia

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Mechanical wear analyses of the dentition have been extensively applied in mammals for functional inference, diet, and habitat reconstruction, and even to deduce past climatic conditions, at individual, species and population level. Over the past 15 years, combined studies of wear analyses on various scales - based on museum material, in-vivo and in-vitro experiments, and simulations - have provided novel insights into the importance of abrasives in the wear process. Yet, this research has raised new questions about how diverse factors such as structure, physical and mechanical properties of the diet influence dental wear. Here, we synthesize recent advances of in-vivo and in-vitro experiments in crickets (*Gryllus bimaculatus*), squamates, American alligators (*Alligator mississipiensis*), rats (*Rattus norvegicus*) and guinea pigs (*Cavia porcellus*), integrating approaches from biomechanical engineering, functional morphology and digestive physiology to highlight both established and emerging players in dental wear. We propose that there is still more potential in applying wear analyses across diverse research scenarios, encompassing both mammalian and non-mammalian vertebrate taxa, extant and extinct species (e.g. dinosaurs), and even to feeding structures in invertebrates (mandibles).

However, with the broader application of dental (and mandible) wear analyses, new challenges have emerged. One critical issue is the need for standardization in experimental and analytical procedures, to enhance repeatability and reproducibility, thus ensuring high data quality and facilitating future data exchange. We propose a solution to improve inter-microscope comparability between different measurement devices by using a reference dataset and introducing correction factors. Our synthesis should be a first step toward a deeper understanding of the biomechanics of wear and the complex, multi-factor interactions that occur on wear surfaces. By addressing these challenges and expanding the application of wear analyses, we hope to advance the field and open new avenues for research across a wide range of taxa and ecological contexts.

The eye of the (mud) dragon

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Many animal phyla exhibit photosensory organs or eyes with highly variable anatomy, origins, and complexity. However, our understanding of photoreception remains limited, with many non-model animal groups being largely understudied. This is particularly true for kinorhynchs, or mud dragons, a phylum of marine microscopic invertebrates that inhabit benthic environments worldwide, from intertidal zones to hadal depths. Kinorhynchs are part of the ecdysozoans (molting animals) and are nested within scalidophorans along with priapulids and loriciferans. Since the discovery of the phylum in 1841, red/orange pigmented structures have been reported in many species, consistently associated with the introvert scalids and varying in number and colour. Despite being phototactic and possessing colored eye spots, kinorhynch “eyes” have never been studied in detail. We employed and integrative approach, combining morphological and molecular methods, to study the photosensory organs in kinorhynchs by: (1) generating comprehensive and comparative ultrastructural data using novel high resolution imaging techniques such as FiB-SEM, serial block face scanning electron microscopy (SBEM), traditional TEM and three-dimensional reconstruction, (2) characterizing and localizing photosensory molecules extracted from transcriptomic datasets, (3) using phylogenetics to understand the evolution of visual pigments within kinorhynchs and across ecdysozoans.

Internal long bone structure of mouse-like rodents (Muroidea) in light of scaling and locomotor behavior

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Muroidea is the largest superfamily of rodents, comprising ca. 1500 species which include, amongst others, mice, rats, voles, and gerbils. These rodents colonized all continents except Antarctica, conquered diverse habitats, and evolved a body mass disparity of two orders of magnitude. Here, we studied how their locomotor behavior is reflected in the morphology of their locomotor apparatus while accounting for body size. We used µCT scans to investigate the internal structure of the humerus and femur using biomechanically informed parameters that describe the epiphyseal trabecular network (e.g., mean thickness of all trabeculae or trabecular connectivity) as well as the cross-sectional properties along the midshaft (e.g., cross-sectional area or second moment of area). We classified the locomotor behaviors into arboreal, fossorial, semi-aquatic and terrestrial. Preliminary results revealed allometric scaling relationships, indicating that body mass has a major influence on the internal structure of these proximal limb bones. The locomotor behavior classes barely differed in their average morphology. However, they differed in their morphological variability, which might be partly related to our limited sample sizes, for now. Nevertheless, similar patterns were described previously in other rodent clades, such as squirrel-related species (Sciuromorpha). This might suggest that rodents, being small-sized mammals, are generally overbuilt in terms of their internal limb bone structure to a degree that does not necessitate pronounced locomotor adaptations as observed in larger mammalian taxa. Yet, it is unclear why certain locomotor behaviors are associated with different degrees of morphological variability despite being remarkably similar on average. Our knowledge of the locomotor repertoires of many species—especially in Muroidea—is extremely limited and further insights into these might help us clarify the observed morphological patterns.

Olfaction with legs – spiders use wall-pore sensilla for pheromone detection

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Chemosensing plays a pivotal role in the survival and reproductive success of most species. In insects, olfaction is performed by hair-like wall-pore sensilla (WPS), and gustation by tip-pore sensilla. Spiders are known to possess tip-pore sensilla, but we do not know how they perform olfaction despite a wealth of behavioral data that prove their ability to do so. The orb-weaving spider *Argiope bruennichi* is one of the few spider species for which the pheromone is known by which females attract males. We combined ultrastructural and electrophysiological analyses to explore this puzzle. We found that WPS do occur on all walking legs of male *A. bruennichi*. These sensilla are specialized in finding a mating partner, since they exclusively responded to the sex pheromone and in a concentration-dependent manner. In a comparative morphological analysis, WPS were found in males of several spider clades. Our data suggests that WPS evolved convergently within Araneae. Further, since they lack in basally branching spider clades, they likely evolved more than once in arachnids and independently in insects from trichoid sensilla.

* Student (eligible for the Student Awards)

How small morphological peculiarities raise big questions: the unique seminal receptacle structure of a Madagascan freshwater crab of the genus *Hydrothelphusa* (Decapoda, Brachyura, Deckeniidae)

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The eubrachyuran crabs are outstanding within the decapods, as they have an internal fertilization system. The paired reproductive counterparts of males and females work together after an elaborate species-specific principle. This makes them highly interesting for research on taxonomic and evolutionary questions. The female reproductive organs consist of a gonopore, a cuticle lined vagina, a seminal receptacle and the ovary that is connected with the seminal receptacle via the tube-like oviduct.

Thereby, the seminal receptacle or receptaculum seminis is of particular importance. It is not only a sperm storage organ, but also the site of fertilization. Numerous studies from recent years support a common hypothesis on the general morphology and the evolutionary development of the seminal receptacle.

Yet, within this research field, freshwater crabs have been almost completely left out although they might represent an original state, due to their basal phylogenetic position. In this project, histological studies have been done on the reproductive organs of a Madagascan freshwater crab of the genus *Hydrothelphusa*. First results already show that the morphology of the seminal receptacle differs from the currently known organisations. As a consequence, the results encourage a re-discussion of the common hypotheses on the seminal receptacle evolution in Eubrachyura.

* Student (eligible for the Student Awards)

Elastic or stiff? New insights on the ultrastructure and material properties of the vagina of the Zuiderzee crab *Rhithropanopeus harrisii* (Gould, 1841) [Panopeidae, Brachyura]

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Eubrachyuran crabs are a highly diverse group and have developed a special feature in their reproduction: internal fertilization. This occurs in one special feature of the female reproductive organs, the seminal receptacle, which also serves as a sperm storage chamber. Two important transport mechanisms from and to this organ take place in the vagina, a cuticle-lined tube. First, the transport of the spermatophores through the vagina into, and second the fertilized oocytes out of the seminal receptacle. To provide these transport mechanisms, the cellular structures of the vagina, especially the cuticle, must perform complex and diverse functions. So far, the vagina has only been investigated using histological methods, and not much is known about its ultrastructure and material properties. Insights into the exact function of the transport processes are also still lacking.

The aim of the project was to investigate these questions using the example of the Zuiderzee crab *Rhithropanopeus harrisii*. The application of electron microscopy and fluorescence microscopy techniques should provide a much more detailed resolution of the fine structure of the cuticle and reveal new information on the cell anatomy of the associated epithelia and the precise interaction with the musculature. With this new combination of microscopic methods, new insights into the structure and function of the vaginal cuticle and the associated musculature were gained. Based on the data, a functional model of the transport processes during spawning of *R. harrisii* can now be presented for the first time.

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Dynamic Loading in Insect Exoskeletons: Structural Adaptations and Fatigue Damage

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The cuticle exoskeleton of insects is one of the most common biological materials on earth, however many fundamental biomechanical questions about this complex material are still open. Previous studies investigating the biomechanical properties of this fascinating material have for example mainly focused on the static properties of cuticle and neglected its responses to dynamic loading.

To better understand how insect exoskeletons withstand cyclic loading and if and how possible fatigue related damage correlates with their function or ultrastructure we performed biomechanical tests with different loading cycles on various body parts of locusts (*Locusta migratoria*) to simulate real stress and induced microdamage. Advanced imaging techniques (X-ray tomography, scanning electron microscopy and light microscopy) was combined with finite element modeling to analyze stress distribution, fatigue related damage patterns and structural adaptations in the cuticle.

This talk will present first results from this ongoing research project and provide insights into the fatigue resistance of insect exoskeletons.

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Life with long appendages: functional, kinetic and morphological adaptations in house centipedes

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The house centipede, *Scutigera coleoptrata*, is known as one of the fastest invertebrate predators. Although not too welcome inside homes, these centipedes are regarded as excellent biological pest control around vineyards. Endemic to the mediterranean region, this species is nowadays also common throughout central Europe. Scutigeromorph centipedes are generally characterized by extremely long legs and antennae, covered with thousands of sensory structures. They are exceptionally fast and agile, and when hunting, they use their slender legs like lassos to immobilize prey before injecting their venom. Most outstanding, and unique to centipedes, is the functional transformation of the last pair of legs, called the ultimate legs. They are not involved in locomotion or prey capture, are longer and have a higher number of sensory structures than normal locomotory legs. Moreover, their position and kinematics greatly resemble those of the antennae. Thus, it is assumed that they have a predominantly sensory function. Focusing on mechanoreception and olfaction, we aim to better understand the neurological and functional aspects of scutigeromorph appendages, using the house centipede as a model. By means of electrophysiology, antennal and leg nerve backfills, as well as immunohistochemistry and morphological investigations we want to determine to which extent the ultimate legs act as "posterior antennae", and how the structure of the corresponding ultimate leg ganglion correlates to this function. Furthermore, we aim to understand the kinematics behind their fast locomotion. High-speed video recordings, as well as step-force measurements will reveal the locomotory mechanism they evolved in order to achieve their exceptional speed and predatorial success.

* Student (eligible for the Student Awards)

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Unravelling structural and mechanical properties of attachment pads in the stick insect *Medauroidea extradentata*

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In Phasmatodea (stick and leaf insects), attachment is facilitated by two cuticular smooth attachment pads on their tarsi enabling them to walk over diverse substrates and adhere to them. The pretarsal arolia preferably generate adhesion and the tarsal euplantulae mainly generate friction, thus complementing each other in the overall attachment process. Despite extensive studies on the functions of the arolium and euplantulae, the ultrastructural differences and mechanical properties responsible for the different functionalities, remain unclear.

Here, we used scanning electron microscopy (SEM) and histological methods to analyse the ultrastructure of the arolium and euplantulae in the stick insect *Medauroidea extradentata*. Additionally, atomic force microscopy (AFM) was employed on live stick insects to quantify the elastic modulus and adhesive properties of both types of pads.

Our findings indicate structural differences between both types of pads, which may explain their functional differences. Both pads exhibit heterogeneous organisation of their procuticle. Their endocuticle consists of multiple thin layers of parallel cuticle fibres, while the exocuticle comprises vertical fibres that increase in density from the proximal to distal regions. In the euplantulae, the overall thickness of the procuticle is lower, while the density of the distal exocuticle fibers is higher. AFM measurements indicate distinct elastic moduli under different indentation depths, attributable to the heterogeneous structure of the pads.

New insights into the morphological and mechanical properties of both pads are discussed regarding their distinct roles in the attachment process.

* Student (eligible for the Student Awards)

Diversity of mandibles of beetle larvae

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Beetles, with approximately 380,000 currently described species, occupy nearly all biotopes globally. Their co-evolution with other species and exposure to diverse selective pressures have led to significant diversity in forms and functional characteristics. This diversity is evident in the anatomical, functional, and morphological differences among beetles, reflecting their varied ecological roles at both adult and immature stages.

One crucial function in the lives of beetles is feeding, and there are many different feeding modes represented within beetles. Even within a single group, different representatives can have different lifestyles. For example, many immature beetles have different ecological roles than their adult counterparts, possibly to avoid competition for food. Therefore, various mouthpart shapes developed over time under different selective processes. Among mouthparts, mandibles are particularly prominent. They are primarily used for biting and chewing, however, they often serve roles in defence and combat. This presentation focuses on the different types of beetle mandibles based on their shape and functionality. For instance, the mandibles of predaceous beetles differ markedly from those of plant or fungus feeders. Shape and additional structures on mandibles, such as hairs, processes, or small teeth, significantly enhance their functionality and can serve as indicators of the feeding mode of the beetle.

We conducted quantitative and morphometric analyses of larval mandibles across various beetle groups. Our study included extant specimens, from both literature and wet samples, and fossil specimens preserved in amber from different origins. These analyses provide insights into the evolutionary adaptations of beetle mandibles and their correlation with feeding behaviours.

Morphology

Shedding X-ray light on the sound-induced motion patterns of hearing structures in fish, focusing on the saccular otolith in three catfish species

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Whereas sound pressure is the main component for hearing in terrestrial vertebrates, fish hearing involves detecting sound-induced particle motion and sound pressure. The ability to detect the latter is especially pronounced in fishes, such as otophysans, possessing a connection between the swimbladder and the inner ears. Traditional methods fail to nondestructively visualize the effects of sound components on hearing structures in real-time. We therefore developed a standing wave tube-like setup to observe the sound-induced motion patterns of the swimbladder, the Weberian ossicles, and the saccular otoliths (= sagittae). Using two miniature inertial shakers at each end of a test tube, we created maximum sound pressure by driving them in-phase or maximum particle motion by driving the shakers out-of-phase. X-ray tomography at the SLS TOMCAT beamline allowed for imaging with high spatial and temporal resolutions. We focused on three different catfish species showing distinct differences in the shape of their sagittae: *Kryptopterus vitreolus* (Siluridae), *Ancistrus dolichopterus* (Loricariidae), and *Corydoras pygmaeus* (Callichthyidae). Under the maximum sound pressure condition, oscillation of the swimbladder walls resulted in a distinct movement of the Weberian ossicles and the sagittae in all three species. In *K. vitreolus*, the elongate sagittae revealed a rotational motion pattern. The sagittae in *A. dolichopterus* is broader in shape than in the former species and showed an overall similar motion. In contrast, *C. pygmaeus*, possessing a thick, angular-shaped sagittae, revealed a complex tilting motion. The findings suggest that the sagitta shape affects motion patterns and thus contributes to our understanding of otoliths' role in fish hearing. Our approach allows for a real-time, non-destructive visualization of fish hearing structures. Future studies will further quantify these motion patterns, offering deeper insights into the relationship between sagitta morphology, frequency response, and the mechanics of the swimbladder and Weberian ossicles in fish auditory systems.

Morphology and Foraging Behaviour in Ants: A Model for Future Functional Trait Studies

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Studying functional traits is essential for understanding how organisms are adapted to their environments and interact within ecosystems. By linking morphological characters with functional traits, we aim to understand how form affects function. In our recent study, we investigated the relationship between ant morphology and foraging behaviour, focusing on the possible impact of head and mandible shapes on the size of items carried by ants. Conducted across diverse habitats in Kyrgyzstan, we recorded and analysed morphometric data from 136 individual ants and additionally from 90 specimens from AntWeb (www.antweb.org). We searched for ants carrying materials from or to their nest, hand-picking and documenting them with a phone camera and magnifying glass in the field. Utilising principal component analysis (PCA) and Bayesian linear models, we identified significant morphological traits influencing foraging efficiency. Especially shape variations in the clypeal region were found to play a crucial role, underlining the importance of this region for item transportation. Building on this foundational work, our upcoming project aims to link ant morphology with other functional traits, such as walking speed. By expanding our morphometric approach, we expect to uncover new significant predictors of ecological performance, complementing morphometric analyses. Furthermore, this methodology holds the potential to make predictions about these functional traits in fossil ants, providing valuable insights into their evolutionary history and ecology in past ecosystems. Our study highlights the importance of shape variation in understanding the ecological roles of ants and demonstrates the value of morphometric analyses in ecological research.

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* Student (eligible for the Student Awards)

Developmental gene expression patterns illuminate the evolutionary origin of the proboscis in sea spiders (Chelicerata, Pycnogonida)

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Deciphering the evolution of the arthropod head and its affiliated appendages has challenged generations of zoologists. Based on various lines of evidence, the segmental composition of all but the anterior-most protocerebral region is by now firmly established, including the homology of the raptorial chelicera in Chelicerata and the sensory (first) antenna in Mandibulata as the appendages of the deutocerebral segment. By contrast, the evolutionary origin of the preoral arthropod labrum (upper lip) and its potential derivation from a protocerebral appendage remains more debated.

Notably, sea spiders (Chelicerata, Pycnogonida) are the only extant arthropod group for which the presence of a labrum is debated. They feature the unique proboscis, a suctorial apparatus composed of three longitudinal antimeres that enclose the pharynx with the mouth at the tip. Evolutionary interpretations of the proboscis nature diverge significantly. Over the centuries, it has been alternatively suggested to represent either a formation sui generis versus a fusion product of a morphologically cryptic labrum anlage with postoral pedipalpal gnathobases, or even a composite of outgrowths from two additional anterior body segments.

