



118th
Annual Meeting
German Zoological Society

7–11 September 2026
Münster

BOOK OF ABSTRACTS

118TH ANNUAL MEETING OF THE GERMAN
ZOOLOGICAL SOCIETY



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PLENARY TALKS



Unraveling the hijacking strategies of zombie-making parasites: A tale of ants and fungi

Charissa de Bekker

Utrecht University

Nature harbours many parasites that can induce extended behavioural phenotypes in their animal hosts. *Ophiocordyceps* fungi that evolved to infect and manipulate the behaviours of social insects are an evident example. The so-called “zombie behaviours” that are induced are thought to aid the fungal parasite in evading social immunity, promote fungal development, and increase transmission rates. My team’s research revolves around the elucidation of these fungal-insect interactions to learn how fungi can hijack social insect behaviour and which host pathways give rise to them.

To do so, we developed the interaction of *Ophiocordyceps camponoti-floridani* with its carpenter ant host *Camponotus floridanus* as a model. In this host-microbe interaction we have observed significant changes in host daily activity rhythms, locomotion and communication, followed by summitting behaviour, which is highly characteristic for *Ophiocordyceps* and other manipulative infections. To investigate the interacting fungal molecules and ant host pathways that elicit these behavioural changes, we integrate omics technology with functional genetics techniques and quantitative behavioural assays.

With this approach, we found that *Ophiocordyceps* secretes a novel cysteine-rich peptide that binds to insect scramblases, thereby inducing aberrant odour-related behaviours. Moreover, we discovered that fungal indole diterpenes cause tremors in ant hosts and affect locomotion and grooming behaviours. Additionally, we found that the ant circadian clock is significantly affected during *Ophiocordyceps* infection. These are some of the first results to connect *Ophiocordyceps* genomes with carpenter ant phenomes, thereby answering how these specialist fungi hijack ant behaviour and how those behaviours are regulated at a molecular level.

Neurophysiological adaptations of hibernation: solutions to environmental challenges

Elena Gracheva

Yale University School of Medicine

Hibernation was first documented by Aristotle in 350 BCE, who noted that some creatures conceal themselves in a sleep-like state during winter. During hibernation animals undergo dramatic adaptive changes, including a reduction in heart and respiration rate and a decrease in core body temperature from 37°C to 4°C. Yet, despite being cold and deprived of oxygen for up to 8 months, they do not experience cold-induced pain, and their organs continue to function! Moreover, because these animals often do not eat or drink during hibernation, they must rely solely on the management and utilization of their internal resources. Hibernators exist in almost all mammalian groups, suggesting that hibernation results from modification of existing physiological pathways rather than evolution of novel traits. However, the mechanisms that support hibernation remain enigmatic.

Our goal is to reveal cellular, molecular, and circuitry mechanisms that induce and support hibernation in mammals. We seek to understand what enables hibernators' survival during prolonged periods of hypothermia, water deprivation and starvation. Our research model is the thirteen-lined ground squirrel, an obligatory mammalian hibernator. We employ a wide array of experimental approaches, including single-molecule biophysics, cell biology, chemo- and optogenetics, neurophysiology and behavior. By combining cutting-edge molecular tools with the naturalistic animal model, we seek to revolutionize our understanding of the mechanisms underlying hibernation.

Our research program tackles fundamental physiological questions from the unique perspective of mammalian hibernators. This work will lay foundation for rational design of pharmacological tools to understand how life in mammals can persist under extreme conditions of prolonged periods of hypothermia, cold exposure, starvation, and dehydration. Our discoveries will allow us to predict whether hibernation can be induced in other mammals, including humans.

Ant Societies: From Behavior to Neural Circuits

Daniel Kronauer

Rockefeller University

The colonies of social insects are complex biological systems in which manifold interactions between individuals give rise to emergent properties that are adaptive at the group level. However, most social insects cannot be propagated in captivity or genetically manipulated, severely limiting the scope for experimentation. Over the past fifteen years, we have developed and utilized the clonal raider ant, *Ooceraea biroi*, as a new model species that overcomes many of these limitations, allowing us to study social dynamics and underlying mechanisms under controlled laboratory conditions. Our work has led to a deeper understanding of how ants within a colony assume distinct behavioral roles and efficiently divide labor, how they communicate, both as adults and across different developmental stages, and how these interactions result in collective behavior. Additionally, our research has shed light on how evolution has repurposed and expanded genetic, neural, and physiological mechanisms from solitary ancestors to produce highly social organisms. In this seminar, I will provide an overview of this work and discuss future directions in our research program aimed at understanding the evolution and organization of insect societies, spanning from genes to neural circuits and behavior.

From a simple idea to global biodiversity observation: the (e)DNA revolution and its unfinished business

Florian Leese

University of Duisburg-Essen

Over twenty years ago, a simple proposal — identify an animal from a short, standardised gene fragment — met a discipline running out of capacity. Morphological identification could not keep pace with the vast numbers of new species reported worldwide, growing monitoring demands, or with shrinking taxonomic expertise. At the same time, animal biodiversity loss accelerated drastically. The new approach, termed "DNA barcoding", offered a solution, and over two decades it grew beyond its original idea into a global observation network. With the advent of identifying many specimens in a bulk sample — or merely from traces in environmental samples, i.e. via "eDNA metabarcoding" — a second revolution extended the principle from single specimens to entire communities, from the deep sea to alpine headwaters, from the poles to the tropics, cost-effectively. In the aquatic realm, such community data now start entering statutory assessment. However, one example captures both the promise and the problem: for under 100,000 €, 1,800 Malaise trap samples from 75 sites across Germany were analysed over two years, yielding >30,000 insect species. Yet, many remain undescribed or without a reliable name, and the data carry no strong quantitative signal. That gap defines today's challenge: sequences bear a risk of becoming detached from ecological knowledge, reference databases are incomplete, error-prone, and analytical routines vary wildly between laboratories. Closing it demands renewed investment in method and data standardisation, new ways of describing species, harnessing digital imaging, and ways to make the data more quantitative, so that detections can be interpreted ecologically. Solutions exist!