With the aim to clarify the developmental origin of the pycnogonid proboscis, we used HCR-FISH to study the expression patterns of evolutionarily conserved anterior patterning genes (e.g. six3, FoxQ2, Nkx2.1, otx) coupled to selected segment polarity and Hox genes during embryogenesis of the sea spider *Pycnogonum litorale*. We show that the entire proboscis originates from the six3+/otx+ precheliceral lobe and refute an involvement of elements from more posterior body segments. Further, the anterior patterning genes studied display prior and during proboscis outgrowth circumoral expression domains. While their expression in the developing proboscis aligns with the arthropod upper lip, these circumoral territories challenge the presence of a clearly delimitable, preoral labrum anlage in pycnogonids, supporting recent morphological studies on sea spider embryogenesis.

Evolution of the hexapod tracheal system

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Hexapods breathe with a system of tubes running through the entire body, the tracheal system. This highly complex and 3-dimensional system was difficult to visualize and study with traditional morphological methods. As a result, our knowledge of the shape and evolution of the tracheal system is very limited.

In the present talk, we will address the ground plan and major transitions in the hexapod tracheal system with a specific focus on the apterygote hexapods. We can show that the current knowledge is too fragmentary to derive any sound evolutionary conclusions. In the second part of the talk we will show the possibilities, that the application of synchrotron based µ-computed tomography and the subsequent creation of 3D models provide for the study of the tracheal system. We developed a pipeline that automatically analyzes numerous morphometric and network-based traits of the tracheal system such as volume, surface, radius, distance to the body surface, length, branching patterns, betweenness or density. We will use the hypothesized case that the relative volume of the tracheal system increases with body size in hexapods to show the potential of this approach.

Neurobiology

Pigment-dispersing factor neuropeptides act as multifunctional hormones and modulators in tardigrades

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Tardigrades (water bears) are ecdysozoans (molting animals) and the closest relatives of arthropods (chelicerates, myriapods, crustaceans and hexapods) and onychophorans (velvet worms), with which they are united in Panarthropoda. Due to their key phylogenetic position and ability to survive extreme environmental conditions, such as freezing and desiccation, tardigrades play an important role for understanding animal evolution and clarifying the function of cells and tissues. One open issue concerns the expression, processing and functionality of pigment dispersing factor neuropeptides (PDFs) and their receptor (PDFR). PDFs or PDHs (pigment dispersing hormones) are evolutionarily conserved peptides that are found in protostomes and play multiple roles related to circadian or non-circadian activities. Three pdf homologs have been identified previously in the genome of the eutardigrade *Hypsibius exemplaris*. To localize the individual PDF-immunoreactive (PDF-ir) neurons, we carried out immunolabeling using specific antibodies and in situ hybridization in combination with three-dimensional reconstruction in *H. exemplaris*. The data show that the three PDFs of this species are co-localized in two pairs of inner lobe cells within the brain, whereas only one PDF occurs in four additional cerebral and two extracerebral cells. The axons of the inner lobe cells pass through the contralateral brain hemisphere, descend to the ventral nerve cord and terminate in two pairs of potential release sites in the posteriormost trunk ganglion. Using in vitro assays (Bioluminescence Resonance Energy Transfer), we further demonstrate that all three PDFs of *H. exemplaris* and their deorphanized receptor are functional. By using in situ hybridization, widespread localization of PDFR across tissues and cells suggests that the tardigrade PDFs act as multifunctional hormones and neuromodulators. Whether the three PDFs are co-expressed with the circadian clock genes and whether or not they are rhythmically released into the hemolymph remains to be clarified.

* Student (eligible for the Student Awards)

Distinct selection regimes shaping the evolution of integrative centres in the brains of Heliconiini butterflies

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Central neural circuits integrate sensory and internal information to cause a behavioural output. Evolution modifies such circuits to generate adaptive change in sensory detection and behaviour, but it remains unclear how selection does so in the context of existing constraints. We have explored this question by analysing evolutionary dynamics in the circuits of the insect mushroom body and central complex. While the central complex seems to be largely conserved in term of size and shape, there is huge diversity in the mushroom body circuit. However, an empirical framework as well as a general understanding of how evolution modifies the function and architecture of these circuits is largely lacking. To address this, we leveraged the recent radiation of a Neotropical tribe of butterflies, the Heliconiini (Nymphalidae), which show a massive amount of variation in mushroom body size over comparatively short phylogenetic timescales, linked to specific changes in foraging ecology, life history and cognition. We combined immunostainings of structural markers and neurotransmitters as well as neural injections with comparative, quantitative datasets to understand the mechanism by which such an extensive increase in mushroom body size is accommodated through changes in its internal as well as its external circuitry. Inside the mushroom bodies, we identified that only some Kenyon cell populations expanded with a higher rate than others, in those Heliconiini faced with specific cognitive demands for their foraging ecology. We also identified that feedback neurons external to the mushroom body show a large increase in cell number. This is accommodated with large conservation inside central complex and peripheral circuitries, with highly intriguing specific differences. Our results demonstrate an interplay of evolutionary malleability inside the mushroom body lobes and functional constraints inside connected circuits as an evolutionary pathway guiding adaptation in cognitive ability through distinct selection regimes.

The influence of tooth morphology on the feeding efficiency of paludomid gastropods

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A deeper understanding of the interaction between the radula and the preferred food is lacking, complicating the inference of the precise ecological roles of radular structures. The radula, displaying distinct morphologies throughout the molluscan phylum, is a crucial adaptation for molluscs and a key to their ecological success.

This study focuses on the distinct tooth morphologies of taenioglossan radulae from paludomid gastropods. In this approach, we tested how tooth morphology relates to feeding efficiency to relate the tooth diversity with the feeding mode. For this, 3D models of the teeth were created – and then morphologically altered. After 3D-printing, the stability of the teeth was determined through bending tests. The feeding efficiencies were determined in pulling tests trough agar gels with different densities. Here, the force generated by the models and, by taking the mass of the removed gel into account, the performance of the radulae could be determined. The models exhibited diverse biomechanical behaviors and performances and small morphological changes had large effects on tooth behavior. Stability determined whether teeth could handle difficult substrates and whether successive rows could support each other, creating a „collective effect“. Surprisingly, more work did not equate to more food; the maximum food collected was limited by tooth morphology. Interestingly, the slender teeth removed and transported a significant amount of gel, while the broader teeth often failed to grip and remove the substrate effectively.

Overall, the study highlights the complex interplay between radular tooth morphology and ecological function, suggesting that even minor morphological alterations can significantly impact the efficiency of food gathering. Understanding these interactions can shed light on the ecological adaptations that contribute to the success of mollusks in diverse environments.

Body mass loss as an early warning signal in the garden dormouse (*Eliomys quercinus*)?

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The garden dormouse (*Eliomys quercinus*, 60-110 g) is a hibernator belonging to the family of Gliridae. Originally widespread in Europe, populations have disappeared from over 50 % of their former range in the last 20-30 years. The reasons for this decline are still not completely understood. As an omnivorous species, the garden dormouse feeds on various food resources, with a high amount of insects and other arthropods. Therefore, insect decline can negatively affect this species. In wild animals, body mass is a good indicator of fitness, especially in hibernating species like dormice. The aim of this study was to investigate changes in body mass and juvenile growth as a proxy for fitness during the last two decades. We therefore conducted a capture-mark-recapture study between 2018 and 2021 and compared body mass and juvenile growth of captured garden dormice with data from dormice captured between 2003 and 2005 in one of their last natural distribution areas in Germany, the Black Forest. Furthermore, we investigated the dietary spectrum of this species by faecal analyses. Results showed that insects represent the main food resource, especially during juvenile growth and pre-hibernation fattening. Before hibernation adult dormice have nowadays a significantly lower body mass (12 %) than two decades ago (body mass difference: males 13.2 ± 6.2 g; females 10.1 ± 4.4 g). Juveniles showed a significantly lower body mass gain in the years 2018-2021 compared to 2003-2005. As insects represent the main food resource of this species, insect decline may display a major threat for this species and the observed body mass decline represents an early warning signal for this population. Insufficient availability of high quality food can prevent dormice from meeting their nutritional requirements, with serious consequences for their reproductive success and survival.

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Effects of the neonicotinoid Acetamiprid on the social bee *Lasioglossum malachurum*

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Wild bees play a crucial role as pollinators and therefore provide a key ecosystem service. However, like other insects, wild bees are highly threatened, among others by the intensification of land use. This includes the use of pesticides, which can affect wild bee behaviour, health and physiological traits. Acetamiprid, the only neonicotinoid still authorised in the EU, is still the subject of debate as to whether, like the other neonicotinoids, it also causes serious negative effects for bees. Various effects for different bee species are known, but the effects on ground-nesting species, which make up the majority of bees, are rarely investigated in pesticide studies.

We therefore investigate the effects of Acetamiprid on *Lasioglossum malachurum*, a ground-nesting social wild bee species. It is a common species in agricultural landscapes that also forages on oilseed rape, which is usually treated with Acetamiprid. Furthermore, the chemical communication of this species is well studied, which makes it a good study organism in this context. We investigated the chemical communication of *L. malachurum* under the influence of Acetamiprid as well as the development of the ovaries and the gut microbiome as fitness parameters - captured in the wild and under controlled treatment in the laboratory.

We found effects of Acetamiprid on the chemical composition of cuticular lipids, so that effects on the communication and social behaviour of this species cannot be excluded. However, we found no clear effects of Acetamiprid on ovarian development and gut microbiota composition. Nevertheless, the gut microbiome changed when brought to the laboratory compared to the field, questioning the relevance of pesticide studies which are performed in laboratory experiments.

Our study shows that it is important to include soil-nesting wild bees in pesticide studies and that further studies are needed because the effects can be subtle and complex.

Sublethal effects of insecticides on sexual communication and host finding in parasitoid wasps

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Insecticides are used worldwide on a large scale in plant protection and can also kill useful non-target organisms. In addition to lethal effects, insecticides can also have less obvious, sublethal effects. Parasitoid wasps play an important role in ecosystems as natural enemies of other arthropods. They can come into contact with sublethal doses of insecticides through direct contact with treated plants or through the ingestion of contaminated nectar, honeydew, or guttation water. We investigated the sublethal effects of four insecticides targeting cholinergic neurons of the insect nervous system, i.e. acetamiprid (neonicotinoid), dimethoate (organophosphate), flupyradifurone (butenolide), and sulfoxaflor (sulfoximine) on the parasitoid wasps *Nasonia vitripennis* (Pteromalidae), *Lariophagus distinguendus* (Pteromalidae), and *Leptopilina heterotoma* (Figitidae). The wasps were treated with sublethal doses of the four active substances and tested in bioassays with regard to pheromone-mediated mating behaviour and olfactory host finding. Sublethal doses of all four compounds interfered with pheromone communication and/or olfactory host finding in at least one of the species studied. In *N. vitripennis* and *L. distinguendus*, the mating frequencies of treated wasps were significantly reduced. Experiments with *L. heterotoma* revealed furthermore, that bioactive amounts of dimethoate can reach parasitic wasps via the food chain (host breeding medium – host larvae – parasitoid). Overall, the strength of sublethal effects depended on the active substance and the wasp species tested, with *L. distinguendus* reacting most sensitively. The results indicate that sublethal doses of insecticides targeting cholinergic neuron impair the olfactory capabilities of parasitoid wasps. The sense of smell is of central importance for the ecosystem service provided by parasitoid wasps. It must therefore be assumed that sublethal effects of insecticides negatively influence the important function of parasitoid wasps as natural enemies. This work was funded by the Bavarian State Ministry of the Environment and Consumer Protection within the research network BayÖkotox.

The comparatively simple genetic basis of sexual attractiveness in parasitic wasps

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Chemical signaling, the most ancient and widespread form of communication, has permeated through all known taxa of life. However, how exactly biologically relevant information is chemically encoded in the vast number of compounds with signalling capabilities remains poorly understood. Cuticular hydrocarbons (CHCs), long-chained lipids occurring on the epicuticle of insects, are an excellent example for this, encoding and conveying a vast array of differential chemical information. CHC profiles constitute complex mixtures of up to hundreds of different compounds, where unravelling the main signalling components is notoriously difficult. Similarly, our knowledge of the genetic basis of CHC biosynthesis remains limited and heavily biased towards the single insect species *Drosophila melanogaster*. Utilizing a model system for parasitic wasps, *Nasonia*, we attempt to close these knowledge gaps and provide a more universal understanding of the genetic architecture and signaling properties of complex CHC profiles. In this genus, female CHCs can generally be perceived and discriminated as species-specific sex pheromones by the males, and we identified specific methyl-branching patterns as the main conveyers of sexual attractiveness in these profiles. We achieved this by functionally characterizing three fatty acid synthase genes mainly responsible for biosynthesizing the key methyl-branched CHCs and upholding the integrity of female CHC profiles above a detection threshold for the males. This largely advanced our understanding of how genetic information can be translated into biologically relevant chemical information and reveals that sexual attractiveness can have a comparably simple genetic basis. These findings also provide a promising basis for further investigating the chemoreceptive mechanisms governing CHC perception in *Nasonia* males. Our general knowledge on how exactly individual signaling compounds are perceived and processed remains surprisingly scarce, rendering the *Nasonia* olfactory communication system particularly suited for obtaining a more holistic view of the delicate interplay between sender and receiver.

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Aging virgin females of the false widow spider (*Steatoda grossa*) engage in dishonest pheromone signaling

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The terminal investment concept proposes that decreased expectation of future reproduction (e.g., arising from increasing age) induces greater investment in current reproduction including greater efforts to locate or attract mates. Typically, aging female animals become less fecund thus males achieve greater reproductive fitness by mating with younger females. Here, we tested the hypothesis that aging females of the false widow spider, *Steatoda grossa*, engage in dishonest signaling, thus 'lying about their age'. Female *S. grossa* are known to deposit on their webs courtship-inducing contact pheromone components which pH-dependently hydrolyze, giving rise to airborne mate-attracting pheromone components. Females can regulate their webs' pH, thus manipulating the rate of hydrolysis and thereby the release rate of mate-attractant pheromone components. Using high-performance liquid chromatography-mass spectrometry, we quantified the contact pheromone components that virgin females deposit on their web over their multi-year lifetime, and we recorded the females' fecundity and attractiveness to males. As females aged, they produced fewer viable offspring and deposited less contact pheromone components but altered their webs' pH to elevate the release of mate-attracting pheromone components equivalent to levels of young females. Essentially, this tactic made old females as attractive as young females, as shown in mate-choice experiments with males, despite diminished fecundity. Our data support the conclusion that female *S. grossa* engage in dishonest signaling, thereby increasing their reproductive fitness to the detriment of male spiders that would achieve greater reproductive potential by mating with younger females.

Guardians of the Grave: Microbial Management in Burying Beetles and its Implications for Carrion Preservation and Rival Avoidance

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Burying beetles (*Nicrophorus* sp.) belong to a wide range of arthropods engaging in parental care. During the breeding process, both parents exhibit various care behaviors, including pre-hatching care, such as preparing a small vertebrate carcass as a food source for their offspring, and post-hatching care, such as the regurgitation of carrion food to the larvae. While the larvae benefit in terms of growth and survival from post-hatching care, the exact function of the parents‘ investment in pre-hatching care remains unclear. Recent studies suggest that pre-hatching care and the associated microbial management via excretions have, on one hand, positive effects as they manipulate the cadaveric VOC emissions to conceal the carrion from rivals, but also negative effects as they impede larval self-feeding by forming an inaccessible ball and removing microbes that act pre-digestively. Here, we show in *Nicrophorus vespilloides* that when using natural forest soil as a substrate, larval survival was much higher on parentally prepared than non-prepared carcasses. Moreover, we found that parentally prepared cadavers emitted different amounts of sulfur-based volatiles, already known for their attracting or deterring effects on *Nicrophorus*, than aged carcasses. Finally, a field experiment revealed that the aged and prepared carcasses were discovered at different frequencies by rivals. In summary, our results reveal that the management of the microbial community in the pre-hatch phase serves a double function: it makes the carcass a less toxic environment and manipulates the VOC emissions to conceal the carcasses and offspring from rivals.

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Larval *Drosophila melanogaster* development and expression of life history traits in a symbiont-by-environment defined niche space

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Microbial symbionts are vital in shaping insect developmental niches, providing essential nutrients for larval growth and influencing adult phenotypes. On various plant substrates, primarily fruits, larval development of *Drosophila melanogaster* relies on the growth and metabolic activity of maternally transmitted bacterial and fungal symbionts. Fruit substrates vary significantly, potentially altering microbial communities that may then be carried by female flies thus impacting future offspring through both temporal and spatial variations in substrate type. We show that it is the interplay between microbial symbionts and fruit substrate type that influences larval development and thus the expression of adult life-history traits, which is linked to substrate-dependent shifts in bacterial communities and fungal diversity. Our work establishes symbiont-environment interactions as a new conceptual framework that helps to understand sources of variation in the evolution of mutualistic dependence.

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Combining empirical data with individual and population-level modeling to predict the effects of environmental change on *Macoma balthica*

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Global climate change together with other anthropogenic pressures such as nutrient loading significantly alters coastal ecosystems through changes in e.g. temperature, salinity and primary production as a base for the food-webs. It is logistically difficult to test the effects of multiple drivers across a large gradient of levels in empirical studies. Process-based models provide a powerful tool to investigate such complicated effects. We have developed a model combining individual bioenergetic and population dynamics of the bivalve *Macoma balthica*, a key species dominating benthic communities in the Baltic Sea and beyond, to study the effects of multiple drivers on individual and population growth. To parameterize the model, empirical studies of metabolism, growth and survival in relation to salinity, quality and quantity of food as well as temperature are being performed. Preliminary results show that the ability to withstand stress is strongly dependent of the availability of energy from food sources. Thus, increasing sea temperatures and decreasing salinity as a consequence of climate change combined with reduced food availability trough efforts to combat eutrophication may lead to a meagre future for *M. balthica* and other deposit-feeding benthos.

The endosymbiont *Spiroplasma poulsonii* increases resistance to pathogens

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Facultative endosymbiotic bacteria, such as *Wolbachia* and *Spiroplasma* species, are commonly found in association with insects and can dramatically alter their host physiology. Many endosymbionts are defensive and protect their hosts against parasites or pathogens. Despite the widespread nature of defensive insect symbioses and their importance for the ecology and evolution of insects, the mechanisms of symbiont-mediated host protection remain poorly characterized. Here, we utilized the fruit fly *Drosophila melanogaster* and its facultative endosymbiont *Spiroplasma poulsonii* to characterize the mechanisms underlying symbiont-mediated host protection against bacterial and fungal pathogens. Our results indicate a variable effect of *S. poulsonii* on infection outcome, with endosymbiont-harbouring flies being more resistant to *Rhyzopus oryzae*, *Staphylococcus aureus*, and *Providencia alcalifaciens*, but more sensitive or as sensitive as endosymbiont-free flies to the infections with *Pseudomonas* species. Further focusing on the protective effect, we identified Transferrin-mediated iron sequestration induced by *Spiroplasma* as being crucial for the defense against *R. oryzae* and *P. alcalifaciens*. In case of *S. aureus*, enhanced melanization in *Spiroplasma*-harbouring flies plays a major role in the protection. Both iron sequestration and melanization induced by *Spiroplasma* require the host immune sensor protease Persephone, suggesting a role of proteases secreted by the symbiont in the activation of host defense reactions. Hence, our work reveals a broader defensive range of *Spiroplasma* than previously appreciated and adds nutritional immunity and melanization to the defensive arsenal of symbionts.

InsectMow - Development and Evaluation of insect- and spider-friendly mowing techniques

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Several studies have shown that a large proportion of spiders and insects living on agricultural grassland are damaged and/or killed during mowing. Therefore, it can be assumed that intensive mowing of agricultural grassland, which damages not only adults, but also larvae and nymphs, has resulted in an “overfishing effect” that has contributed to the current insect decline on agricultural land. The interdisciplinary project “InsectMow” is investigating how the negative effects of mowing on grassland ecosystems can be reduced by a technical modification of standard disc mowers. Therefore, the project aims at pursuing the development of (1) a modified disc mower that causes fewer arthropod losses without economic disadvantages, and (2) an effective insect flushing bar that enables insects to flee. In the light of the ongoing loss of biological diversity this project intends to gain a deeper knowledge on the direct, medium-, and long-term effects of mowing by testing various mowing technologies and their effects on spiders, as well as important pollinators, herbivores, and predatory insects.

Here, we present results from our first two years of testing several mowing techniques and an insect flushing bar prototype. Our results show that mobile insects such as dipterans or cicadas are able to escape from the mower when the flushing bar and mower are tested together at low operating speeds. In addition, we have been able to show that, contrary to previous assumptions, bar mowers affect the arthropod fauna similar to disc mowers. Immediately after mowing, the average number of arthropods was approximately 35 % lower for both mowing techniques compared to the unmown control plots. We have also detected medium-term effects of mowing (two to four weeks after mowing) regardless of the mowing technique, with 27 to 90 % less arthropods depending on the group on mowed plots compared to untreated controls.

* Student (eligible for the Student Awards)

Lessons Learned from the Old and New World: Exploring the Interplay between Biodiversity and Zoonotic Diseases in Wildlife

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Understanding the relationships between biodiversity and zoonotic diseases is crucial for safeguarding human and animal health. We investigated the diversity-disease relationships in wildlife, focusing on bat communities exposed to Coronaviruses in Ghana and small mammal communities (rodents and marsupials) exposed to *Trypanosoma* infections in Panama. Using spatiotemporal variations in species community assemblages, we revealed in both settings and study systems that anthropogenic disturbances and subsequent biodiversity loss are reshaping species communities, favoring the proliferation of generalist species that act as main reservoirs for pathogens. As a consequence, infection probability and prevalence increased in less diverse species assemblages. In Ghanaian bats, we could demonstrate that closely related species can differ in their resilience and thus amplify or reduce Coronavirus infection likelihood. In Panama, we could show that *Trypanosoma* infection likelihood was associated with human disturbance affecting species diversity, marsupial density, and host genetic diversity. Combined, both host-pathogen systems highlight aspects of diversity-disease relationships compatible with the dilution effect hypothesis. Overall, our findings emphasize the urgent need to prioritize conservation efforts that maintain healthy and resilient ecosystems to mitigate the risks associated with zoonotic disease transmission.

Multifaceted Analysis of Arthropod Vision

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Compound eyes are found in most arthropods and are thus the most abundant eye type on earth. They may consist of up to tens of thousands of single ommatidia, each equipped with a light-focusing lens (facet) and a photoreceptive unit. The acuity of a compound eye depends on the visual field that each ommatidium covers, and thus on the angle between neighbouring facets. Sensitivity depends on the visual field of each facet as well as on the size of these light-collecting entities. Topological differences of facet properties within one compound eye, interpreted as adaptations to differing optical needs of each eye region, have already been found in several insect taxa. However, data gathering was tedious and limited to a few taxa. Here, we present a suite of scripts in R, ImageJ macro language, and Blender Python to extract the 3D positions, sizes and inter-facet angles of all ommatidial facets of a compound eye based on a µCT-scan. Using the new pipeline, we extracted visual topologies of myriapods, crustaceans and various insects, identified topological differences in acuity and sensitivity across each of their eyes, and visualized these in 2D and 3D. The method was also applied to fossil specimens to get visual properties of extinct taxa. The quick workflow enables multifaceted investigations ranging from studying differences within one population to the macroevolutionary path through visual compound eye properties with trade-off relations throughout the megadiverse arthropods.

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* Student (eligible for the Student Awards)

Morphology, Development and Function of the heart in *Daphnia* revealed by light-sheet fluorescence microscopy

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Water fleas of the genus *Daphnia* are not only interesting indicators for limnological and toxicological research. Cladocera in general are characterized by a highly derived morphology compared to other representatives of the Branchiopoda, which is intriguing from the perspective of evolution and character transformation. This concerns not only the external habitus but also the internal morphology. The hearts of Cladocera are significantly shortened compared to those of other branchiopod crustaceans and appear as delicate hollow sacs. While other imaging methods for examining the three-dimensional morphology of the heart have drawbacks in various aspects that limit detailed visualizations, light-sheet microscopy enables this delicate organ to be depicted in a state as native as possible and yet in great detail.

We have performed histochemical fluorescence staining on adult *Daphnia magna* and late developmental stages and imaged them using our in-house modular Flamingo light-sheet microscope. Additionally, we developed a protocol to stain live *Daphnia* with live dyes and to study the function of the beating heart in vivo.

With light-sheet microscopy, we were able not only to show the later morphogenesis and detailed adult morphology of the heart in *Daphnia* but also to depict the contraction pattern of the heart and the function of the ostia in 4D.

The obtained data contribute to a reconstruction of the evolutionary transformation of heart morphology within the Branchiopoda. Furthermore, our live-staining protocol can be adapted for other crustaceans - and more broadly other invertebrates - to study heart function, especially in such non-model organisms of which transgenic lines are unavailable.

ABCB transporters and the transport network for sequestered cardenolides

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Many phytophagous insects not only tolerate and detoxify noxious compounds present in their host plants but even sequester the toxins for their defence. This necessitates specific mechanisms, especially carrier proteins that regulate uptake and transport to specific storage sites or protect sensitive tissues from toxic compounds. We focus on the milkweed bug *Oncopeltus fasciatus*, which sequesters cardenolides from its Asclepias host plants, and investigate the involvement of ATP-binding cassette subfamily B (ABCB) transporters in this process. Bioinformatic analyses could identify four ABCB full transporters and five ABCB half transporters in transcriptomes of adult bugs that show a pronounced tissue specific expression. Knock-down experiments by RNAi under cardenolide exposure compared to non-exposure identified ABCB transporters involved in the protection of the sensitive nervous tissue but also those responsible for transfer into the defense fluids of O. fasciatus. On the other hand, enzyme assays with heterologously expressed transporters were used to analyze the substrate spectra of the some ABCB transporters. Both approaches confirm the crucial role of ABCB transporters for sequestration of cardenolides.

Navigating ontogenetic pathways: amphibian developmental plasticity in a changing world

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The interaction of widespread stressors such as nitrate pollution and increasing temperatures associated with climate change are likely to affect aquatic ectotherms such as amphibians. The metamorphic and physiological traits of amphibian larvae during the critical onset of metamorphosis are particularly susceptible to these stressors. We conducted a common-garden experiment using *Rana temporaria* larvae subjected to four constant acclimation temperatures (18, 22, 26, 28 °C) crossed with three environmentally relevant nitrate concentrations (0, 50, 100 mg × L-1) to investigate the interactive and individual effects of these stressors on metamorphic (i.e., growth and development) and physiological traits (i.e., metabolism and heat tolerance) at the onset of metamorphosis. Larvae exposed to elevated nitrate concentrations and thermal stress displayed increased metabolic rates but decreased developmental rate, highlighting interactive effects of these stressors. However, nitrate pollution alone had no effect on either metamorphic or physiological traits, suggesting that detoxification processes were sufficient to maintain homeostasis but not in combination with increased acclimation temperatures. Furthermore, larvae exposed to nitrate displayed diminished abilities to exhibit temperature-induced plasticity in metamorphosis timing and heat tolerance, as well as reduced acclimation capacity in metabolic rate and heat tolerance to higher temperatures. These results highlight the importance of considering the exposure to multiple stressors when investigating how natural populations respond to global change.

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Trends in early larval traits and responses to chronic vs. acute exposure across a latitudinal gradient: the European shore crab *Carcinus maenas*

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The oceans are warming at unprecedented rates, heatwaves are increasing, particularly in the Arctic. Larval stages are particularly susceptible to environmental drivers, and their vulnerability is likely to vary across latitudinal gradients due to variations in traits like size and thermal tolerance. We examined latitudinal patterns in body mass, elemental composition, and thermal tolerance of first-stage larvae of shore crab *Carcinus maenas* from populations spanning a 25° latitudinal gradient (Vigo (Spain), Bergen, Trondheim, and Bodø (Norway) and re-analysed data from populations in Helgoland, Bangor, Brest, and Cádiz. For thermal tolerance, two laboratory experiments were carried out with larvae from Vigo and the Norwegian populations (experiment-1: larvae reared from hatching to Zoea II at eight temperatures: 6–27 °C; experiment-2: larvae were exposed to ramps of increasing or decreasing temperature: up to 40 °C and down to 3 °C respectively. Dry mass, carbon and nitrogen content of freshly hatched larvae increased with latitude, towards the Arctic. Norwegian larvae exhibited higher survival at 9 °C compared to larvae from Spain. We did not find evidence of a relationship between dry mass at hatching and thermal tolerance. Larvae from Bodø (northern range edge) had longer LT50 at low temperatures than southern populations. All populations demonstrated low survival at 27 °C, but high survival at 12 – 24 °C. We did not find evidence of relationships between survival to Zoea II and thermal tolerance as quantified from the ramp experiment, suggesting different aspects of thermal tolerance are measured under chronic vs. acute exposure. Tolerance to low and high temperatures was positively correlated, suggesting that general physiological quality rather than trade-offs drive relationships between upper/lower thermal tolerance limits. Overall, this study provides evidence for a potentially adaptive increase in larval body mass and tolerance towards low temperatures with latitude across the native range in *C. maenas*.

* Student (eligible for the Student Awards)

How to succeed in novel habitats? Successful development through alternative pathways

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Quantifying species responses to the combined effects of multiple environmental drivers is critical for better understanding the effects of climate change on performance of native and invasive species. Here, we quantified the combined effects of temperature and salinity on survival and growth of the larval stages of the crab *Hemigrapsus sanguineus*, invasive to the North Sea coast. Larvae of *H. sanguineus* were reared at 12 combinations of four temperatures (15 – 24 °C) and three salinities (20, 25, 32 ‰), from hatching to megalopa. Survival and growth rates showed complex responses to salinity and temperature. Larvae were able to metamorphose to megalopa with high survival and growth rates at high temperatures (18 – 24 °C) irrespective of salinity. However, at 15 °C successful development varied among salinities, and occurred through alternative developmental pathways (short or long) characterised by either five or six zoeal stages. The proportion of larvae developing through the long pathway was determined by the salinity (highest proportions at 32 ‰); those larvae metamorphosed to megalopa with increased body mass and carbon and nitrogen content. The ability of *H. sanguineus* to successfully develop at moderately low salinities, along with its high performance at high temperature may enhance the likelihood of establishing populations in regions of freshwater influence.

The evolution of cornified skin appendages was associated with the origin and loss of transglutaminases in vertebrates

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Transglutaminases (TGMs) cross-link proteins by introducing covalent bonds between glutamine and lysine residues. Here we investigated the evolution of TGM genes in relation to adaptations of the skin and skin appendages in vertebrates and basal chordates. We determined the catalog of TGMs in the main clades of vertebrates and two chordate species, performed a comprehensive phylogenetic analysis of TGMs and localized TGMs in different tissue types of selected vertebrate species. Our data suggest that TGM1, which is crucial for normal skin development in humans and is linked to severe skin diseases when mutated, is the phylogenetically oldest epithelial TGM, with orthologs being present in the lancelet. Proteomic detection of TGM1 orthologs in the epithelial teeth of the lamprey, a basal vertebrate, suggests that TGM1 contributes to the cornification of these primitive skin appendages. Gene duplications led to the origin of TGM2 in stem vertebrates and an increasing number of epithelium-associated TGM genes in the lineage leading to terrestrial vertebrates. We identified a previously uncharacterized protein, TGM9, in the epithelial egg tooth of birds. The corresponding gene is conserved in crocodilians, turtles and the platypus, which also utilize a cornified egg tooth to break the egg shell during hatching. In mammals, TGM1, TGM3 and TGM6 contribute to the cornification of keratinocytes during the growth of hair. The evolutionary loss of hair in whales was associated with the loss of TGM3 and TGM6. Taken together, this study suggests that the gain and loss of vertebrate TGM genes was associated with the evolution of cornified skin appendages in vertebrates.

Analysis of the DUOX pathway in *Tribolium castaneum*

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Insect immunity involves the IMD, Toll and DUOX-ROS signalling pathways that trigger different antimicrobial responses. The IMD and Toll signalling pathways result in the production of antimicrobial peptides (AMPs) secreted in response to recognition of pathogen-associated-molecular-patterns. AMPs are probably the most effective part of the immune response in insects, but other defence mechanisms as the formation of reactive oxygen species (ROS) by the dual oxidase (DUOX) also contribute. ROS are important regulators of intestinal homeostasis. It is known that DUOX activity is stimulated by uracil, leading to the production of ROS and hypochlorous acid (HOCl). Uracil is released by pathogenic but not by commensally living bacteria and it presumably binds to a yet unidentified G-protein-coupled receptor (GPCR) triggering the activation of the DUOX gene expression. In an attempt to identify the GPCR that binds uracil in insect immunity, we performed a simple bioinformatic approach using a human purinergic GPCR, which is able to bind also UTP as well as uracil, as a template for searching the genome of the red flour beetle, *Tribolium castaneum*, for putative orthologues. We selected four potential candidates and analysed their expression profiles in different tissues and in response to feeding the larvae with an uracil-supplemented diet. Two promising candidate genes were further analysed by RNA interference (RNAi). We found that the knockdown of one of the candidate genes resulted in DUOX no longer being induced by uracil. Using the HOCl-reactive chemical R19-S, we further found that DUOX activity was reduced in the gut when the uracil receptor candidate was silenced by RNAi. Finally, dsRNA injected larvae to silence the candidate gene exhibited a similar developmental delay and mortality in response to a Bacillus thuringiensis challenge as observed in dsTcDUOX injected insects, indicating a crucial role for pathogen recognition.

Keep or lose: Inheritance and elimination of songbird germline-restricted chromosome

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Recently, it was discovered that many birds combine compact genomes and stable karyotypes with extremely rapidly evolving and highly repetitive genomic element. How do they achieve this? This phenomenon is related to the germline-restricted chromosome (GRC) present in every studied songbird, which represents the only known example of programmed DNA elimination in birds. The elimination of GRC occurs during the differentiation of somatic cells in embryogenesis of both sexes and during meiotic divisions in spermatogenesis. However, the timing of GRC elimination during embryogenesis and mechanism of this process remain unknown.

Preserved only in germ cells, two GRC copies enter female meiosis, where they form a normal bivalent and recombine. Male meiotic cells typically contain one GRC copy, which undergoes epigenetic modification and transcriptional inactivation before being expelled. Usually absent from sperm, GRC is transmitted via females, exhibiting non-Mendelian inheritance. When and how sex differences occur, and what is the mechanism of GRC inheritance are still unknown.

Using GRC-specific microdissected probes, we examined the dynamics of GRC elimination in the early development of the zebra finch and sand martin. We showed that elimination begins before egg laying and continues for at least 24 hours afterward. We assessed the epigenetic characteristics of GRC in embryogenesis and compared them with those during spermatogenesis to reveal whether elimination at these stages utilize the same mechanisms. We assessed the GRC copy number at different stages of embryogenesis to understand when and how sex differences in GRC behavior may occur.