What amphibians can teach us about the evolution of parental care

Eva Ringler

University of Bern

Parenting is considered a key evolutionary innovation that contributed to the diversification and expansion of vertebrates. Amphibians are an ideal group in which to identify the ecological factors that have facilitated or constrained the evolution of different forms of social behaviour, including parental care. In my research group we aim to better understand the ecological factors that have shaped highly specialised and complex social behaviours, assess causes and consequences of individual differences in behavioural profiles, and also identify cognitive abilities associated with distinct behavioural traits. We use dendrobatid frogs and glassfrogs as models to answer diverse questions regarding their reproductive behaviour, parental care, space use, learning and memory. We study these animals in their natural habitat as well as in the lab, by combining a diverse set of methodological approaches, including behavioural experiments, molecular parentage analysis, bioacoustics and spatial analyses. Our research has shown that tropical frogs are very dedicated parents, exhibit remarkable spatial behaviour, as well as behavioural flexibility across various contexts.



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Plenary Talk



Drosophila glia: from development to behavior

Christian Klämbt

University of Münster

Münster 2026

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KEYNOTE TALKS



Enduring together: The role of social behaviour in lizards' resilience to novel environments**Isabel Damas Moreira**

Bielefeld University

Humans are changing the world. These changes have driven the current global biodiversity crisis, marked by widespread species decline and extinction, as many species struggle to cope with rapid environmental changes. Yet, some particular species seem to be able to survive and succeed in novel conditions. These species can demonstrate an exceptional ability to adjust to drastic environmental changes within their habitat, as seen with urban dwellers, or to even establish and thrive in novel environments, as happens with invasive species. It is central to understand how these particular species can successfully cope with rapid and profound environmental changes.

As a critical first step, individuals can modify their behaviour to better cope with unfavourable changes, providing an immediate and flexible mechanism for survival. However, individuals do not exist in isolation; they interact with others. Plausibly, social behaviour and social adjustments may play a crucial role for the entire population to succeed in novel conditions, even in species typically considered "less social". Despite this, the contribution of social behaviour to species persistence remains understudied, even though it can directly impact individuals' interactions, reproduction, and ultimately their fitness. To explore this, I have been studying two lizard species that rank among the most successful lizards in anthropogenic settings: the Italian wall lizard (*Podarcis siculus*) and the common wall lizard (*Podarcis muralis*). Both species have invasive populations across multiple countries and are also commonly found in urban areas within their native ranges. Intriguingly, individuals of these two species are territorial and live within small home ranges, traits that make it challenging to quickly relocate to more suitable habitats. Instead, these lizards must rapidly adjust to environmental stressors in situ to survive, positioning them as exceptional models for studying anthropogenic-related resilience.

In this talk, I will take you through a journey exploring how social behaviour could be important to species resilience, flowing from biological invasions to urban ecology, with lizards leading the way. These studies raise important questions about the role of social behaviour in adaptive responses to an increasingly anthropogenic world. Understanding the behavioural mechanisms driving species' responses to anthropogenic change can be essential for predicting species resilience and guiding conservation efforts.



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Keynote Speaker

Behavioural Biology



The ecology of electrostatics: pollination, parasitism, and predator-prey interactions

Sam England

Museum für Naturkunde Berlin

Electricity, a fundamental force in the universe, is all around us. The potential for this force to play a role in ecological interactions, moving organisms and objects in the environment, or being sensed, is therefore a promising avenue for biomechanical and neuroethological research. Here, I put forth my case for naturally occurring static electricity to be considered a driver of ecology and perhaps even evolution. I present our findings that pollen is attracted by the natural static charges of butterflies and moths, and similarly how ticks are electrostatically pulled onto hosts. From this, I build to our new evidence of an electrostatic sense in insects, in the context of predator detection by caterpillars and treehoppers – showing that this sense may be widespread and even a driver of morphological evolution.

A dark blue silhouette of the Münster skyline, including various church spires and the Teleferik cable tower, spanning the bottom of the page.

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Signaling centers of appendage regeneration: from frogs to mammals**Can Aztekin**

Friedrich Miescher Laboratory of the Max Planck Society

Why mammals cannot regrow their lost limbs remains one of the biggest mysteries in biology. Unlike mammals, *Xenopus laevis* tadpoles possess a remarkable ability to regenerate lost appendages. In our previous work (Aztekin et al., 2019; 2021), we identified key signaling-center cell types that orchestrate amphibian tail and limb regeneration. Through cross-species comparisons (Zhong et al., 2023), we identified equivalent cell populations in mammals and developed simplified mammalian stem cell-based models, including limb bud organoids, to investigate the properties of these regenerative cells (Skoufa et al., 2025). In this talk, I will present our recent findings comparing frog tadpoles and embryonic mouse limbs, revealing that regenerative amphibians exhibit reduced oxygen sensing. This altered oxygen sensitivity shapes cellular biomechanical, epigenetic, and metabolic states that are conducive to regeneration initiation. In contrast, mammalian limbs exhibit heightened oxygen sensitivity. However, altering environmental oxygen levels reprograms mouse limbs toward a tadpole-like regenerative state and induces regeneration initiation (Tsissios et al., 2026). Together, these results reveal a conserved mechanism underlying limb regeneration initiation across species and suggest potential pathways for reactivating this dormant capacity in mammals.

Losing the Essential: Evolution of Neuropeptide Processing Genes**Vera Terblanche Hunnekuhl**

University of Göttingen

The evolution of animal genomes is shaped by differential gene loss on different phylogenetic levels, often assumed to result from functional redundancy between related genes. However, experimental evidence addressing the prerequisites and consequences of gene loss remains limited. In bilaterians, neuropeptide signalling relies on conserved processing enzymes, including prohormone convertases (PCs) and carboxypeptidases (CPs). Although the enzymes PC1/3 and CPE are broadly conserved, they have been lost in dipteran insects, including *Drosophila melanogaster*, which instead relies on single orthologues for peptide processing. Using the beetle *Tribolium castaneum*, which retains the ancestral complement of these genes, we investigated their functions in insects.

We show that both genes perform essential, non-identical roles. PC1/3 is specifically expressed in the suboesophageal ganglion and midgut enteroendocrine cells. Its disruption causes a metabolic syndrome in which larvae fail to accumulate lipid stores required for growth and instead shift energy metabolism toward glycogen and circulating trehalose. Cpe, which we show originated from a partial duplication of an ancestral cpd/svr gene but has been repeatedly lost in major insect lineages, is specifically expressed in the nervous system, as in vertebrates. Its knockdown severely impairs development from egg to larva, indicating subfunctionalisation between paralogues. A cross-species rescue experiment further demonstrated molecular redundancy, which along with increased isoform diversity, but not lack of functional importance, facilitated the gene loss in flies. Beyond the evolutionary implications of these functional analyses, I will also discuss the cell-specific expression of prohormone convertases, as revealed by novel reporter lines, and their potential for the further characterisation of peptidergic cell types in an evolutionary context.

Traits in a Warming World:

Understanding Heat Tolerance in Zooplankton

Maja Ilić

University of Cologne

Predicting how elevated temperatures will reshape populations, ecosystems, and evolutionary processes requires the identification of ecologically relevant traits. Zooplankton such as *Daphnia* are particularly promising models for such approaches due to their key role for pelagic food webs. Heat tolerance has emerged as a candidate trait that is likely to influence community composition and evolutionary trajectories of *Daphnia* in warming environments. For the past two decades, heat tolerance research has focused on two proxies: the critical thermal maximum measured along a temperature gradient (CT_{max}) and time until immobilization measured at a constant temperature (Timm). Despite recent developments such as video tracking, which enables robust and reproducible quantification of CT_{max} and Timm, and advances in identifying the physiological traits associated with heat tolerance, an in-depth understanding of the mechanisms linking heat tolerance to fitness and population dynamics is still lacking. This specifically applies to potential trade-offs between heat tolerance and other fitness-related traits, and the role of heat tolerance in intra- and interspecific competition. In this talk, I will present our recent findings from heat tolerance experiments with different *Daphnia* species and discuss future perspectives and potential challenges in heat tolerance research.

Beetle Minds and Microbial Management: Behavioral and Immune Adaptations in the evolution of (bi)parental care

Maximilian Körner

University of Bayreuth

Harsh ecological conditions are thought to favor the evolution of cooperation, particularly during early stages of sociality. These effects are especially pronounced when organisms face transient or challenging environments, such as colonizing novel habitats or breeding under severe resource constraints. Here, I present new findings from *Nicrophorus* burying beetles, a model system ideally suited for studying social evolution during niche construction on ephemeral vertebrate carrion. The volatile and competitive nature of this resource has selected for complex biparental care, varying levels of offspring dependence, and sophisticated microbial management mediated in part by personal and social immunity. By experimentally manipulating parental care, resource availability, and microbial pressure, we investigate how biparental coordination, social immune interactions, and offspring dependency emerge during and in turn shape family life on an ephemeral resource. In my talk, I highlight three facets of our work: (i) how parents coordinate their investment during facultative yet stable biparental care, (ii) how personal and collective immunity of parents and offspring interact to stabilize family groups, and (iii) how resource stability affects terminal investment thresholds and thus future reproduction. Together, these findings provide new insight into how subsocial associations can consolidate into interdependent social systems under adverse ecological conditions.

How culture leaves a genomic signature: learned song and the evolution of reproductive isolation

Ulrich Knief

University of Freiburg

Many mating signals have a genetic basis. Bird song is different. In many songbirds it is learned, allowing an individual's song and its genetic ancestry to become uncoupled. This raises a fundamental question in evolutionary biology: can a culturally inherited mating signal shape patterns of gene flow and ultimately contribute to reproductive isolation and speciation?

The willow tit (*Poecile montanus*) provides an exceptional opportunity to address this question. Across the Palearctic, the species exhibits geographically separated song traditions that have persisted over evolutionary timescales despite their cultural transmission. At finer spatial scales, multiple contact zones between song types provide natural experiments for investigating the mechanisms maintaining these boundaries.

In this talk, I will combine continental phylogeography with studies of European hybrid zones to explore the evolutionary consequences of learned song in willow tits. I will first reconstruct how historical range dynamics shaped the present-day association between song traditions and the species' major evolutionary lineages across the Palearctic. I will then focus on European hybrid zones, where geographic patterns of song and genomic variation, complemented by behavioural experiments, reveal an apparent paradox: although song can become decoupled from genetic ancestry at the level of individuals, it nevertheless leaves a lasting genomic signature at the population level through its effects on patterns of gene flow and reproductive isolation.

More broadly, I will argue that culturally inherited mating signals can leave lasting genomic signatures despite being transmitted independently of DNA, highlighting the importance of integrating population genomics, behaviour, and evolutionary history to understand the evolution of such reproductive barriers. Even if culturally inherited mating signals did not drive the initial divergence, they may nevertheless play a key role in maintaining divergence following secondary contact.



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Keynote Speaker

Evolution



Evolution in Real Time: Understanding Adaptation in the Wild

Maria Moiron

Bielefeld University

Understanding and predicting how organisms adapt to their environments remains a central challenge in evolutionary ecology. Addressing this challenge in the wild requires an integrative approach that bridges ecological and evolutionary processes, from the genetic architecture of trait variation and phenotypic plasticity to the role of environmental variability in shaping selection and population dynamics. Such an understanding is increasingly important for predicting population resilience in the face of rapid environmental change, including climate warming and disease outbreaks. Drawing on 33 years of individual-level data from a natural population of common terns (*Sterna hirundo*), I will show how long-term ecological change can shape selection, phenotypic change, and population dynamics, and how these processes might interact to generate eco-evolutionary feedbacks. I will further discuss what long-term individual-based data can reveal about the mechanisms underlying adaptive responses to environmental variability, and highlight future directions for developing a more predictive evolutionary ecology of natural populations.