In my talk, I will present recent results on GRC elimination and overview the current models of GRC inheritance. I will also demonstrate what cytogenetic analysis can tell about variability of GRC at different scales and the efficacy of processes maintaining this chromosome in the germline and throughout the evolutionary history of songbirds.

Expanding the phasmatodean tree of life: new insights from targeted enrichment in stick and leaf insects

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Employing genomic data such as genomes and transcriptomes has become the standard tool to investigate phylogenetic relationships. However, many less well-studied insect lineages have so far only been analysed using traditional morphological and behavioural traits or molecular data of few selected loci. Despite their popularity as masters of plant masquerade, the stick and leaf insects (Phasmatodea) also long remained one of those taxa for which phylogenetic hypotheses have been mostly incongruent. Contributing to this was undoubtedly the prevailing notion that morphological adaptations, for instance to resemble a particular plant part and occupy a similar niche, were the result of common ancestry and not convergent evolution of morphology and behaviour in unrelated taxa. Eventually, with the advent of phylogenomics, the backbone tree of Phasmatodea could be largely resolved. While this one previous phylogenomic analysis based on transcriptomic data covered 38 phasmatodean species, it lacked representatives of many significant lineages and the entirety of the African taxa. In order to address this shortcoming, we used the available transcriptomes to design baits for enriching 1,384 single-copy protein-coding genes of nearly 100 additional species. Our aim was to construct a comprehensive phylogeny with which we can resolve the remaining systematic questions regarding all principle taxa and shed light on the global biogeography of stick and leaf insects. Moreover, this expanded tree not only forms a solid foundation for future taxonomic studies but will also play a major role in understanding convergent evolution, trait evolution and other phenomena within the Phasmatodea. Thus, the insights gained from this research may contribute to a broader comprehension of evolutionary processes that might be applicable beyond this fascinating lineage of insects.

Crabs on Crete: How apparent taxonomic contradictions led to new paleobiogeographical insights in the Aegean region

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Freshwater crabs of the genus *Potamon* are widely distributed, with a particularly high diversity in the Aegean region. The species of this genus can be distinctely distinguished by characters of the first gonopods (male copulatory organs). The resulting classification was further confirmed by molecular genetic studies - with one exception: a population on Crete. These crabs were previously morphologically assigned to the species *Potamon potamios*. Recent molecular genetic studies, however, refuted this assignment and suggested an independent species being endemic to Crete (*Potamon kretaion*) with a surprisingly close relationship to *Potamon ibericum* from the Black and Caspian basin. The first gonopods of this species differ considerably morphologically from the gonopods of *P. kretaion* and in addition, *P. ibericum* is distributed far away from Crete. The aim of this study was to shed light on these taxonomic and biogeographic contradictions. For this purpose, the morphology of the first gonopods was carefully studied and compared with the other Aegean species. In addition, the palaeogeographical development of the Aegean was reconstructed and related to the current distribution patterns of the species. In this way, not only was the mystery of *P. kretaion* solved, but it was also shown that the distribution history of *Potamon* in the Aegean is a result of drastic geographical changes, such as the almost complete desiccation of the Mediterranean Sea.

* Student (eligible for the Student Awards)

Small worms, big surprises: Uncovering Hidden Diversity within the genus *Amphiglena* (Sabellidae: Annelida)

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Amphiglena Claparède, 1864, is a genus of tiny polychaetes (Sabellidae, Annelida) that typically do not exceed a few millimetres in length and dwell within photophilic algae and coarse sand in shallow marine environments. *Amphiglena mediterranea* (Leydig, 1851), described from European waters, was long regarded as a cosmopolitan species. However, molecular analyses have revealed a cryptic species complex in the Mediterranean Sea, leading to the description of several new species. These new species were solely based on morphological distinctions, and a link between the genetic data and available species names is still missing. New samples collected along the Italian coastline — including the type localities for the named *Amphiglena* spp. — allow for a more comprehensive investigation of the diversity within this previously underestimated genus, which is now understood to be significantly more species-rich than once assumed. By following an integrative approach, combining morphological and molecular analyses, we aim to link sequence data to available names, clarifying the taxonomic status of Italian *Amphiglena* species and reconstructing the phylogenetic relationships within this group. We also present the first mitochondrial genome for this genus, which unveiled a novel gene order that is significantly different from the putative ground pattern (PGP) found in most other polychaetes.

* Student (eligible for the Student Awards)

Dusting Off the Phylogeny of Feather Dusters

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Sabellidae, affectionately named flowers of the sea or feather duster worms, is a family of polychaete annelids inhabiting soft tubes and known for their radiolar crowns with feathery appendages. With over 500 recognized species, Sabellidae is one of the most diverse family-ranked groups within polychaetes. Their position on the annelid tree of life and their sister group has only recently been resolved through phylotranscriptomic methods. However, the internal phylogeny of Sabellidae remains poorly understood. Building upon our published dataset of 17 sabellid transcriptomes, we have now sequenced over 500 loci for approximately 100 sabellid species. This comprehensive approach combines baited target enrichment and exon capture, as well as genome skimming and in-silico capture of the selected loci. Here, we will present this newly constructed and robust phylogeny, propose a systematic revision of the family, and clarify the delineation of subfamilies and tribes within Sabellidae. Our taxon sampling spans the group's vast diversity, including numerous new species, such as a remarkable deep-sea Bispira species with methanotrophic symbionts. This new phylogeny not only provides an essential foundation for the much-needed systematic revision of Sabellidae but also offers a valuable tool for exploring the evolution of diverse life-history strategies, body sizes, and morphologies within the family.

Development of an automated plankton biodiversity sensor for a biohybrid monitoring system

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Due to anthropogenic changes in the environment and fast advancing climate change, it is particularly important today to obtain up-to-date data on biodiversity. Aquatic environments are of particular interest in this context, as it is especially difficult to collect long-term and high-frequency data on biodiversity. The EU FET open project Robocoenosis is currently developing a new optical sensor that can autonomously and automatically record the plankton biodiversity of freshwater ecosystems. This system is designed to monitor not only species composition but also changes in biodiversity over a long period of time. This data can be used to provide information on species fluctuations in freshwater bodies, as well as to infer the current health of the aquatic environment through the utilisation of many plankton organisms as bio-indicators. This system will also be used to test the extent to which the actual behaviour of plankton organisms can be observed in relation to changes in water quality. We will present the state of the art of different systems as well as the current development and experiences with the new optical system in Robocoenosis. The results of the first field experiments carried out in the spring and summer of 2024 in Lake Millstatt (Austria) will be presented.

* Student (eligible for the Student Awards)

Costly Courtship: Condition Dependence of a Multimodal Courtship Signal in a Parasitoid Wasp

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Signals that mediate mating decisions are often considered to be condition dependent and therefore function as a cue for an individual's quality. However, much of this research has focused on a single signal modality. But despite the additional cost associated with the use of multiple modalities, multimodal courtship signals are common in animals. Therefore, it is important to consider all modalities when assessing if a multimodal courtship signal is condition dependent.

Here, we test whether the two components of the multimodal courtship of the parasitoid wasp, *Leptopilina heterotoma*, are condition dependent. *L. heterotoma* male courtship consists of a chemical signal (cuticular hydrocarbons (CHCs)) and a vibratory signal (wing fanning). Previous research has shown that larger males and males with a higher fundamental frequency when wing fanning are more likely to mate. However, there was no difference in the CHC profile between successful and unsuccessful males. To determine if any of these signals are affected by a male's condition, we manipulated the males in two ways (nutritional state and age) and then conducted courtship trials. During the courtship we recorded the wing fanning frequency with a laser Doppler vibrometer and analyzed the male CHC profiles using gas chromatography–mass spectroscopy (GC-MS).

We show that male CHC profiles differ depending on male condition in both, the nutritional stage and age treatments. The analysis of our wing fanning data is still in progress. However, previous research suggests that the starved and older males have a lower fundamental frequency wing fanning compared to their fed and young counterparts. Therefore, it is likely that all elements of *L. heterotoma's* courtship signal are condition-dependent and may serve as a cue of individual quality.

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* Student (eligible for the Student Awards)

Leaving No One Behind – Social Dispersal in a burying beetle

66

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The timing of dispersal of offspring from their birth site is an important life-history trait with tremendous effects on future reproductive success. While often genetically determined, the timing of dispersal is also influenced by environmental and social cues. As part of family interactions individuals are even able to adjust their dispersal time in response to their surrounding family to increase their indirect fitness gains. For example, in the house wren, fledging-ready chicks delay their own dispersal when growing alongside younger chicks to increase the survival chances of their younger siblings. While avian and mammalian dispersal behaviours have been extensively studied, similar investigations into sub-social insect species remain sparse. Here, we investigated sibling interactions and dispersal behaviour in the burying beetle *Nicrophorus vespilloides*, a species with facultative brood care, whereby offspring profit from the presence of parents but can also survive and develop in the absence of parental care. We tested how older and therefore more independent siblings affect their younger counterparts in the absence of parents. To this end, we compared growth rates and dispersal behaviour of newly hatched *N. vespilloides* larvae cohabitating with older larvae to those residing with age-matched siblings. Surprisingly, the older larvae induced dispersal behaviour in their younger siblings, resulting in an earlier dispersal from the carcass resource. Compared to conditions with age-matched siblings, dispersing larvae were thereby associated with a lighter mean larval weight. This has tremendous implications for the beetles, as larvae weight at dispersal highly correlates with adult beetle size, which in turn determines their reproductive success. Our results indicate that the positive effects of social dispersal outweigh the negative consequences of an early dispersal.

* Student (eligible for the Student Awards)

Social environment effects the substantial individual variation in clock-controlled behaviour of *Tribolium castaneum*

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Virtually all organisms possess a biological pacemaker, the so called circadian clock. Those clocks enhance organisms' fitness by allowing them to anticipate, rather than simply react to, the 24-hour environmental changes caused by the Earth's rotation. The general mechanisms of these pacemakers are evolutionarily highly conserved. Nevertheless, the interspecific variation in the molecular composition of these pacemakers and its outputs such as behaviour or metabolism demonstrates remarkable evolutionary flexibility. So far, our understanding of the circadian behaviours as well as their molecular underpinnings in the important model organism and pest species *Tribolium castaneum* remains limited.

We conducted a comprehensive analysis of the circadian activity patterns in *T. castaneum* and their entrainment to light and temperature cycles. These environmental cycles entrained the beetles' diel activity patterns, and they further persist in constant environments, proving control by an internal pacemaker. However, in contrast to most organisms employed in chronobiological studies, this species exhibits substantial individual variation in rhythmicity. This variation was of such a magnitude that a notable proportion of individuals behave arrhythmically, whereas others exhibit clear rhythmicity. Interestingly, behavioural measurements in groups of ten animals revealed more stable rhythmic activity patterns than measurements of isolated individuals. This indicates that social contacts enhance rhythmicity in this species. We presume that such a social rhythmicity could be evolutionary significant, since it could mask newly evolving variation in individual rhythms. This would allow a population to build up variation, on which evolution could act upon later.

Our findings provide insights into the circadian biology of *T. castaneum*, demonstrating the extent of individual variation in clock-controlled behaviour in this species and underscore the impact of social factors on individual variation in behaviour.

* Student (eligible for the Student Awards)

Fine-scale navigation: searching ants are guided by the visual environment

79

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Navigation is of crucial importance for the survival of many animal species. To guarantee the successful completion of a journey, insects engage in highly efficient area-restricted searches to finally pinpoint their target. The resulting search patterns are highly structured – systematic – while retaining strong adaptive flexibility. Yet, it remains unclear how this sophisticated behaviour is generated by the insect central nervous system. Our current knowledge suggests that it involves the integration of several distinct navigational steering mechanisms in the insect brain. Here, I investigate the extent to which previous visual experience guides ants during their systematic searches for the nest entrance. When experimentally restricting the area around the nest to prevent foraging ants from forming visual memories, I found that subsequent unrestricted nest searches retained their systematic structure but suffered from reduced precision. The highest level of restriction resulted in the lowest levels of search precision and interestingly, asymmetrical restriction led to asymmetrical searches. This indicates that searching ants employ visually guided steering mechanisms, in which the perceived visual environment is matched to visual memories. Where such memories are lacking, the steering mechanism is impeded. The detailed analysis of searching behaviour reveals the spatial layout of unrestricted visual memories, and shows that such memories are formed in an area of at least one square metre around the nest entrance. As a whole, these findings reveal how recognised navigational routines can give rise to sophisticated systematic searching behaviour, and how such routines interact with external cues during searching. More broadly, the outcomes allow us to ask questions of fundamental importance about how brains work to produce adaptive behaviour.

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POSTER ABSTRACTS

Timing of chitin/chitosan assembly in insects

D02

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Locomotion requires the cooperation of different leg tissues for completion. In insects, the muscles, their motoneurons, sensory organs, the nutrient and the oxygen delivery systems, haemolymph and tracheae, respectively, and the exoskeleton co-ordinately ensure correct locomotory behaviour. We are interested in understanding the function of the leg cuticle in this matter. Focussing on the hip (trochanter together with the coxa), we ask how these leg segments are formed to accommodate locomotion. Along the proximal-distal axis, the cuticle of the trochanter is subdivided into distinct regions defined by chitin/chitosan-binding proteins that conceivably account for their physical properties. We will report on the trochanter structure in different insect species and show primary results on the assembly of the trochanter cuticle in the fruit fly *Drosophila melanogaster*.

Silencing of β-catenin1 blocks tail regeneration, but does not induce head regeneration in the flatworm *Macrostomum lignano*

D03

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β-Catenin enables the interaction of classical cadherin to the cytoskeleton filament actin and is modulating the Wnt signal, thus mediating cell differentiation, proliferation, and determining the body axis. 4 β-catenin homologs have been described in the highly regenerating planarian flatworm *Schmidtea mediterranea*. Among them, only Smed-β-catenin1 is involved in establishing posterior identity. Silencing of Smed-β-catenin1 during regeneration leads to the formation of a head at the wound site, even at the posterior end. In regeneration-deficient planarians, i.e. planarians that cannot regenerate a head from pieces posterior to the pharynx, β-catenin1 RNAi also rescues head regeneration in posterior pieces.

Using phylogenetic inference with β-catenin homologs from a diverse range of flatworms, we found that duplication of β-catenin occurred not in all flatworms, but only in *Rhabditophora*. In *Macrostomum lignano* (*M. lignano*) there are 3 β-catenin homologs. RNA interference of Mlig-β-catenin1, but not of Mlig-β-catenin2a or Mlig-β-catenin2b blocked tail regeneration and resulted in the lack of a blastema and a strong reduction of cell proliferation at the wound site. After knockdown, tails frequently regenerated imperfectly. Not at any amputation level could RNAi of any β-catenin rescue head regeneration in *M. lignano*.

Together, these findings demonstrate the requirement for Mlig-β-catenin1 in determining posterior polarity and affirms the conserved role of Wnt/β-catenin in specifying the Anterior-Posterior axis. The failure of head regeneration in β-catenin1 knockdown in *M. lignano* suggests that the rescue of head regeneration in the absence of β-catenin1 is not a conserved feature in flatworms, but possibly an apomorphy of planarians.

* Student (eligible for the Student Awards)

Predator induced cellular plasticity in *Daphnia longicephala* antennules

D05

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The freshwater crustacean *Daphnia* is well known to adapt to an increased predation risk through the expression of predator specific inducible defenses. The expression of these inducible defenses is initiated upon the perception of predator specific chemical cues, so called kairomones. The aesthetascs located on the antennules serve as a central element of kairomone perception. However, the distinct cellular and molecular mechanism that enable predator perception are not understood. In order to obtain a deeper insight into the involved cells and chemoreceptors, we first quantified the number of olfactory sensory neurons (OSNs) in the antennules in response to predator exposure via immunohistochemistry. In a second step we stained IR25a, a ionotropic coreceptor previously identified to be essential for predator perception. We observed an ~15 % increase of OSN number during predator exposure independent of normal cell division in the antennules. In addition, IR25a is more abundant in predator exposed specimen. Our results show cellular plasticity at the OSNs in form of nerve cell number and IR25a abundancy upon predator perception and provide important insights into how the nervous system reacts to the presence of their predators.

* Student (eligible for the Student Awards)

Hedgehog signaling, apical constriction and cilia dynamics in the patterning and segmentation of the vertebrate hindbrain

D07

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During vertebrate head development, the embryonic hindbrain orchestrates nervous system morphogenesis along the anterior-posterior axis. It is subdivided into metameric units, the rhombomeres, which express a specific molecular code to guide the correct growth of cranial nerves and the migration of neural crest cells. To ensure segmental identity, specialized structures called rhombomere boundaries (RhBs) prevent mixing of cells between adjacent rhombomeres.

We have previously shown that RhBs in *Xenopus laevis* can be identified by two unique features: 1) RhB cells constrict apically, forming a morphological furrow; 2) RhBs contain bona fide stem cells and progenitor cells. These observations lead us to hypothesize that RhBs in *Xenopus* serve two essential functions: 1) They reinforce initial patterning signals, converting an expression boundary through apical constriction (AC) into a physical compartment boundary, thereby restricting the mixing of cells with different fates and 2) they maintain stem cells to regulate tissue growth via controlled proliferation and differentiation.