Keynote Speaker

Morphology

How cuttlefish stick to their prey in milliseconds**Guillermo Amador**

Wageningen University

Cuttlefish are ambush predators that use specialized, sucker-lined appendages to capture their prey in milliseconds. Their suckers generate high suction forces while remaining dynamic, versatile, and reversible. The prey they capture include crustaceans, like crabs and shrimp, scaly fish, and even other cuttlefish. Therefore, the substrates they attach to can vary significantly in roughness and stiffness. Here, I will present a novel, passive, cuttlefish-inspired, artificial suction cup and use it as a tool to explore the functional adaptations underlying the remarkable attachment performance of cuttlefish suckers. Cuttlefish suckers have a characteristic plunger shape with a stalk that, together, are hypothesized to generate suction passively upon contact with a surface, with minimal preloading. Their interior is lined with a stiff proteinaceous ring that provides structural support to resist collapse under the low internal pressures exerted during suction. The top of the ring bears teeth that can penetrate soft tissues. Additionally, they possess micro-structures on the rim, which enable attachment to rough substrates. By translating these morphological adaptations to our design, we created a bio-inspired suction cup that can attach to challenging substrates and be utilized by robotic systems in agriculture, deep-sea operations, and medicine without the need of external air or fluid compressors.

Big Teeth, Microscopic Traces: Reconstructing Dinosaur Ecology through Dental**Microwear Texture Analysis****Daniela E. Winkler**

University of Bonn

Over the past two decades, advances in palaeobiological methods have transformed our understanding of dinosaur biology. Stable isotope analyses, bone histology, biomechanical modelling, and studies of fossil melanosomes have provided new insights into physiology, locomotion, and appearance. Dietary ecology, however, has increasingly emerged as another key aspect for reconstructing dinosaur life histories.

My research aims to understand how extinct vertebrates interacted with their environment by integrating experimental studies on extant vertebrates with quantitative analyses of fossil tooth wear. Together, these approaches bridge neontology and palaeontology, using feeding ecology as a window into the ecological and evolutionary processes that shaped ancient ecosystems. Central to this approach is Dental Microwear Texture Analysis (DMTA), which provides a quantitative record of feeding behaviour preserved on tooth surfaces. Originally developed for extant mammals, DMTA has been experimentally validated across a growing range of vertebrates, including reptiles, providing an increasingly robust comparative framework for interpreting fossil taxa. Recent studies have demonstrated the potential of DMTA for reconstructing dinosaur ecology across Theropoda, Sauropoda, and Ornithomimiformes. Rather than simply distinguishing herbivores from carnivores, microwear textures preserve a short-term record of feeding behaviour that enables addressing ecological questions at multiple biological scales, from individual dietary shifts during ontogeny to resource partitioning within communities and ecosystem responses to environmental change. For example, in Late Jurassic dinosaur assemblages, DMTA has revealed ecological differences among sympatric sauropods and found evidence for remarkably stable dietary niches across geographically distinct populations, distinct habitat signals, and possible migratory behaviour.

In this presentation, I will provide an overview of recent advances in dinosaur dental microwear research while illustrating how experimentally grounded approaches from modern zoology can be integrated with palaeontological data to reconstruct feeding ecology and ecosystem dynamics in deep time.

Keynote Speaker

Neurobiology

Evolution of sensory information integration – lessons from comb jellies

Maike Kittelmann

Oxford Brookes University

How neurons and the first nervous systems evolved and how they facilitated signal transmission remains one of the most exciting problems bridging the fields of Neurobiology and Evolutionary and Developmental Biology. As one of the earliest-branching metazoans, comb jellies - marine animals with a subepithelial nerve net - have been providing crucial insights into early forms of signal transmission between cells and tissues. Using high resolution 3D electron microscopy, we previously reported the syncytial organisation of the nerve net neurons with predominantly neuropeptidergic vesicles in *Mnemiopsis leidyi*. Now we have expanded this morphological investigation to their aboral organ - a sensory hub that detects motion, light, and pressure and coordinates ciliary movement. 3D reconstruction of the aboral organ revealed new cell types, including non-synaptic vesicle-rich cells likely involved in volume transmission, as well as condensation of the nerve net surrounding the apical organ and its direct synaptic connections to balancer cells. We suggest that the aboral organ relies on synaptic as well as non-synaptic signal transmission and represents a multimodal integrative sensory system critical for behavioural regulation.

Sleep deprivation enhances decision making in larval zebrafish

Hanna Zwaka

Leibniz Institute for Neurobiology

Sleep deprivation is known to drastically affect cognitive functions, including decision-making and attention, across many different species. In our lab, we leverage the small size and conserved brain structure of larval zebrafish to investigate sleep and the consequences of sleep disruption across a range of behaviors. I will present how sleep disruption leads to improved performance in a visual decision-making paradigm. Specifically, we show that lack of sleep slows fish down and increases their reaction time. Using a drift diffusion model, we attribute this behavioral change to a specific strategy switch: sleep-deprived animals require a higher level of decision certainty before committing to a response. Together, these findings show that sleep loss does not simply impair behavior, but can alter how evidence is evaluated and when a decision is made.

Keynote Speaker

Physiology

The puzzle of torpor regulation in the Djungarian hamster.

Annika Herwig

Ulm University

Daily torpor is an important physiological strategy that enables Djungarian hamsters (*Phodopus sungorus*) to reduce energy expenditure during winter. During torpor, metabolic rate decreases by approximately 80%, while body temperature falls to 15–25 °C for several hours per day. Our research aims to uncover the mechanisms underlying this remarkable physiological adaptation, with a particular focus on the hypothalamus, a key brain region regulating energy balance.

Over the past years, we have combined gene expression analyses and in vivo studies to investigate the roles of hypothalamic thyroid hormone signalling and blood glucose availability in torpor regulation. Our findings indicate that local thyroid hormone availability within the hypothalamus contributes to torpor control, whereas blood glucose availability is not necessarily involved. In parallel, next-generation sequencing has identified molecular adaptations of the torpid hypothalamus, including enhanced neuronal plasticity and increased biomolecule transport. Building on these findings, we integrated anatomical mapping with nucleus-specific transcriptomics to identify neuronal circuits involved in torpor control. This work identified the suprachiasmatic nucleus (SCN) as hypothalamic region exhibiting increased neuronal activity during torpor, while SCN-specific transcriptomics revealed dynamic expression of genes associated with circadian rhythms, metabolism, mitochondrial function, and transcription. Together, these findings support an active role of the SCN in torpor regulation. Future studies will aim to elucidate which hypothalamic systems are involved in coordination of different torpor forms.