To our knowledge, RhBs are unique in their dual functionality as both compartment boundaries and stem cell zones. This raises the question of how RhBs orchestrate the maintenance of stem cells while at the same time ensuring cell segregation. We suggest a potential mechanism could be provided by the Hedgehog (Hh) signaling pathway. Preliminary data shows: 1) RhBs exhibit active Hh signaling, 2) Hh overactivation increases RhB cilia length, and 3) loss of cilia disrupts both apical constriction and stem cell maintenance. Basing on this data, we propose the existence of a developmental module in which Hh signaling, AC and cilia dynamics collectively interact to instruct compartment formation and cell segregation as well as neural stem cell maintenance.

* Student (eligible for the Student Awards)

Morphogenetic roles of extraembryonic structures in red flour beetle, *Tribolium castaneum*

D09

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Many studies in morphogenesis focus on embryonic development, often neglecting the significance of extraembryonic structures such as the yolk, amnion, and serosa. However, these structures are pivotal in embryogenesis and provide valuable insights for evolutionary developmental biology (evo-devo) comparisons.

The red flour beetle, *Tribolium castaneum*, is an emerging model organism in insect research. It offers a better representation of insect biology compared to *Drosophila melanogaster* (Schmitt-Engel et al., 2015). For example, while *Drosophila* has a combined amnioserosa, *Tribolium*, as the majority of insects, has 2 separate extraembryonic membranes (Panfilio, 2008). *Tribolium* is a holometabolous insect and positions its embryo above the yolk, with the germband curling around its poles.

In this study, we explore novel morphogenetic events related to *Tribolium*'s extraembryonic structures. Yolk of *Tribolium* does not stay one yolk cell as it happens in *Drosophila*. Instead it forms membrane bound spheres early in development (Benton et al., 2013). We observed that yolk cleavage cycles align with germband pulsations, potentially influencing its elongation. Additionally, prior to dorsal closure, yolk spheres compact into a dense mass, exhibiting pulsations during this phase. Our research into extraembryonic membranes revealed repetitive contraction waves in the serosa preceding dorsal closure and persisting through withdrawal of extraembryonic membranes. Individual pulsations of amnioserosa cells are known for *Drosophila* (Solon et al., 2009), while in *Tribolium* we clearly detected propagating contraction waves. We suggest that this happens due to natural synchronisation effect (Mirollo & Strogatz, 1990). Emergence and propagation of contractile waves in serosa pose as an elegant example of self-organisation in biological systems. While the exact function of these contraction waves remains elusive, they seem to aid in withdrawal of extraembryonic membranes, with each wave accelerating the withdrawal process.

These findings underline the significant role of extraembryonic structures in insect morphogenesis, emphasising the need for further exploration in this area.

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* Student (eligible for the Student Awards)

Phoretic *Poecilochirus* Mites use Methyl-Alkanes as Kairomones to Identify their Burying Beetle Hosts

Ev40

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The stability of many symbioses depends on the recognition of symbionts, because recognition allows repeated interactions and thus the evolution of specialized traits. Because arthropods live in a chemical world, their recognition systems are often based on semiochemicals. We studied host recognition in the phoretic mite *Poecilochirus carabi*, which lives in close association with burying beetles of the genus *Nicrophorus*. The mites can actively select beetles for transport and are specialized to exploit one particular burying beetle species, but they are often found on related beetle species as well. We show that *P. carabi* selects among host species in a hierarchical manner that reflects the suitability of the beetle for mite reproduction. We further show that the mites use kairomones from the cuticle of their hosts to discriminate among potential host beetles. We separated the cuticular substances into different fractions and found that methyl-hydrocarbons are sufficient for the mites to find their preferred host species, while they do not appear to use any other class of substances.

Love your data

Ev42

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Research Data Management (RDM) is a fundamental part of daily research work and increasingly acknowledged as such. More and more funding agencies demand Data Managements Plans, the National Research Data Infrastructure (NFDI) is getting up to speed, and data stewards are hired.

With this slightly interactive talk I aim to raise awareness for this topic among researchers and provide them with terms and motivation to talk about and improve their data handling. Questions to ask yourself here are for example „How do I name my files so I can find them again?“, „What does this variable name stand for?“, or „Will I know in 6 months time how I measured this parameter?“.

Answers to these and many more are required to write a Data Management Plan and thus ultimately to acquire funding. Here, I will outline the basic concepts, benefits, and resources available to setup and maintain good data management in compliance with good research practice.

Remember: Documenting your research is like writing a love letter to your data. Love your data!

How gene accessibility orchestrates defenses in a freshwater gastropod

Ev51

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Phenotypic plasticity describes the ability of genomes to be able to produce multiple phenotypes based on environmental cues. The globally invasive freshwater gastropod *Physella acuta* is an established model system for phenotypic plasticity. Upon the perception of conspecific damage-released alarm cues, which are indicative of predation events, they plastically alter their behavior, morphology and life-history. Our project explores the epigenetic patterns underlying such phenotypic changes. Using a split-clutch design, we raise individual *P. acuta* from hatching onwards either in a high-risk environment (i.e., exposure to conspecific alarm cues) or a low-risk water control. At sexual maturation, we assessed their behavior and morphology and obtained genetic samples. With ATAC-sequencing, we will then measure patterns of chromatin accessibility in each individual. Applying our recent curated annotation of the *P. acuta* genome will allow us to first determine which genes are epigenetically enhanced or repressed. Second, we will be able to correlate patterns of chromatin accessibility with phenotype expression to identify the underlying mechanisms of antipredator phenotypic plasticity in our freshwater gastropod species.

* Student (eligible for the Student Awards)

Latitudinal Variation and Urban Evolution of Seasonal Plasticity

Ev53

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Urban environments are rapidly changing environments, hence, the organisms living there must adapt to the changes. Cities enable the study of rapid evolutionary processes as a response to environmental changes. One important kind of anthropogenic change in cities is altered seasonality. This can create mismatches between cues and environmental changes, leading organisms into developmental traps. For example, the Urban Heat Island effect warms environments, which might extend the growing season of the urban populations. Moreover, light pollution can create a perception of longer days, misleading organisms that rely on photoperiod for the timing of seasonal plasticity. In multiple taxa, differences between urban and rural populations have been demonstrated to evolve in a relatively short period of time. Comparing populations at different latitudes can lead us to understand how different populations respond to similar environmental changes or, alternatively, how populations respond to latitude-specific selection pressures.

To test the evolutionary response of *Pieris napi* butterflies to urban changes, we have collected female individuals of urban and rural populations associated with cities at different latitudes throughout Europe. We used their offspring in common garden experiments to analyze their photoperiodic reaction norms for diapause induction. These findings will reveal whether urban evolution in this trait stays consistent across different latitudes or if it varies with latitude due to increased light pollution's disruptive effects further south. With urban land cover expected to increase in the coming years, making urban evolution an important field of study, our results will provide valuable insights into how conservation and management strategies may need to vary among cities to better support organisms living in urban environments.

* Student (eligible for the Student Awards)

Recurring phenotypic loss, the evolutionary origins and developmental plasticity of scopae in bees

Ev55

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Corbiculate bees collect and carry pollen pellets on their corbiculae, located on the hind tibiae. The corbiculae (pollen baskets) are polished areas surrounded by fringes of long setae. Scopae serve a similar role in bee species without corbiculae. This trait is an evolutionary novelty and expressed in a sex- and caste-specific manner, demonstrating developmental plasticity. In several independent kleptoparasitic bee lineages, this trait has been lost. The repeated loss is an excellent model to study the developmental basis of evolutionary novelty, developmental plasticity, and phenotypic loss on the levels of genomes and transcriptional regulation.

In this study, we focus on the corbicula and two additional types of scopae. We will 1) sequence and assemble genomes from approximately 50 bee species, enabling comprehensive comparative analyses between kleptoparasitic lineages (phenotype lost) and their closest non-kleptoparasitic relatives (phenotype retained). This will yield insights into gene content (gene loss), gene family expansions/contractions, protein domain rearrangements, and selection, in particular relaxed selection within lineages where the phenotype has been lost. 2) We will study the transcriptional (RNA-seq) and epigenomic (ATAC-seq) regulation during development of the scopae, and compare kleptoparasitic lineages with those retaining the phenotype. For three pairs of host bees and kleptoparasite species, each representing different scopae and their evolutionary loss, we will obtain pupal tissue to study the regulatory landscape and differences, derive regulatory motifs and provide insights into the mechanisms controlling these evolutionary innovations.

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* Student (eligible for the Student Awards)

Recurrent genomic dynamics linked to parallel evolution of secondary phytophagy in Hymenoptera

Ev57

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The phytophagous lifestyle is a key innovation in insects and has evolved in only one third of all insect orders. The evolution of phytophagy likely involves fundamental behavioural and morphological changes accompanied by chemosensory and metabolic adaptations. To date, the genomic basis and genetic innovations related to evolutionary dietary shifts are poorly understood. Here we focus on two monophyletic groups within the Hymenoptera, Aculeata and Chalcidoidea, that secondarily developed larval phytophagy independently. To shed light on evolutionary processes that shaped the diversity of nutritional adaptations in Hymenoptera we address the following main research questions: (1) Is parallel evolution at the phenotypic level reflected by parallel genome evolution? And (2) did similar genomic innovations appear when independent lineages realized convergent dietary transitions? On my poster I want to present the goals, methods and the current status of the project. The latter will comprise first insights into newly sequenced genomes and preliminary results of a computational identification of novel genes for representative aculeates. Project results will be of major interest to scientists in the fields of functional genomics, systematic biology and protein function analysis of insects, including insects of economic importance.

* Student (eligible for the Student Awards)

Changes in visual acuity and sensory weighting reflects patterns of neural investment during ecological divergence in *Heliconius* butterflies.

Ev59

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As populations diverge across environmental gradients, the reliability of sensory modalities may change, favoring divergence in neural investment and sensory perception. Neotropical *Heliconius* butterflies provide an excellent opportunity to study how different sensory environments shape the sensory and neural systems during the early stages of divergence. *Heliconius cydno* from forests and *H. melpomene* from forest-edge habitats have evolved distinct brain morphologies and eye sizes, with the former investing more in vision. Molecular and anatomical studies suggest that these changes are driven by selection, but their behavioral effects remain uncertain. We hypothesized that differences in visual investment, associated with changes in habitat use, may lead to behavioral shifts such as differences in visual acuity (the ability to perceive detail) and sensory weighting. Tests based on an optomotor response assay revealed higher visual acuity levels in *H. cydno* compared to *H. melpomene*, as well as higher resolving power in males than females. Interestingly, we also found that visual acuity differs between age groups, with mature individuals exhibiting higher visual resolution. To assess whether these changes are associated with post-eclosion brain development, we compared volumetric changes in the optic lobe among young and adult individuals, as well as neuroanatomical differences between both species. Finally, to test differences in sensory weighting, we trained individuals in an associative learning experiment using both colour and odour cues. When positively rewarded stimuli were presented in conflict, i.e. pairing positively trained colour with negatively trained odor and vice versa, *H. cydno* prioritized visual cues more strongly than *H. melpomene*. Our results suggest that differences in visual performance and sensory weighting may evolve early during divergence and are predicted by neural investment. These findings highlight how sensory adaptations can influence behavioural shifts contributing to behavioural isolation and ultimatively, speciation.

* Student (eligible for the Student Awards)

Does sessility simplify nervous systems? A case study in Annelida

M30

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Some animals such as ascidian tunicates are prominent examples for a correlation between simplification of the nervous system and sessility. Pelagic larva of the species possess a much more complex nervous system than the adult sessile form. The anatomical complexity of a nervous system is influenced by the environmental challenges and the lifestyle of a species. Accordingly, vagile, predatory animals are expected to have a more complex neuroanatomy than sessile, filter-feeding species. Annelids are ideal to test these assumptions. Recent phylogenomic analyses show that sessility is an ancestral trait, maintained in the basal most branching annelids, like in oweniids and chaetopterids. According to these analyses, certain higher annelid taxa, like sabellids, secondarily returned to sessility. By comparing the brain structures of these taxa, one would expect (1) that the brain structure of vagile species is more complex than that of sessile species and (2) that secondary sessility simplifies the brain structure, probably in such way that it is similar to primarily sessile species in terms of character reversals. We therefore generated complete series of Azan-stained histological sections of the brain of approximately 80 annelid species from different subgroups. We used aligned stacks to reconstruct the anatomy of the central nervous systems and to infer the evolution of this organ system based on recently published molecular phylogenies. Additionally, we performed ultrastructural investigations on chosen taxa. We can show that the brain of vagile species turned out to be highly complex, while basally branching sessile groups possess a simple basiepidermal, ring-like brain. In contrast to our expectation, secondarily sessile species possess a brain that is far more complex than that in basally branching taxa. This result advises caution about interpreting observed correlations as examples for general rules or causal relations.

Morphology and ultrastructure of tarsal organs in *Scutigera coleoptrata* (Chilopoda)

M32

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Arthropod legs are an evolutionary key innovation, as they take up a vast diversity of morphologies and functions beyond locomotion. Transformations are particularly evident when it comes to food capture and uptake, communication, copulation and reception of various stimuli. Moreover, certain arthropod appendages can take up multiple functions, seen in e.g. locomotory legs in flies that can also taste and stick to smooth surfaces. In centipedes, evolutionary transformed appendages, such as their ultimate legs (their last pair of legs) are known to possess morphological adaptations for diverse functions like sensing, predator avoidance or presumably pheromone production. However, little attention has been given to "ordinary" locomotory legs. House centipedes (Scutigeromorpha) possess fourteen pairs of locomotory legs with elongated tarsi (the fifteenth pair is the ultimate legs). The tarsus 2 can exhibit up to 25 annuli that are covered with cuticular specializations including many trichomes. Ventrally, each annulus houses clusters of long obelisk-shaped sensilla, shorter hitherto unknown sensilla, as well as beak-shaped sensilla, also known from the antennae. We present anatomical details on these structures and focus on a new type that is associated with a massive glandular tissue, comparable to was has been shown in geophilomorph ultimate legs. However, this type is a combination of sensory and glandular elements, comprising two sheath cells (one with massive secretory activity) and a conducting canal connected to the sensillum's shaft. Five to seven receptor cells innervate the glandular elements and project as cilia into a conspicuous central mass. The function of this sensillar/glandular organ is still unknown, however, based on our ultrastructural results, we discuss probable mechanisms such as adhesion.

Form and Function of the Neck-Trunk Boundary in Artiodactyls

M34

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Exemplified by the iconic long neck of giraffes, artiodactyls exhibit strikingly variable neck lengths while maintaining the usual mammalian count of seven cervical vertebrae. To gain insight into the evolutionary morphology of the neck and specifically its boundary to the trunk, we used an integrative investigation at the interface of form, function, and evolution. We leveraged non-destructive imaging techniques to conduct a clade-wide comparative and quantitative analysis of 3D shape and structure within a phylogenetically informed framework. Computational modelling of the form-function relationship identified performance differences, in terms of a potential trade-off between joint mobility (assessed by range of motion analysis) and vertebral robustness (assessed by finite element analysis) across a comparative dataset of artiodactyl species (N=32). This combined analysis not only revealed new insight into the unique morphology of the giraffe's neck-to-trunk boundary, but, more generally, also shed light on the evolutionary dynamics of artiodactyl neck evolution.

M36

Exploring moving fish hearing structures: Tomographic Imaging using an experimental standing wave tube-like setup and its implications for aquatic research

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The morphological composition of hearing structures in modern bony fishes has been studied for centuries. Fishes show a considerable variation in the morphology of their auditory system, structures and their auditory capabilities. However, the precise interaction and contribution of individual structures to enhanced hearing remain unclear. Experimental evidence on the in-situ motion of fish auditory structures and their interrelations, while avoiding invasive damage through direct intervention, is limited. A new method was required to non-invasively visualize the movements of fish auditory structures. Synchrotron radiation-based tomography has enabled the investigation of morphofunctional relationships in biological systems with unprecedented spatial and temporal resolutions, offering a non-invasive alternative to traditional methods. We designed a miniature standing wave tube-like setup to meet both the requirements of tomography and those of tank acoustics. Previous attempts have already characterized moving fish auditory structures using radiography. Our current setup allows for a highly precise and improved adjustment of the acoustic field within the test tube. Sound Pressure Levels (SPLs) were now determined and adjusted during the tomographic measurements and phases were precisely regulated to project maximum sound pressure or particle motion at the center of the test tube. Additionally, we were able to generate and measure frequencies up to 2kHz that fall within the relevant hearing spectrum of fish. With this updated setup, we successfully visualized the dynamic interactions and movements of fish auditory structures in response to acoustic stimuli. This advancement not only enhances our understanding of fundamentals in fish bioacoustics but also sets a new standard for non-invasive, high-resolution imaging techniques in the field of aquatic sensory biology.

Effects of inducible defences and environmental factors in *Daphnia* predator-prey interaction

M38

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The freshwater crustacean *Daphnia* is well-known to adapt to changing predator environments by forming phenotypic plasticity, especially inducible morphological defences. While defensive behavioural and morphological traits have already been described in many species, the actual mode of action reducing the predation rate is unknown in almost all of them. This is e.g., the case in *D. longicephala*, an Australian species known to form an exuberant head morphology protruding the back of its head to a crest-like structure in the presence of the backswimmer *Notonecta*. Using morphological measurements of the crest and the second antennae, we found that the so-called antenna parachute, crucial for locomotion, is increased in *Notonecta* presence. In behavioural studies we detected that the crest, like a keel, appears to reduce the left-right deviation during swimming, potentially reducing the perceptibility of *D. longicephala* to *Notonecta*. With the recorded predation trials under different light and acoustic settings, we also determined the role of the crest in direct predator contact by investigating the puncture sites, revealing a so far undescribed defensive feature of the crest. In our experiments, *Notonecta* appeared to be mainly visually guided, but can also hunt successfully in absolute darkness. Therefore, we also used particle image velocimetry (PIV) to visualize and compare the flow fields around defended and undefended *D. longicephala* to understand the cues *Notonecta* relies on in darkness. Based on these results we get deeper insights into the influence of morphological defences and environmental factors on predator-prey interaction between *D. longicephala* and *Notonecta*.