Scales of change: Eco-physiological responses of marine benthic invertebrates to environmental variability in a changing Baltic Sea

Christian Pansch-Hattich

Abo Akademi University

Climate change is shifting not only mean environmental conditions but also the frequency, intensity and structure of short-term variability and extreme events. Using laboratory assays, flow-through systems, custom-built indoor and outdoor mesocosms, and field studies in the Western Baltic Sea, I present work that explores how environmental variability shapes physiology to ecological interactions in marine benthic invertebrates across scales ranging from hours to seasons. Drawing on concepts of thermal performance curves and Jensen's inequality, we found that the biological consequences of fluctuating conditions depend critically on their amplitude and frequency relative to the species' physiological optimum: fluctuations can buffer stress when centred on extreme average temperatures, yet exacerbate it under milder conditions, with underlying shifts in metabolic demand and recovery capacity. At longer, weeks-to-months timescales, sequential extreme events such as repeated marine heatwaves and hypoxic upwelling reveal the importance of stress memory and cross-stress tolerance, in which prior exposure to one stressor can attenuate or amplify sensitivity to a subsequent stressor. Together, these findings across scales, from diurnal fluctuations to multi-month sequences of extremes, demonstrate that variability itself, and not only shifting means, is a key determinant of organismal performance. This body of work illustrates how integrating physiological theory on variability, tolerance, and stress memory with multi-scale experimental approaches can improve our understanding, and ultimately our predictions, of how coastal marine ecosystems will respond to an increasingly variable and extreme ocean climate.

Evolution of social parasitism and biodiversity of *Acromyrmex* leaf-cutting ants

Daniela Mera-Rodríguez

University of Hohenheim

Social parasitism is a form of brood parasitism in which a parasitic species depends on their hosts' social organization for survival and reproduction. Social parasitism has evolved repeatedly throughout the ant tree of life, which raises questions about the convergent origins of these specialized species interactions. Leaf-cutting ants offer an exceptional system for studying these questions because the genus *Acromyrmex* includes at least five inquiline social parasite species, each having distinct combinations of morphological, behavioral, and life-history traits, while also representing one of the most ecologically dominant and economically important insect groups in the Neotropics. Yet, despite centuries of biological research, species boundaries are ambiguous, and the current taxonomic classification is highly convoluted. Therefore, the evolutionary relationships among *Acromyrmex* species are poorly understood.

To address the evolutionary history and species diversity of *Acromyrmex*, we reconstructed a comprehensive population-level phylogeny for all 32 currently described species in the genus, placing a special emphasis on host and parasite populations across their biogeographic distribution, using Ultraconserved Elements (UCEs) as molecular markers. This phylogenomic framework served two complementary goals. First, it allowed for testing competing hypotheses regarding the origins and evolution of social parasitism, asking whether social parasite species arose in direct sympatry from their hosts via the intra-specific route of social parasite evolution, or in allopatry via the inter-specific route. Second, we used this integrative phylogenomic framework, combined with morphological, population genetic, and biogeographic data, to reconstruct the evolutionary history and delimit biological species within *Acromyrmex*.

Our results suggest that social parasitism evolved at least three times in leaf-cutting ants, with both sympatric and allopatric speciation contributing to the diversity of parasitic life histories. These findings show that convergent outcomes can arise through multiple distinct evolutionary pathways. Moreover, our findings clarify long-standing taxonomic ambiguities, reveal previously unrecognized species diversity within *Acromyrmex*, and establish a robust evolutionary framework that opens new avenues for investigating the biogeographic and ecological conditions that repeatedly give rise to social parasitism in the Neotropics.

Can Proteins Identify Species? Ten Years of MALDI-TOF Mass Spectrometry in Marine Biodiversity Research

Sven Rossel

German Centre for Marine Biodiversity Research

MALDI-TOF mass spectrometry has become a standard tool for the identification of microorganisms, yet its application in zoology remains comparatively limited. Over the past decade, the potential of proteomic fingerprinting as a rapid and cost-effective approach for species identification and biodiversity assessment in marine metazoans has been extensively explored.

Using taxonomically challenging meiofaunal copepods as a model system, standardized workflows for specimen preparation, data processing and automated species identification were established. Subsequent studies demonstrated that proteomic fingerprints are highly informative for species discrimination and frequently recover biologically meaningful entities that are congruent with morphology and DNA-based approaches. The method was subsequently expanded to a broad range of marine taxa, including fish eggs, cnidarians, corals, echinoderms and deep-sea crustaceans, revealing its applicability across diverse phylogenetic groups and ecological settings.

Beyond specimen identification, proteomic fingerprinting proved valuable for biodiversity assessments in ecosystems where taxonomic knowledge remains incomplete and species diversity is still largely unknown, ranging from coastal habitats to Arctic and deep-sea ecosystems. Several studies also revealed that proteomic fingerprints contain information beyond species identity, including ontogenetic stage and sex. While this can increase the biological resolution of the method, it also emphasizes the importance of comprehensive reference libraries and careful interpretation of proteomic patterns, particularly in recently diverged species complexes.

Drawing on more than a decade of research, the development of MALDI-TOF-based proteomic fingerprinting is traced from a proof-of-concept approach for marine meiofauna to a broadly applicable tool for biodiversity research across marine metazoans. Together, these studies demonstrate that proteomic fingerprints can reliably identify species across a wide range of marine metazoans while simultaneously providing biological information beyond species identity. They further highlight both the opportunities and current challenges of proteomic fingerprinting and illustrate how the method can complement morphology and DNA-based approaches in zoological systematics, biogeography and biodiversity assessment.



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PUBLIC TALK



Die Grenzen der Anpassung - Über das Schicksal der Tiere im Zeitalter des Menschen

Norbert Sachser

University of Münster

Tiere sehen sich im Zeitalter des Menschen, dem Anthropozän, großen Herausforderungen gegenüber. Dabei können sie sich überraschend gut und schnell an anthropogene Veränderungen ihrer Umwelt anpassen, wie zahlreiche Studien an Wild- und Haustieren zeigen. Wildtieren gelingt dies vor allem durch Mikroevolution und phänotypische Plastizität. Haustiere sind aufgrund genetischer Veränderungen im Laufe der Domestikation für ein Leben in menschlicher Obhut gut geeignet.