Ontogenetic development of the shoulder joint and forelimb muscles in *Xenopus tropicalis* (Gray, 1864)

M43

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It has recently been revealed that there are inaccuracies in the naming and homologization of shoulder joint muscles within frogs and toads (Lissamphibia: Anura) and that muscle ontogeny and innervation are valuable to derive hypotheses on muscle homology. So far, the clawed frogs (*Xenopus* Wagler, 1827), a genus that is of particular interest because of its routine use as model organisms, has not been investigated in this context. To fill this knowledge gap and expand previous work by the muscles of the forelimb, the ontogenetic development, innervation, and morphology of the shoulder joint and arm muscles were described based on tadpoles of *Xenopus tropicalis* (Gray, 1864) (Nieuwkoop and Faber stages 53 to 65). Digital dissections of volumes acquired by histological serial sectioning were performed and three-dimensional reconstructions were derived. The results indicate that, like in all tetrapods, the muscles of the shoulder joint and forelimbs are ontogenetically derived from the dorsal and ventral pre-muscle masses in the developing limb bud. During ontogeny, these pre-muscle masses split up and differentiate into individual muscles. With regard to the muscles crossing the shoulder joint, the mm. anconaeus, dorsalis scapulae, latissimus dorsi, and the group of scapulohumeralis muscles derive from the dorsal pre-muscle mass while the mm. cleidohumeralis, episternohumeralis, supracoracoideus, coracoradialis, subcoracoscapularis, coracobrachialis and pectoralis originate from the ventral pre-muscle mass. In the same way, divisions of these two pre-muscles masses also give rise to the muscles of forelimbs, which make up those of the upper arm, forearm, and hand.

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* Student (eligible for the Student Awards)

New insights on the biodiversity and distribution of Xanthidae on the East African Coast

M45

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Brachyuran crabs are a dominate part of the eu- and sublittoral of marine cohabitations in the west Indian ocean. In order to understand the biodiversity and evolution of a region and to be able to assess and recognize current changes, a sound knowledge of the diversity and distribution of individual species is essential. Adult brachyuran crabs are well suited for these investigations due to their small range of movement. The aim of this project was to gain new information on the distribution of brachyuran crustaceans in the western Indian Ocean, using their largest family, the Xanthidae, as an example. Due to their species richness and wide distribution, Xanthidae are an ideal indicator to gain new information on marine habitats of the African east coast.

The investigations are based on historical collections from the Zoological Museum Kiel and the Museo di Storia Naturale dell'Università di Firenze, which have not yet been analysed. They document the fauna of the East African coastal waters from Egypt to Tanzania in the period between 1875 and 2006. The results provide new insights into the speciation processes and distribution of the Xanthidae as well as the comparability of the regional diversity of East African eu- and sublittoral habitats.

* Student (eligible for the Student Awards)

Function of *D. longicephala*'s defensive crest thwarting *Notonecta*

M47

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Many species of the genus *Daphnia* are well know for their ability to thwart perdators by developing defensive morphologies. *Daphnia longicephala* for example forms an extensive crest in response to the presence of the predator *Notonecta*. These crests make *D. longicephala* less prone to predators and thereby increase organism fitness. However, the mechanisms through which the crest protects *D. longicephala* from *Notonecta* predation is not understood. It was previously hypothesized that the distinct body shape that the crest generates, imposes handling difficulties on the predator, through which *D. longicephala* have better chances to escape the predator's grasp. Because of this we then documented the site where *Notonecta* initially stings *D. longicephala*. In fact, *Notonecta* stings the crest significantly more often than other body parts. We manually mimicked these punctures with a fine needle and penetrated the crest. These wounds healed efficiently and did not reduce *D. longicephala* survival. These results indicate that the crest directs the attacks away from the vulnerable body parts to the invulnerable crest, thereby increasing escape chances during predator handling. These observations add a plausible explanation to the array of hypotheses on the function of the defensive crest in *D. longicephala*.

* Student (eligible for the Student Awards)

Ecology in deep time: Morphological specialisations of predatory and anti-predator strategies of insects in the fossil record

M49

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Insects are a very important part of ecosystems today and most likely were in the past as well. It is crucial to reconstruct potential ecological roles of fossil insects to better understand the evolution of ecosystems and food webs. There are approaches that are useful in reconstructing predator-prey interactions, such as investigating 1) group fossilisations and ‘frozen behaviour’, 2) morphological specialisations, 3) trace fossils, and 4) the phylogenetic position. Cases of group fossilisations contain several individuals fossilised in close connection. If these organisms are fossilised in a specific moment of interaction, these can fall into the category ‘frozen behaviour’.

Morphological specialisations in this context can be specific structures or appearances that are associated with a predatory or defensive lifestyle. Predatory specialisations that occur in insects can be predatory appendages, like e.g. the raptorial forelegs of praying mantises (Mantodea). Defensive specialisations can e.g. be structures associated with evasion tactics, like e.g. the enlarged hindlegs of grasshoppers (and relatives; Orthoptera) for jumping (away). Specific structures may also be associated with both predatory and defensive lifestyles, e.g. camouflage. Trace fossils that may give hints towards past predator-prey interactions are e.g. fossilised regurgitate or coprolites (fossilised excrements) which may indicate predation pressure on the contained prey organisms.

The phylogenetic position of insects gives hints towards potentially exhibited lifestyles (phylogenetic bracketing concept), but is best used in combination with the approaches above, as comparison with extant animals is necessary to interpret morphological structures and reconstruct potentially associated lifestyles of fossil insects. Here we present several fossil insects from Cretaceous to Cenozoic localities (100-35 Million years ago) that show different types of morphological specialisations towards a predatory and defensive lifestyle and also cases of frozen behaviour associated with predator-prey interactions and discuss implications of the evolution of these ecological strategies over time.

* Student (eligible for the Student Awards)

Bumblebees trade off costs and benefits of multi-cue learning and decision-making in a foraging task

N04

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When animals and humans make decisions based on their sensory input, they often rely on multiple cues at once. These provide complementary sources of information, which can help overcome ambiguity and noise, and increase the accuracy of decisions. While most studies have focused on the benefits of multimodal and within-modal integration for learning and decision making, their costs have received less attention. Processing multiple inputs, and learning and memorizing them requires more neural resources than single cues, and might also require more time. When a decision can be made with high accuracy based on a single cue alone, adhering and memorizing multiple ones simultaneously might thus concur higher costs than benefits, and not be an optimal decision-making strategy.

In this study, we explicitly tested if insects trade-off the costs and benefits of learning multiple cues in a foraging task, using the buff-tailed bumblebee *Bombus terrestris*. To maximize comparability between cues, we presented combinations of visual-only features, such as are found on real flowers: colours of varying discriminability, paired with shapes or patterns. We found that the bees relied exclusively on colours when these were easy to discriminate, and did not learn pattern or shape features presented simultaneously. With harder to discriminate colours, the bees learned both colour and shape or pattern features, and relied on the colours to a much smaller degree when these were set in conflict with patterns or shapes. Our results demonstrate that bumblebees flexibly adjust their learning strategies when presented with visual features of varying discriminability, to balance the costs and benefits of multi-cue learning. When cues are easy to discriminate, they trade off increased information for learning speed, and rely on single cues, while they learn and base their decisions on multiple cues under more ambiguous conditions.

Pioneering Genome Editing in Stick Insects: CRISPR/Cas9-Mediated Genetic Modifications in *Medauroidea extradentata*

N06

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Stick insects have long been used as experimental animals to investigate the neural basis of locomotion and belong to the most thoroughly studied creatures in that respect. Experimental work would markedly profit from an in-vivo visualization or identification of neuron classes within the central nervous system, for which molecular genetic interventions are needed. Despite their relevance to study the neurobiology of complex behaviors, and the accessibility of their nervous system, genetic tools for the manipulation of their neurons haven't been developed until now, even though their parthenogenetic life cycle offers unique advantages. Here, we successfully implement Clustered Regularly Interspaced Short Palindromic Repeats/Cas associated protein 9 (CRISPR/Cas9) as a technique to modify the genome of the stick insect *Medauroidea extradentata*.

As proof of concept, we targeted genes involved in the ommochrome pathway of eye pigments transport and formation (cinnabar and white), performing eggs microinjection within 24h after oviposition to generate knockout (KO) mutants. Cinnabar and white KO resulted in distinct eye and cuticle colour phenotypes. Homozygous cinnabar KOs showed pale pigmentation of eyes and cuticle, while white KO was lethal to developing embryos, which display a completely unpigmented phenotype.

In conclusion, we showed that CRISPR/Cas9 can be successfully applied on the genome of *M. extradentata* by creating phenotypically different and viable animals. This genetic toolbox can now be implemented to create genetically modified lines to enable further unravelling of motor control using state-of-the-art methods in a parthenogenetic upcoming model organism.

Isogenic vs. non-isogenic crayfish: Establishing a microCT based pipeline to compare variability in numbers of olfactory glomeruli

N11

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The olfactory lobes of aquatic crustaceans are the primary centers for olfactory processing and are structured/subdivided into complex subunits, the so-called olfactory glomeruli, areas of high synaptic density. Their morphology and number can vary between crustaceans but also between individuals of one species. Differences in number of glomeruli are thought to mirror differences in their ability to discriminate olfactory stimuli. We currently investigate to what extent these inter- and intraspecific differences in number of glomeruli are driven by the genetic background and ask the question whether isogenic crayfish have a less variable phenotype of their olfactory system than non-isogenic crayfish possibly linked to their lack of genetic diversity. We will compare the olfactory system of the parthenogenetic marbled crayfish (*Procambarus virginalis*; Lyko, 2017) with its close relative, the sexually reproducing *Procambarus alleni* (Faxon, 1884); both reared under similar controlled experimental conditions. In order to clearly differentiate the glomeruli within their olfactory lobes and thus quantify them, we chose X-ray micro-computed tomography (µCT) which has proven to be a fast and non-invasive method for analyzing the neuroanatomy of crayfish. We performed an exploratory series of protocols for determining the optimal sample preparation using different fixatives and staining agents. So far, phosphotungstic acid (PTA), in our hands, has proven to be an ideal contrast agent to identify and thus quantify smaller structures such as glomeruli. After establishing a suitable method for quantifying the glomeruli in *Procambarus virginalis* and *Procambarus alleni*, we want to shift our focus on identifying individual cellular elements in the sensory system of these animals.

* Student (eligible for the Student Awards)

When winters get warmer – effects on metabolism and fatty acids in overwintering *A. bruennichi* spiderlings (Arachnida, Araneae)

Ec16

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Climate change has ecological effects ranging from the individual level to the entire ecosystem. Little is known about the specific effects of climate change on overwintering arthropods, although higher temperatures can influence individuals’ metabolism and energy balance. We investigated the effect of increased winter temperatures on the warm-adapted populations of the spider species *Argiope bruennichi* in Southern France. In *A. bruennichi*, spiderlings hatch from eggs and overwinter in the egg sacs with a limited amount of yolk. We hypothesize that increased overwintering temperatures influence the spiderlings´ metabolic rate, which in turn affects fatty acid consumption and survival probability. To this aim, we exposed egg sacs with spiderlings to two warmer winter treatments (+3.7 and +4.8 °C) as projected by the IPPC and compared them to a control treatment (average temperature over winter). We demonstrate that mortality increased with higher ambient temperatures, with no difference between the two warmer treatments. The metabolic rate was higher in the warmer treatments and was correlated with a significant reduction in energy-storing fatty acids such as saturated and monounsaturated fatty acids. We suggest that the decrease in energy stores led to higher mortality. Consequently, even small increases in winter temperatures, as chosen here, are likely to impact *A. bruennichi* on both individual and population levels, possibly leading to a shift in the range of this abundant species.

Non-linear effects of fungicide on Collembola reproduction and microbiota

Ec18

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The use of pesticides poses a significant threat to biodiversity, including belowground habitats. While the targeted effects of specific pesticides, such as insecticides, are well-documented, the indirect effects mediated through third-party interactions remain less understood. Springtails (Collembola) are soil dwelling hexapods. They make good model organisms, because of their cosmopolitan distribution and their role in soil microbiota regulation, thus directly influencing soil biodiversity. This study investigates whether the widely used fungicide Fontelis 20 SC (active ingredient penthiopyrad) influences the expression of life-history traits in soil-dwelling Collembola (*Folsomia candida*) by potentially affecting their microbial symbionts residing the animals' gut. We observed juvenile number, egg size, egg number, reproduction investment and hatching success. A miniaturized Collembola reproduction test was conducted; then the animals were transferred to plaster for 10 days. To collect fecal material, a parallel population was fed on filter paper on both soil and plaster, so the fecal material could be collected. We used 16S-markergene for taxonomic identification of the bacterial community. Our results indicate that intermediate concentrations of the pesticide exerted the strongest impact on microbial diversity. Notably, these concentrations also represented a critical threshold for the expression of several reproductive traits in Collembola. At this concentration, juvenile number changed from increase to reduction. The hatching success had shown no sign of toxicity whereas lower and higher pesticide concentrations led to reduced hatching success. Reproductive investment was highest at this concentration, while investment was not increased in the neighbouring concentrations. The first results indicates that the non-linear toxicity was likely driven by the non-linear changes in the collembola gut microbiota. In conclusion, soil biodiversity as fostered by Collembola species may be driven by pesticide usage, affecting the microbial community within and around the host.

When winters get warmer: Impact of increased winter temperatures on body condition of overwintering *A. bruennichi* spiderlings (Arachnida: Aranae)

Ec19

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Climate change and global warming affect species distribution, phenology, and survival. The orb-weaver *Argiope bruennichi* has undergone rapid latitudinal range expansion from southern Europe to Scandinavia in the last century. Previous studies have investigated adaptation and plasticity to colder climatic conditions in the northern regions. However, it remains unclear how spiders of the core populations in the Mediterranean will react to warmer temperatures. We explored whether warmer winters affect the body condition of *A. bruennichi* spiderlings that overwinter in the egg sac. Adult females were collected after mating and before oviposition from three locations in southern France. They produced egg sacs under a simulated local temperature regime in the laboratory. Three temperature treatments were simulated: control, warmer (+3.7°C), and even warmer (+4.8°C). Spiderlings hatched inside the egg sacs within a few weeks and stayed there over winter. Egg sacs were randomly assigned treatments. At the beginning of spring, the egg sacs were opened. We investigated the body condition of the living spiderlings using light microscopy and µ-CT. Spiders that underwent either of the warmer winter treatments had a similar body size but a lower body condition index compared to those in the control temperature. We, therefore, surmise that spiderlings that experienced the IPCC-predicted warmer winter conditions will emerge in spring with fewer resources that may impact their viability. Thus, we anticipate a trailing edge of this abundant species in the south, leading to unforeseeable ecological consequences.

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* Student (eligible for the Student Awards)

Cuticular hydrocarbon plasticity does not affect chemotype stability in an insect using polymorphic CHC profiles for sexual communication

Ec21

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The cuticula of insects is covered by a layer of lipids, primarily hydrocarbons. Cuticular hydrocarbons (CHCs) protect the insect from desiccation, while the species-specific CHC profiles can additionally be used for within-species communication. Successful communication requires stable signals. In contrast, CHC profile plasticity in response to high temperatures or dry conditions may be essential to prevent desiccation. Enzymes involved in the biosynthesis of CHCs are genetically determined; however, internal and external factors may influence the regulation of these pathways. To understand the effects of CHC profile variability on communication, it is necessary to first disentangle the influences of genetic and other factors. Here, we studied *Tachinaephagus zealandicus*, a parasitoid wasp that uses CHCs in mate recognition and in which females exhibit a CHC profile polymorphism with three distinct chemotypes. We investigated CHC heritability, and variability in response to four factors (age, mating status, host species, and temperature during development). Chemotypes remained distinct across the four tested factors, indicating a genetic basis for the polymorphism. Chemotype variability was only influenced by age and temperature. Age-dependent changes in CHC composition may be important for mate recognition by signaling the state of sexual maturity of individuals. Changes in CHC composition related to temperature may be an adaptation to climatic conditions, which could affect CHC-based communication. Future bioassays shall investigate the potential trade-off of the dual role of the CHC profile in this species.

* Student (eligible for the Student Awards)

Interaction of *Bryacis puncticollis* (Staphylinidae: Pselaphinae) with Ants (Hymenoptera: Formicidae)

Ec23

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Pselaphinae represent a species-rich subfamily of Staphylinidae (ca. described 10,000 sp.) with extreme morphological disparity unparalleled in Coleoptera. A notable aspect of their biology is myrmecophily -the intricate relationships they maintain with ants (Hymenoptera: Formicidae). These beetles often reside in ant colonies or live closely associated with ants by sharing their habitat. While there is information on the morphological adaptations in Pselaphinae towards a myrmecophile lifestyle, particularly their body development into a limuloid direction, little is understood about potential chemical defenses in these beetles. Unlike other staphylinids, pselaphines exhibit a loss of abdominal defensive glands, raising questions about their survival strategies within ant-dominated habitats.