Doch die Anpassungsfähigkeit aller Tiere hat ihre Grenzen – und diese werden immer häufiger erreicht. Der Lebensraum von Wildtieren verändert sich dramatisch, ihre Bestände schrumpfen und Arten sterben aus. Tiere in der Landwirtschaft erfahren extreme Haltungsbedingungen und leiden. Und auch Heimtiere sind häufig durch Vermenschlichung und fragwürdige Zuchtziele in ihrer Anpassungsfähigkeit überfordert.

In meinem Vortrag werde ich auf dem aktuellen Stand der zoologischen Forschung thematisieren, was es für Wild- und Haustiere heißt, im Zeitalter des Menschen zu leben, und kurz skizzieren, welche Lösungswege es für die hieraus resultierenden Probleme gibt.



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AWARD TALKS



The Parallel Evolution of Complex Cognition

Onur Güntürkün

Biopsychology, Institute of Cognitive Neuroscience

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The evolution of brain and cognition is full of strange twists. Take the following example: Great apes such as chimpanzees have complex cognitive abilities and a brain weighing approximately 400 g, which includes a large neocortex. In comparison, birds such as corvids and parrots have a brain weighing between 3 and 25 g and no neocortex. This should make it impossible for birds to develop high cognitive abilities. However, studies over the past two decades have shown that there is not a single cognitive ability in chimpanzees that has not also been demonstrated in corvids and parrots. And not only that, also the mechanisms of cognition are absolutely the same. How is this possible? This question keeps me awake at night because it challenges fundamental assumptions about the neural basis of complex cognition. I have come to realize that I must travel back to the depths of vertebrate evolution to identify the “hard-to-replace” neural mechanisms of cognition in mammals and birds to find answers. This talk is about that journey.



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Functional Identification of Predator-Sensing Ionotropic Receptors in *Daphnia*

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Inducible morphological defences are a prime example of phenotypic plasticity, which is the ability of a single genotype to produce distinct phenotypes in response to environmental signals. *Daphnia*, a freshwater zooplankton genus, is a well-established model for this phenomenon. Across the genus, different species can detect and distinguish a diverse array of predators, to which they develop specific morphological responses. While the ecological basis of this phenomenon is well studied, the chemosensory detection and distinction of predator cues remain rather unresolved.

Ionotropic receptors (IRs) are a family of ligand-gated ion channels evolved from ionotropic glutamate receptors. Functional IR complexes are heterotetramers composed of two broadly expressed co-receptor subunits and two stimulus-specific tuning receptor subunits. We previously demonstrated that IR co-receptor subunits are involved in predator detection in *Daphnia*, suggesting that IRs are essential for chemosensory-mediated defence induction. However, with hundreds of tuning IR paralogs encoded in *Daphnia* genomes, the identity of the receptors responsible for predator cue detection remained unknown.

To address this, we identified, annotated, and phylogenetically characterized the complete IR repertoire across eight *Daphnia* species. Gene tree–species tree reconciliation and orthology assignment revealed approximately 480 ortholog groups distributed across roughly 1,000 gene loci, reflecting both conserved ancestral clades and substantial lineage-specific expansions. In parallel, tissue-specific RNA-seq in *D. longicephala* followed by differential expression analysis identified a subset of tuning IRs significantly upregulated in antennule tissue, the primary chemosensory organ. Their antennule-enriched expression suggested a direct role in sensory detection, which we tested through targeted RNA interference-mediated knockdown. Silencing these receptors specifically impaired the induction of morphological defences. The comprehensive IR repertoire established here now provides a framework for systematically identifying the tuning receptors underlying distinct predator-prey chemosensory interactions across the *Daphnia* genus.

Can manipulative parasites modify host-mediated trophic effects? Experimental evidence from *Schistocephalus solidus* and three-spined sticklebacks

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Parasites can alter host traits, thereby reshaping host interactions and modifying density- and trait-mediated effects on trophic cascades. Despite increasing research in parasite ecology, the cascading effects of parasitism from individual hosts to population and community levels remain underexplored. Here, we conducted a large-scale mesocosm experiment replicating key phases of the parasite's development to test our hypothesis that the trophically transmitted tapeworm *Schistocephalus solidus* weakens stickleback-driven trophic cascades by altering host performance, feeding behaviour, and diet. We quantified its effects on three-spined sticklebacks (*Gasterosteus aculeatus*) and their prey communities. *S. solidus* infection reduces stickleback body condition and shifts zooplankton biomass, transiently dampening the likelihood and strength of stickleback-driven trophic cascades at specific time points of the infection. Using structural equation models, we show that parasite-driven trait-mediated indirect effects (TMIEs) are equivalent to density-mediated indirect effects (DMIEs) on trophic cascades; However, their net ecological impact is often constrained by their influence on host population density. Our findings highlight the complexity of host-parasite interactions and their community and ecosystem-level consequences.

Unlocking the genomic architecture of *Gordionus violaceus*: new perspectives on Nematomorpha evolution and development

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Nematomorpha, or horsehair worms, are a widely neglected clade of parasitic protostomes essential for understanding evolutionary dynamics within the Ecdysozoa. Despite their remarkable life cycles—characterized by terrestrial host manipulation and an aquatic free-living phase—genomic and molecular resources for this phylum are severely lacking. This study focuses on the gordiid species *Gordionus violaceus* to establish a high-quality molecular foundation for the phylum.

We present a chromosome-resolution annotated genome assembly of *G. violaceus* generated through a combination of PacBio HiFi and HiC sequencing. This genomic resource enables the analysis of gene complement, the identification of molecular signatures related to parasitism, and the resolution of the debated phylogenetic position of Nematomorpha within the Ecdysozoa. To further characterize the organism, we employ single-nucleus RNA sequencing (snRNA-seq) to produce a comprehensive cell atlas, bridging the gap between existing ultrastructural data and transcriptional profiles.

Additionally, we investigate the unique developmental biology of nematomorphs, which exhibit a rare deuterostomic mode and highly regulative early cleavage. By applying bulk RNA-seq to multiple embryonic stages, we map the differential gene expression governing cell fate determination and differentiation.