We hypothesize that Pselaphinae may possess an alternative chemical defense mechanism to ward off ant predation, compensating for the absence of abdominal defensive glands. Although *Bryaxis puncticollis* exhibits morphological adaptations towards a myrmecophilous lifestyle; their role as myrmecophiles or hemi-myrmecophiles remains unknown. To investigate the interactions between *B. puncticollis* and ants, we used different camera setups including high-speed vidiography to observe, analyze, and quantify noticeable reactions by the ants after contact with *B. puncticollis*. Our experimental runs showed that after contact, ants entered a nervous state and exhibited antennal grooming behavior, suggesting a potential chemical defense mechanism in the beetle.

To explore a possible correlation between ant reactions upon contact and morphological features, we captured images of *B. puncticollis* using a scanning electron microscope, where we found secretions inside foveal openings of *B. puncticollis*. This could imply that *B. puncticollis* indeed possesses a chemical defense. However, this defense is not associated with abdominal defensive glands, as in other staphylinids, but with the foveal thoracic openings. Although these results are intriguing, more experimental runs are needed to better understand these interactions and the connection between the secretions and the foveal pits found on Pselaphinae.

* Student (eligible for the Student Awards)

Do coexisting fruits flies form species-specific symbiont microbial communities?

Ec25

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Independent intraspecific aggregation across fragmented resources mediates the coexistence of different species in a shared ecological niche, for example, different *Drosophila* species utilizing the same plant substrate as breeding sites. While the "aggregation model of species coexistence" does not assume niche separation, locally established symbiont microbiota may lead to species-specific habitats affecting larval development differently. We hypothesize that during their life cycle, *Drosophila* form species-specific associations with symbiont bacteria and fungi, which benefit their own but not the development of other species. This was tested on both apple and tomato substrates using three *Drosophila* species, *D. melanogaster*, *D. hydei*, and *D. immigrans* and their associated microbiota. Larval survival, development time, and weight of the flies reveal species-specific and context dependent responses to microbiota origin. These findings add a symbiont-mediated mechanism driving species coexistence in a shared environment.

* Student (eligible for the Student Awards)

Do *Drosophila* larvae have chemical control over their microbial symbionts?

Ec27

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The interactions between larvae and their microbial environment are key to the survival and development of *Drosophila melanogaster*. The ability to selectively control the growth of microorganisms and thus shape the functional properties of their microbiota may positively influence larval development. While it is known that the presence of larvae affects the growth and composition of bacteria and fungi in decomposing fruit, the specific factors responsible for these effects remain unknown. We hypothesize that, in addition to their physical presence, larvae may induce chemical changes in the substrate, thereby influencing the substrate-associated microbiome. To investigate the potential for chemical interactions, we conducted experiments monitoring yeast growth in the presence and absence of larval excretions. Preliminary results indicate that larval excretions can delay yeast growth, suggesting that *D. melanogaster* larvae may disrupt microbial growth and dynamics not only by moving through the substrate but also by secreting chemical compounds.

* Student (eligible for the Student Awards)

Differential adaptation strategies of bacteria and fungi in earthworm gut under diverse litter support the paradox of enrichment hypothesis

Ec29

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Georg-August-Universität Göttingen, Germany

Understanding the adaptation strategies of bacteria and fungi in earthworm guts is essential for elucidating soil microbial ecology. However, the response of these microbial communities to varying litter qualities remains poorly understood. We investigated the diversity and stability of bacterial and fungal communities in foregut, midgut, hindgut, soil, and litter samples using high-throughput next-generation sequencing (NGS) analyses in a microcosm experiment with two earthworm species (*A. caliginosa* and *L. terrestris*) and two litter types (rape leaves and wheat straw). Our results revealed that bacterial alpha diversity in the gut was consistently lower than in soil but higher than in litter. In contrast, fungal alpha diversity varied significantly with litter type, being higher in wheat straw compared to rape leaves. Furthermore, bacterial communities exhibited greater flexibility in gut adaptability compared to fungi. Network analysis showed that wheat straw treatment resulted in microbial communities with higher negative correlations, clustering coefficients, and weighted degrees, suggesting increased stability compared to rape leaves. Overall, our study provides novel insights into the microbial ecology of earthworm guts and their interactions with soil and litter environments, extending our understanding of the microbial mechanisms in earthworm guts in response to different litter qualities.

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* Student (eligible for the Student Awards)

Influences of the antidepressant Sertraline on the freshwater crustacean *Daphnia magna*

Ec31

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Global change continuously impacts freshwaters world-wide. Especially the continuous release of micropollutants such pharmaceuticals of the antidepressant type are continuously being released into freshwater habitats due to increasing prescription rates and low removal rates in wastewater treatment plants. In consequence, concentrations in lakes, rivers and ponds are rising continuously. However, the effects of the widely prescribed antidepressant sertraline on freshwater specimens are mostly unkown. We here investigate the effects of the sertraline and predator presence on the morphology and behavior in the model freshwater crustacean *Daphnia magna*. We first determined the effective concentrations (EC50) for the three *Daphnia magna* clones in an immobilization test. Based on the EC50 values we exposed juvenile *D. magna* to low concentrations of sertraline as well as predator kairomones and determined growth rates, and activity patterns over a period of 5 days. We found *D. magna* growth rates were significantly slowed down. In line, sertraline exposed *D. magna* clones showed significantly slower swimming velocities. Furthermore changes in predator perception and development of inducible defenses were observed.

We conclude, that sertraline does have an impact on juvenile development, behaviour and predator perception in different *D. magna* clones. Here we provide a first insight on how antidepressants like sertraline affect freshwater organisms on multiple levels.

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* Student (eligible for the Student Awards)

Establishment of a bioassay to investigate predator-induced escape behaviour of macroinvertebrates in riverine ecosystems

Ec33

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In rivers, drift is one of the most important modes of locomotion for macroinvertebrates. It is used to search for food, to colonise new habitats or to rapidly leave an area in the event of disturbance, for example by predators. Evading potential predators such as fish is vital for many invertebrates. In response to predation pressure, aquatic invertebrates evolved the ability to perceive and respond to kairomones emitted by fish. When fish kairomones are perceived, defenses are induced. These defenses include escape behavior by drifting with the water flow or a reduction in this drift behavior and hiding from predators.

Environmental factors can potentially influence kairomone perception and therefore, the defense mechanisms against predators. Since altered drift behavior can have a major impact on the interactions between species in ecosystems, it is essential to understand the process of drift, the substances involved, and how they are influenced by environmental factors. However, so far only a few substances have been identified as kairomones and previously applied experimental setups for experiments with stream invertebrates are prone to environmental disturbance and therefore, unsuitable for setup and implementation under controlled laboratory conditions.

Therefore, in this work, a new system was developed in which the drift behavior of macrozoobenthos invertebrates from rivers can be researched. In the future, this system will be used to analyze substances for their ability to influence drift behavior. To validate if changes in drift behavior can be detected in the developed system, the influence of several fish species across different macrozoobenthos taxa was examined. Our results show that the system is suitable for some invertebrate taxa under certain conditions and that changes in drift behavior can be detected.

* Student (eligible for the Student Awards)

Effect of fluctuations in CO_2 partial pressure (pCO_2) on the development of predator-induced defenses in the freshwater crustacean *Daphnia longicephala*

Ec35

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Human activities release CO_2 into the environment, which builds up in the global carbon cycle and is expected to disrupt global carbon fluxes. Through ongoing human activities such as land-use changes, agricultural runoff, and rising temperatures, CO_2 concentrations in freshwater lakes are increasing. In lab experiments a continuously high CO_2 partial pressure (pCO_2) was shown to have a profound impact on the transcriptional, physiological, and behavioural responses of different aquatic organisms. For example, the freshwater crustacean *Daphnia* showed a reduced ability to defend against predators due to impaired sensory capacities. However, aquatic pCO_2 levels are never stable but fluctuate due to several dynamic processes e.g. with diel dependent changes in respiration and photosynthesis. We hypothesized that fluctuations in pCO_2 levels may have weaker effects in comparison to in continuously increased pCO_2 levels, as low pCO_2 phases could be used as recovery phases.

We analyzed the effect of fluctuations in aquatic pCO_2 by exposing *Daphnia longichephala* to distinct changes in pCO_2 levels incomparison to norm pCO_2 and constantly elevated pCO_2 levels. We then measured *D. longicephala*'s ability to develop defensive crests by exposing them to their predartor the heteropteran *Notonecta* spec.. Both continuous and fluctuating pCO_2 levels reduce the defenses in a similarly strong manner. These results again show that rising pCO_2 in freshwater environments negatively affects predator sensitivity in *D. longicephala*. pCO_2 fluctuations affect defence development as strongly as continuously high pCO_2 so that low pCO_2 levels during fluctuating conditions cannot be used recovery periods. Rapid and unpredictable changes in pCO_2 can cause physiological stress in freshwater species. Fluctuation e.g. may disrupt homeostasis, forcing organisms to constantly expend energy to maintain internal balance, which can impair growth, and reproduction. The energy diverted to cope with these fluctuations may be energy that is not available development of defensive features.

* Student (eligible for the Student Awards)

Medium-term effect of mowing on spiders (Araneae) in agricultural grassland

Ec37

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Several studies have shown that a large proportion of spiders and insects living on agricultural grassland are damaged and/or killed during mowing. It can therefore be assumed that intensive mowing of agricultural grassland, which damages not only adults but also larvae and nymphs, has led to an “overfishing effect” that has contributed to the current decline of arthropods on agricultural grassland. In the light of the ongoing loss of biodiversity, the interdisciplinary project “InsectMow” aims to gain a deeper understanding on the direct, medium-, and long-term effects of mowing by testing various mowing techniques and their effects on spiders as well as important pollinators, herbivores, and predatory insects. As part of the “InsectMow” project, we have investigated the medium-term effects (2-4 weeks after mowing) of a conventional disc mower versus a double-blade bar mower on the spider fauna of agricultural grasslands in South Germany. We captured eight spider families (7,988 individuals) using standardized sweep net catches and pitfall traps and directly compared (a) an unmown control, (b) a double-blade bar mower, and (c) a disc mower. We could show that the most abundant families in the pitfall traps, Lycosidae and Linyphiidae, were little affected by mowing, as similar numbers of individuals were recorded in unmown and mown plots both two and four weeks after mowing. However, fewer individuals were found in the mown plots by sweep netting, with Thomisidae being the most abundant family.
This demonstrates the importance of complementary sampling methods for investigating the medium-term effects of mowing as well as considering the diverse ecology of different arthropods. Importantly, it also highlights that generalized statements about the effects of mowing must be treated with caution, as various arthropod groups, e.g. spiders are affected by mowing to different degrees.

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* Student (eligible for the Student Awards)

P24

Diversity of hirudins and hirudin-like factors in *Hirudo troctina*, the North-African medicinal leech

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The genus *Hirudo* comprises at least seven different species, namely *Hirudo medicinalis* (Linnaeus 1758), *Hirudo verbana* (Carena, 1820), *Hirudo orientalis* (Utevsky and Trontelj, 2005), *Hirudo nipponia* (Whitmann, 1886), *Hirudo sulukii* (Saglam, Saunders, Lang and Shain, 2016), *Hirudo tianjinensis* (Liu, sp. nov.) and eventually *Hirudo troctina* (Johnson, 1816). The hematophagous leech is exclusively found in the northwestern regions of Africa and the southern Iberian peninsula. Despite being used in leech therapy for a long time, the anticoagulant repertoire of *H. troctina* remained largely unexplored. The aim of our project was hence to identify and functionally characterize putative hirudins and hirudin-like factors (HLFs) of *H. troctina*. Our data indicate that the genome of *H. troctina* comprises at least 11 different genes that encode four putative hirudins and eight HLFs, respectively. Most strikingly, we revealed the presence of three chimeric (or hybrid) hirudin and HLF genes that are composed of exons and introns of various origins. The diversity of hirudins and HLFs in *H. troctina* is remarkably high compared to the European members of the genus *Hirudo*.

Investigations on the Sex-Dependence of DIPA-CRISPR in *Tribolium castaneum*

P26

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A novel CRISPR/Cas9-based technique termed DI(rect)PA(rental)-CRISPR was employed in *Tribolium castaneum* to facilitate gene-editing for physiological studies and pest management strategies. Tailored sgRNA-Cas9-RNP complexes are directly injected into the hemocoel of *T. castaneum* four days after pupal-adult molting. The resulting gene-editing effects, such as knock-outs or knock-ins, are observable in the subsequent generation. DIPA-CRISPR appears to involve a transmission pathway akin to parental RNA interference (RNAi), where injected dsRNA presumably enters the oocytes from the hemolymph during vitellogenesis, passing gene-silencing effects to the progeny. Consequently, both techniques were initially thought to be restricted to females due to the requirement for the injected molecules (dsRNA or sgRNA-Cas9-RNP) to be uptaken by oocytes. Using commercial Cas9 enzymes fused with viral nuclear localization sequences, we demonstrate that DIPA-CRISPR knock-outs of the tryptophan 2,3-dioxygenase encoding gene vermilion (VER) are not exclusively dependent on females. We injected VER-sgRNA-Cas9-RNP to both male and female beetles and mated them with un-injected beetles of the opposite sex. This experiment revealed successful knock-outs of VER in both sexes as indicated by the white-eye phenotype and sequencing. Additionally, we explored CRISPR by injecting VER-sgRNA-Cas9-RNP into 1.5 mg fourth instar larvae, further investigating potential applications of this gene-editing technique in biological studies and pest control. Our results show that the DIPA-CRISPR approach is suitable to establish stable functional homozygous genome-edited *T. castaneum* lines through both sexes.

P28

Metabolite profiling reveals energetic and osmoregulatory differences in *Mytilus* spp. populations from different salinity habitats

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Mussels from the *Mytilus edulis* species complex experience a salinity gradient from the North Sea into the Baltic Proper ranging from 32 to 5. As osmoconformers, mussels adjust their internal osmolarity to match that of their surroundings. This adaptive strategy poses a significant challenge to the metabolic machinery of the mussels, including their mitochondria. Thus, populations from different sites have adapted to reach their highest mitochondrial function at a salinity close to their respective habitat salinity. We hypothesised that this adaptation is accompanied by a change in accumulated metabolites. To test this hypothesis, mussels from three populations along the salinity gradient were assessed: north Baltic Sea (*M. trossulus* zone), south Baltic Sea (transition zone) and North Sea (*M. edulis* zone). Metabolites from gill tissue were measured via liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS) and their abundances were analysed using a principal component analysis (PCA) and pathway enrichment analysis (MetaboAnalyst 6.0). The measured metabolites separated the populations from one another either by osmoregulation or by energy metabolism. Additionally, the pathway enrichment analysis identified three pathways that differed between each population. γ-aminobutyric acid (GABA) was one of the main drivers of the population specific differences, along with amino acids that are directly or indirectly connected to the citrate cycle. The citrate cycle in turn feeds the mitochondrial electron transport system (ETS). Overall, our findings suggest population specific differences in osmoregulatory compounds, drivers of the citrate cycle as well as differences in the utilisation of sources for the mitochondrial respiration.

The role of oxygen for the thermo-tolerance of *Daphnia magna*

P44

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Increasing water temperature challenges poikilothermic aquatic animals as oxygen demand is exponentially increased while oxygen solubility declines. The oxygen and capacity limited thermo-tolerance model (OCLTT, e.g. Pörtner et al, 2017, J Exp Biol 220, 2685-2696) has, however, been questioned (Jutfelt et al, 2018, J Exp Biol 221, jeb169615).

For the planktonic crustacean *Daphnia magna* raised at various temperature and oxygen conditions, the effect of oxygen availability on its motility was analysed. The swimming activity index and the time of immobilisation (Timm) was determined under heat stress. Increasing the oxygen content of the water prolonged the animals' motility. The hemo¬globin content of the hemolymph was decisive, and enhanced oxygen transport capacity positively affected Daphnia's ability to tolerate elevated temperatures.

Accordingly, the results were in line with the oxygen and capacity limited thermo-tolerance hypothesis, showing that for this species the physiological performance in water of elevated temperature is closely linked to the oxygen supply of tissues and cells. Thus, physiological constraints can be assumed to determine the distribution and the ecological potential of these zooplankton key species also in its habitat.

Mitogenomics in Nemertea – uncovering the diversity of basal branches

S08

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In the majority of Metazoa, mitochondrial genomes contain a stereotypic set of genes, but the gene order of the circular mitochondrial genome is vastly diverse between different lineages. In Nemertea, a taxon of worm-shaped, mostly marine Spiralia, besides mitochondrial genomes of the derived neonemertean taxa Heteronemertea and Hoplonemertea, data are presently only available for one clade of the basally branching palaeonemertean taxa, the Archinemertea. With a genome skimming approach, we were able to significantly enlarge the database on complete mitochondrial genomes of Nemertea and to gain data on members of Palaeonemertea outside of Archinemertea for the first time.

Our results show that the gene order in the non-archinemertean lineages of Palaeonemertea is very different from the gene order in Archinemertea, which in turn differs from the gene order in Hoplonemertea and Heteronemertea. The new data sheds light on mitochondrial genome diversity in Nemertea and how it has been underestimated in the past. With a growing coverage the evolution of mitochondrial genomes in Nemertea will lead to a deeper understanding of related spiralian clades.

Diversity of heelwalking: attachment systems in Mantophasmatodea

S10

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The tarsi of Mantophasmatodea (heelwalkers) comprise a highly modified tarsal attachment system. All extant species use their euplantulae (“heel pads”) for locomotion and lift the arolium (“toe pad”) usually off the substrate. While the tarsal morphology of single species is well known, its infra-order diversity remains unexplored. We examined the tarsal attachment system of Mantophasmatodea based on a representative taxon sampling covering 11 species (52 % of all described species) of this group and compared morphological differences across species and sexes. Our scanning electron microscope study showed that the ground pattern is very consistent and revealed almost no specific adaptations. There are minor, but mostly clade-specific differences in the shape of the adhesive setae on the tarsal euplantulae and in the morphology and density of the acanthae on the pretarsal arolium. Both features differ primarily between Austrophasmatidae and the remaining groups. The strong specialization of the mantophasmatodean tarsal attachment system likely either interferes with further adaptability, or sufficiently copes with the diversity of substrates the insects walk on.