Our multi-stage datasets provide insights into the nematomorphs debated phylogenetic position and the deep ancestry of prominent model systems such as *C. elegans*. By integrating genomics, transcriptomics, and developmental observation, this work establishes Nematomorpha as a powerful model for comparative evolutionary and developmental biology.

Parasite diversity affects individual host immunity and immune plasticity in cavefish**Marc Bauhus**; Robert Peuß

Münster University

Host-parasite interactions are a major driver of immune system evolution. It has been demonstrated that reduced parasite diversity can affect the evolutionary trajectory of host immunity in various ways. Some cave-dwelling populations of the Mexican tetra, *Astyanax mexicanus*, change their immune investment strategy by investing less in costly innate immune responses and more in adaptive immunity. This raises the question of whether adaptation to parasite diversity affects the immune response under natural conditions, including the ability to respond plastically to changes in the parasite environment. To answer this question, we used the Mexican tetra and took the following approach: (1) we measured abiotic and biotic factors of cave and surface environments to identify key environmental factors shaping cavefish immunity, and (2) we performed a fully reciprocal immunological experiment to measure immune-response plasticity under laboratory conditions.

Our data confirmed that some cave populations were infected only with monogenean ectoparasites, whereas other cave and surface populations harbored a more diverse repertoire of macroparasites (e.g., trematodes, nematodes). We present evidence that cavefish are under starvation regimes in the field at both metabolic and transcriptomic levels, indicating limited energetic resources in cave environments. This was accompanied by reduced ratios of innate to adaptive immune cells in the blood and decreased expression of innate immune marker genes in the hematopoietic organ. Finally, when we exposed primary immune cell cultures of laboratory-reared fish to homologous and heterologous parasite supernatants collected from the field, cavefish predominantly upregulated adaptive immune genes upon both treatments, whereas surface fish mounted strong innate responses only to homologous parasite cues.

These results suggest that immune systems retain plasticity under high parasite diversity and become more specialized and inflexible when parasite diversity is reduced. This work provides physiological and genetic insights into how a complex vertebrate immune system functions under reduced parasite diversity.

Wild Animal Welfare Science: The emerging field at the intersection between animal welfare and ecology**Michaël Beaulieu**

Wild Animal Initiative

Animal welfare science has traditionally focused on animals under human management such as farmed or laboratory animals. Similar to animals managed by humans, most animals living in the wild are also expected to experience negative and positive affective states (e.g., suffering because of diseases, starvation, or harsh weather conditions; enjoying life when being healthy, satiated, or exposed to mild conditions). Paradoxically, very little empirical research has been conducted so far to better understand these natural experiences. This is an important gap in our understanding of animals' lives, especially when considering the variety of experiences animals are likely to have in their natural habitat. The emerging field of wild animal welfare science specifically aims to fill this gap by unifying concepts used in the fields of animal welfare science and animal ecology. I will illustrate here how both research fields may constructively intersect by showing how variation in affective state may contribute to determine the response of animals exposed to challenging environmental conditions. Crucially, I will also emphasize that such important research questions can be answered only after identifying and validating indicators of animal welfare that can realistically be measured in the field. Finally, I will present the strategy recently developed by Wild Animal Initiative to establish wild animal welfare science as a recognized research field by providing examples of research projects this organization has funded and/or conducted over the last years. By providing the conceptual and practical tools necessary to study animal welfare in the wild, this presentation will hopefully encourage zoologists, irrespective of their backgrounds, to consider wild animal welfare in their future research and join forces to advance this multidisciplinary research field.

A fatty acid-binding protein links lipid handling to chitin synthase-dependent cuticle formation and nanoscale organization in *Tribolium castaneum*

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The insect cuticle is a chitin-containing extracellular matrix whose formation requires coordinated regulation of chitin biosynthesis, fibril organization, and post-synthetic maturation. Although lipids are essential for cuticle barrier function, the mechanisms connecting lipid-associated processes to chitin synthase-dependent cuticle formation remain poorly understood. Previous work in *Drosophila melanogaster* suggested a functional link between fatty acid-binding proteins and chitin synthase-dependent chitin deposition. Building on this, we identified Fabp homologs in *Tribolium castaneum* and selected TcFabp8 as a candidate involved in elytral cuticle formation, prioritized through phylogenetic analysis and qualitative TcChs1 co-immunoprecipitation/mass spectrometry, which detected TcFabp8 among other candidate Chs1 interactors. RNAi-mediated depletion of TcFABP8 caused severe molting and cuticular defects, including reduced cuticle thickness, diminished chitin deposition, and loss of apical Chs1 immunoreactivity. Since TcCHS1 transcript levels were not markedly reduced, these defects point to a post-transcriptional role of TcFabp8 in Chs1 localization, stability, or vesicular delivery. TcFabp8 immunoreactivity was detected in subapical punctate structures and within the developing cuticle, spatially associated with Nile Red-positive lipid-rich compartments, consistent with a role at lipid-cuticle interfaces. Synchrotron X-ray diffraction analysis showed that TcFABP8 depletion preserves α -chitin-associated peak positions but reduces chitin-associated diffraction intensity, and alters fibrillar anisotropy, indicating impaired chitin fibril alignment. Together, these data identify TcFabp8 as a functional link between lipid handling and Chs1-dependent chitin deposition, with direct consequences for nanoscale cuticle organization, raising the question of how lipid-binding proteins more broadly contribute to chitin synthase trafficking and cuticle assembly across insect taxa.