Molecular phylogeny of fire ants: Implications for social evolution

S12

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Fire ants (*Solenopsis geminata* species complex) have emerged as a model system for the study of social organization. In particular, a large supergene, termed Sb, has been intensely studied because it is obligately associated with polygyny in a small clade of fire ants. We test the association between the presence of the supergene and polygynous colony organization using a comparative phylogenetic framework. We present the first multi-locus phylogeny of fire ants with a near complete taxon sampling providing a robust estimate of the evolutionary history of the group. Furthermore, we compile available information from the literature regarding social organization and the presence of the Sb supergene to (a) map the two traits onto the phylogeny, (b) reconstruct ancestral character states, and (c) compare the evolutionary patterns between the two traits. Our analyses suggest that the system may benefit from a critical reappraisal.

Teaching integrative taxonomy using case-based learning: revising Vanuatuan ants in the *Pheidole sexspinosa* species complex

S14

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Because of climate change and human impacts, there is a need for increased taxonomic efforts to describe, catalogue, and better understand the evolutionary history of the globe’s vanishing biodiversity. However, there are a dwindling number of trained taxonomists exacerbating the large discrepancy between the known and predicted level of global biodiversity. To accelerate the taxonomic process as well as make it more robust, an integrative approach to taxonomy combines comparative morphology with molecular approaches such as COI barcoding and phylogenomics. Even with the modern-day integrative approach to taxonomy, there is still a need to train and directly transfer taxonomic expertise to the new generation of scientists. Here, we present a pilot study on teaching integrative taxonomy utilizing collaborative and case-based learning. For this case-based learning study, students applied an integrative taxonomic approach to delimit ant species in the species complex from the Vanuatuan archipelago in the South Pacific, which is part of a broader and ongoing study to provide first insights into the biodiversity and evolutionary history of Vanuatuan ants. Overall, this integrative taxonomic approach supports the presence of three new, morphologically and phylogenetically distinct species in the *Pheidole sexspinosa* species complex and contributes to the growing evidence that Vanuatu is an understudied biodiversity hotspot. Based on student surveys, this collaborative and case-based learning approach to integrative taxonomy provided them a deeper understanding for the mechanisms generating biodiversity, gave them a sense of community, and enhanced their scientific self-efficacy by increasing their confidence in taking on their own taxonomic projects.

A multidisciplinary approach to determine the biodiversity and phylogeography of Tasmania's freshwater isopods (Phreatoicidea)

S13

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The enigmatic Phreatoicidea, a subgroup of Isopoda, are still poorly known. Marine fossils from the late Carboniferous period indicate that current Phreatoicidea species can be regarded as living fossils. It is assumed that representatives of these isopods colonized the freshwater bodies of the supercontinent Gondwana from the sea between the Carboniferous and Triassic periods before all marine representatives became extinct. Today, Phreatoicidea are only found in freshwater of continental fragments (Australia, India, South Africa and New Zealand) that once formed Gondwana. The greatest diversity of the Phreatoicidea is found in Australia, whereas only small species groups are known from other countries. The world's greatest diversity of genera can be found in Tasmania.

For this reason, the focus of this study will be on the biodiversity (species and populations) of the Tasmanian Phreatoicidea and how this biodiversity relates to the unique geological history of this island. A multidisciplinary approach will be used. Firstly, a detailed morphological study of the Tasmanian Phreatoicidea will be carried out. The morphological characters of new species and genera will be included in the DELTA database and added to the existing dataset of Dr. George Wilson with almost 900 characters to describe. The database will be used for extensive taxonomic studies and for the description of new species. In addition, molecular analyses, both classical Sanger sequencing and double-digest restriction site-associated DNA (ddRAD) analyses, will be performed. In view of the ongoing destruction of their habitats, for example through forestry, hydropower and tourism, there is an urgent need for action to improve our knowledge of the Phreatoicidea and thus contribute to the protection of these species.

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* Student (eligible for the Student Awards)

Redescription of *Cyclograpsus escondidensis* Rathbun, 1933 assessing its inclusion within the family Sesarmidae Dana, 1851 (Crustacea: Decapoda: Sesarmidae)

S15

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The aim of this work is to assess the position of *Cyclograpsus escondidensis* within the superfamiy Grapsoidea, and to test an alternative hypothesis to the current view that they are not sesarmid crabs, but varunid crabs based on zoea and megalopa larval morphology and on the molecular phylogeny presented in Schubart et al. (2002). To this end, specimens belonging to *C. escondidensis* were morphologically and genetically compared with other *Cyclograpsus* species. Morphological evidence indicates that *Cyclograpsus escondidensis* as well as *Cyclorma lophopus* share characters that link them to sesarmid crabs, such as the pterygostomial and subhepatic regions of the third pair of walking legs and the telson subcircular. The phylogenetic trees based on the mitochondrial COI and 16S genes and the nuclear 28S gene support the placement of *Cyclograpsus escondidensis* within the family Sesarmidae.

* Student (eligible for the Student Awards)

Integrative approach resolves the convoluted taxonomy of leaf-cutting ants in the *Acromyrmex octospinosus* species complex

S17

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The leaf-cutting ants are the dominant herbivores in the Neotropics and their fascinating biology has inspired seminal studies about the social behavior, ecology, and evolution of eusocial insects. However, the taxonomy of the leaf-cutting ants remains convoluted. Within the leaf-cutting ants, the *Acromyrmex octospinosus* species complex has been subject to scientific inquiry for a couple of centuries and yet, there is no consensus regarding the diagnostic traits defining individual species. In the absence of unambiguously diagnosable species, our understanding of the biology of individual species is easily misled. The *Acromyrmex octospinosus* species complex currently consists of four species and three subspecies, including *A. echinatior*, *A. insinuator*, *A. octospinosus*, *A. octospinosus cubanus*, *A. octospinosus ekchuah*, *A. octospinosus inti*, and *A. volcanus*. Our study aims to delimit the species boundaries in the A. octospinosus species complex using an integrative taxonomic approach that incorporates morphological, genomic, population genetic, ecological, and biogeographical data. We reconstructed the evolutionary relationships within the *A. octospinosus* species complex at the population level using Ultra Conserved Elements (UCEs) as genomic markers. In addition, we re-evaluated morphological characters previously used to delimit „species“ and inferred the evolution of morphological and life history traits. Our study contributes to comprehensively assessing the taxonomy of the leaf-cutting ants and provides the taxonomic foundation for future comparative studies about the complex biology of fungus-growing ants.

* Student (eligible for the Student Awards)

Oasen der Vielfalt - Friedhöfe als strukturreiche Biotope urbaner Biodiversität

S61

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Friedhöfe gelten gerade im Ballungsraum als wertvolle Oasen, die nicht nur der Trauerbewältigung dienen, sondern auch Orte der Entspannung und des Natur-erlebens sind. So spielen sie nicht nur für uns Menschen, sondern auch für Pflanzen und Tiere eine bedeutende Rolle.

Das Ziel der gerade angefangenen Doktorarbeit ist es, vorhandene Biodiversität der Friedhöfe zu erfassen, Parameter für die Erhöhung der Biodiversität zu testen und zu identifizieren, und den biologischen Wert sowie Handlungsempfehlungen zu kommunizieren. Es werden unter anderem Fragen der „richtigen" Flächenpflege, menschlicher Aktivität und Friedhofsgröße bearbeitet.

Dazu werden bestimmte Tierarten genauer untersucht: Fledermäuse, Füchse, Kaninchen & Eichhörnchen, sowie Laufkäfer. Andere Taxa werden mit Bürgerwissenschaft erfasst – Tiere & Co. gesucht – komm schnapp sie dir - eine Mitmachaufforderung an alle.

Ultimatives Ziel dieser Doktorarbeit ist die Erhöhung der Biodiversität im urbanen Raum, um den Erhalt der Friedhöfe zu fördern und Lebensraum für Tier, Pflanze und Pilz zu schützen.

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* Student (eligible for the Student Awards)

S63

Integrative taxonomy is the key: Investigation of the unknown bee fauna of the Gargano region, Apulia, Italy.

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Bees (Hymenoptera, Anthophila) are known as essential pollinators of crops and many flowering plants in terrestrial ecosystems. Given their enormous morphological, behaviorally, and ecological diversity, bees are a frequently studied group. However, despite the broad faunistic coverage in Europe, there are still important gaps of knowledge on the bee fauna of several European regions, such as the Mediterranean area. This is mainly due to a lack of taxonomic experts and identification keys for these areas. An integrative taxonomic approach, combining morphology and DNA barcoding, could be a promising approach, especially for taxonomic beginners. Here, we applied this strategy to document the spring bee fauna of the Gargano region in Apulia, Italy. Although no identification keys are available for the studied region, we were able to identify about two third of the species based on their morphology using identification keys for other regions as well as very antiquated literature. DNA-barcoding was required for identification of one third of the species and was also used to verify all morphological identifications. From a total of 92 identified specimens six remained unidentified. Their identification will require the involvement of taxonomic experts, reference collections, and/or more in-depth molecular work. Our faunistic study demonstrates that in the absence of identification literature and experts, the determination of foreign faunas requires an integrative taxonomy approach, i.e. combining both, molecular and morphological methods. Further, the study demonstrates the need for identification keys for specific geographical regions, to enable taxonomists without access to molecular tools to work with wild bees and to improve the knowledge on the distribution of this important group of insects.

* Student (eligible for the Student Awards)

S65

You can only protect what you know: A taxonomic students project on pollination networks of wild bees

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You can only protect what you know: The worldwide insect decline strongly points out the lack of taxonomic expertise, which is urgently needed to identify, monitor, and protect vulnerable insects. In-depth taxonomic knowledge can only be gained by yearly continued practice and the passion for insects. Therefore, the role of Universities is fundamental by offering and supporting taxonomic courses, field work and projects for students. Here, we present such a taxonomic project on wild bees. Its aim was to study wild bees and their occurence on diverse flowering plants in a Botanical garden. Our main goal was to understand (1) the dietary breadth of identified bee species and (2) the suitability of exotic plants as food sources for native wild bees.

The project was performed within the “Ökoprojekte” which are part of the Modul “Ökologie” of the Biologie Bachelor programme of the University of Hohenheim. Bees were collected between May and June 2024 using sweep nets. All individuals were mounted and morphologically identified to species level using the standard literature for the Central European bee fauna (Gokcezade et al. 2015; Scheuchl 1995, 1996; Schmid-Egger & Scheuchl 1997).

Most bee species were collected on several plant species, some bee species were found only on one plant. Literature research revealed that most of the former species are described as polylectic, while most of the latter are considered oligolectic. Three of the 15 observed plants are exotic plants. They were visited only by the honeybee *Apis mellifera*, but not by other species.

Despite the fact that wild bees are a challenging taxonomic group, this students project was successful in (1) providing and supporting knowledge on the diet breath of common wild bee species in Germany and (2) supporting the assumption that exotic plants might not be suitable food resources for specialized wild bees. Besides taxonomic knowledge, the students were trained in collection techniques for wild bees, the preparation and documentation of collected specimens, and the analysis of ecological data.

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* Student (eligible for the Student Awards)

A fish that escapes towards a looming-disk stimulus

B20

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Escape responses are an essential part of the behavior of most animals. Their direction is usually away from the stimulus that elicited the escape, which could be e.g. an expanding disk that mimics an approaching predator. Recent analyses of such looming-induced escapes in zebrafish and *Drosophila* have identified mechanisms by which a stimulus not only elicits but also directs the response and it has been suggested that such mechanisms could be universal. Here, we report a clear counterexample. We studied escapes of the shell-dwelling *Lamprologus ocellatus*, a small cichlid fish native to sandy areas in Lake Tanganyika that uses aquatic snail shells for cover.

Because shelter is rare in its habitat, we hypothesized that *Lamprologus ocellatus* should escape towards its shell, regardless of the direction of the stimulus. To test this, we elicited escapes in fish (N=3) that rested outside their shells in two scenarios: (I) the experimental fish was able to reach its shell by escaping away from the looming-disk; (II) the fish needed to escape in directions that brought it closer to the looming-disk to reach its shell.

Independent of their initial orientation and position the fish escaped toward their shell, regardless of whether this meant moving away from the stimulus or not: The fish produced escape maneuvers in which the direction was independent from the position of the looming-disk and only depended on the position of the shell. We thus show that a looming-disk stimulus elicits escapes but does play no role in directing them when a shell is available. This contradicts views that the nature of the underlying circuits would cause conserved escape maneuvers that initially would be always away from looming-disk stimuli.

B22

ManyGoats – an initiative to promote open and reproducible research on goat behaviour and welfare

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Studies on farm animal behaviour and welfare are often conducted on groups of animals characterised by specific individual factors and living conditions. Due to the contextual idiosyncrasies of individual testing sites, the results of these individual studies could only be valid for the particular group of animals and thus may not always be reproducible. However, robust results are necessary to ensure that outcomes are broadly relevant; this is vital if such results are intended to contribute to improved husbandry and management conditions, and ultimately better animal welfare. In a scoping review on goat behaviour and welfare, we find that a majority of studies used single breeds and the same age cohorts within their study rationale. In addition, a majority of studies was conducted on single sites, making it prone to site idiosyncrasies. Multi-site approaches can offer a resource-efficient opportunity to tackle these problems and increase the external validity of scientific results. For this reason, we established the ManyGoats initiative; our aim is to increase the generalisability of findings in research on goat behaviour and welfare by implementing identical experimental protocols and simultaneously testing animals across different facilities around the world. The initiative will also adhere to Open Science principles, making our work transparent, inclusive and readily accessible. In our first proof-of-concept study (‘ManyGoats1’), we will focus on goats’ behavioural responses to different human attentional states during an Avoidance Distance test. To increase heterogeneity in our sample and identify the factors that contribute to behavioural variation, we will test a diverse range of subjects (i.e. all sexes, different ages, breeds, uses including dairy, meat, fibre and companionship) in different living conditions (e.g. research facility, farm, zoo settings). The Stage 1 Registered Report of this study is currently being reviewed and we anticipate starting data collection from early 2025.

Goats who stare at Rotating Snakes: Do dwarf goats perceive motion illusions?

B39

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Providing farm animal housing environments with environmental enrichment can improve animal welfare by promoting natural behaviours and offering diverse engagement opportunities. However, many forms of environmental enrichment can lead to habituation effects in the animals, and/or incur significant economic costs to implement and maintain these enrichment options. Motion illusions, a subcategory of optical illusions, have the advantage of being installed as simple stationary images but are perceived as moving stimuli. For prey animals like goats, motion illusions could be a cost-effective long-term form of environmental enrichment. In a looking time paradigm, we confronted 20 female dwarf goats (*Capra hircus*) with 2D stimuli shown either on the left or right video screen of an experimental apparatus, while the opposite screen remained white. In a pretest, we examined their visual attention to rotating or stationary black-and-white circles. In the test, goats were presented with either a motion illusion („Rotating Snake Illusion“) or a control stimulus that does not induce a motion illusion in humans but is of similar complexity to the actual illusion stimulus. All stimuli were presented for 10 seconds each. Both the pretest and the test consisted of four sessions with four trials each (2 x test stimulus, 2 x control stimulus). The looking duration at the stimuli was analysed using generalized mixed models. In the pretest, goats looked longer at the moving stimulus than at the stationary stimulus ($p < 0.001$). In the test, goats showed no visual preference for either of the presented stimuli (motion illusion vs. control stimulus; $p = 0.75$). Goats do not appear to spontaneously exhibit a strong behavioural response to the presentation of motion illusions. This suggests they either are not able to perceptually/cognitively process these illusions or are only marginally affected by them.

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* Student (eligible for the Student Awards)

Daphnia Dating – Fertility of *Daphnia magna* females affects the behaviour of *Daphnia magna* males

B41

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The freshwater crustacean *Daphnia* is known for switching between parthenogenetic and sexual reproduction as a result of declining environmental conditions. When environmental conditions are stable, *Daphnia* reproduce via parthenogenesis and females produce clonal female offspring. When environmental conditions are unpredictable, switching to genetic recombination through sexual reproduction is advantageous. Selection favours females that choose males that enhance their offspring's success. Similarly, males should select a female in the right egg stage to maximize their reproductive success. Because of different abiotic factors in habitats, females in different reproduction modes are simultaneously present in the same environment. Accordingly, males must identify females and their reproductive stage to maximize their reproductive success and should show less interest in other females. However, it is unknown how daphnids locate potential mating partners. Using a 3D-Tracking System we analysed video tracks for characteristic behavioural patterns (e.g. speed, depth selection, crowding) in *Daphnia magna* that males display when encountering fertile females. As it is unknown at what time daphnids are mating, we used day and infrared light. We found differences in swimming speed as an indicator of higher activity when encountering embryo carrying females. Males in general prefer to swim near the water surface, but when egg carrying females are in their vicinity, they swim in deeper water levels. However, females with developing embryos swim in the middle and lower water levels, showing avoidance to males. They surface when being fertile to increase male encounter rates. Additionally, the light setting influenced male behaviour, with reduced behavioural patterns during the night. This suggests that mating occurs during the day. We conclude that males determine the fertility window of females. Our results provide initial insights into mating-associated behaviour in *Daphnia magna*.

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* Student (eligible for the Student Awards)

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