Costly vibes? Male energetic investment in vibratory courtship in response to female feeding condition in the spider *Pisaura mirabilis*

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Elaborate courtship displays are widespread in the animal kingdom and often involve multiple signals of different modalities. The production of such signals is constrained by their underlying energetic costs; and thus, they often function as honest indicators of the quality of the signaling sex. When signaling is costly, selection favors choosiness and differential signal investment by the signaler in response to the quality of the potential mating partner. Males of the nursery web spider *Pisaura mirabilis* are well known for offering a wrapped prey item to females prior to mating. In addition, they produce vibrational signals by tremulating their opisthosoma upon contact with adult female silk, thereby transferring pulses into the substrate through their legs. Both behaviors are considered energetically costly, and therefore likely to function as honest components of courtship in *P. mirabilis*. However, the energetic costs of tremulation have not yet been quantified directly. In this study, we investigate the respiration rate of male *P. mirabilis* spiders as a proxy for energy expenditure during vibrational courtship in response to silk of well-fed and starved females. We exposed 60 males to silk of either well-fed (N=30) or starved (N=30) females and simultaneously recorded CO₂ production and vibrational signals using a custom-built setup combining flow-through respirometry with laser Doppler vibrometry. Males in contact with silk of well-fed females were more likely to engage in vibrational courtship, exhibited longer signaling durations, and produced more pulses. Synchronization of vibrational performance with respirometry will allow us to test for tremulation-specific energy expenditure. We expect that males exposed to silk of well-fed females exhibit higher energy expenditures during active tremulation periods. This study directly assesses the energetic costs associated with vibrational courtship and examines whether males vary their signaling effort based on the feeding condition of females.

Multi-disciplinary insights into active sensing collectives

Thejasvi Beleyur

University of Konstanz

When hundreds and thousands of echolocating bats come together they face a unique sensory and motor challenge. Individuals must track their neighbours, following and avoiding them – while also attempting to make sense of the barrage of echoes and calls arriving from all directions. The fact that bats can even manage to fly and show various kinds of collective behaviour using only sound is a fascinating inverse problem that remains acknowledged but under-investigated due to the logistical, technical and inter-disciplinary challenges involved.

Here I will present our multi-pronged approach at studying these active sensing collectives using sensory modelling, swarm robotics, multi-sensor rigs in the field and cutting-edge acoustic localisation of overlapping sounds. Echolocators perform fine flight maneuvers in groups likely using their own echoes - but how? Our dynamic models of echolocating swarms reveals that individuals may be able to identify their own echoes without the need for special spectro-temporal signatures. Only using the predictability of returning echoes, individuals could filter out others' echoes and calls using what we call the 'spatio-temporal consistency' heuristic. Inferring what echolocators do in the field remains an important frontier aspect that is untouched due to especially the complex overlapping audio that bat groups produce. Using multi-sensor rigs (mic arrays, LiDAR, acoustic cameras, thermal cameras) and cutting edge RANSAC-based algorithms we reconstruct individual flight and call decisions even with overlapping calls in a group at high spatial accuracy of tens of centimeters. Finally, to bridge the simulation-real-world gap, we use swarm robotics to validate biologically plausible sensorimotor heuristics in complex acoustic environments. With our 'SonoRo' robot platform we are able to demonstrate how basic auditorily driven heuristics can generate acoustically mediated collective behaviours like aggregation, dispersion and flocking.

Automatized size measurement of fire salamanders using computer vision: comparison with established methods and application in a large-scale case study

Jonathan Berger; Max Mühlenhaupt; Sean G. Grond; Pia Deimann; Josie Merk; Barbara A. Caspers

Bielefeld University

Body size plays an important role for fire salamanders (*Salamandra salamandra*). A common method to acquire length measurements is taking digital images for post-hoc analysis. However, that process is time-consuming and labour-intensive. This study documents the training of an object detection model that can detect fire salamanders and a size reference in images, and its implementation in a pipeline to measure the total body length of the pictured individual. Compared to manual measurements by hand and digital analysis, the automatic measurement technique produced systematically smaller body length measurements. However, it sped up the process. Since digital analysis is very time consuming and hand measurements are often impractical or harmful, the presented model offers a fast and easy to use alternative.

Using the developed pipeline, an existing dataset was expanded with 1545 body length measurements. A precursor study analysed the distance of fire salamander encounters from various habitat features. Adding body size showed a body size related spatial distribution to several environmental features. Increased distance from refuges with increasing body size indicates that larger individuals are more risk prone, potentially because they are less likely to be preyed upon. The distance to the nearest body of water increased with increasing body size in fall for both adults and subadults likely because smaller individuals face a higher desiccation risk. Overall, this study shows that body size can impact microhabitat choice. Automatizing the size measurement allowed to analyse such a large dataset in a reasonable timeframe which would have been almost impossible otherwise.

Living in the shadows of fungi – the bacterial symbionts of bark beetles**Michelle Borgers**¹; Anna Müller²; Franziska Anni Franke-Gerth²; Stefanos Siozios¹; Michael Gerth¹¹Martin-Luther Universität Halle-Wittenberg; ²Universität Leipzig

To efficiently feed on plant sap, many phloem- and xylem-feeding insects have evolved crucial symbiosis with microorganisms. These symbionts are not only involved in the digestion process but also provide supplemental nutrients and can detoxify plant defense compounds. The specific composition of microorganisms inhabiting the host differs between species, populations, and individuals. Bark beetles are an important component of the forest ecosystem and carry bacterial and fungal microbiota that facilitate the colonization of the host tree's subcortical environment. In recent years, research has focused heavily on ambrosia beetles—a specialized ecological group of bark beetles—and their symbiosis with fungi. In contrast, the bacterial communities associated with these beetles have been largely neglected.

In this study, we aim to gain insight into the bacterial microbiome of bark beetles found in the Leipzig floodplain forest. Using eight cross-vane traps, we collected bark beetles between 26.03.2025 and 13.08.2025, with a collection interval of two weeks. All collected specimens were sorted based on morphological characteristics and a subset of four different morphotypes with high abundance was identified via COI barcoding. The bacterial microbiome of these individuals was determined through near-full-length 16S rRNA metabarcoding using Oxford Nanopore technology. We analyzed temporal variation in symbiont communities both within and across bark beetle species to characterize their associated bacterial microbiomes. Bacterial community composition differed significantly among the four bark beetle morphotypes, and also varied within species across collection time points. These findings suggest that the symbiotic bacterial microbiome is shaped not only by host species identity, but also by seasonal dynamics. We discuss the implications of these findings for our understanding of bark beetle symbiosis and host biology.

Partial Ecological Substitution Over Geological Time Between Praying Mantises and Raptorial Lacewings Uncovered Through Quantifying Prey-Catching Appendage Morphology.

Carolin Haug¹; Christine Kiesmüller²; **KAICHENG CAO**¹; Georgios Kamas¹; Corleone Stahlecker¹; Gideon Haug³; Carsten Gröhn⁴; Patrick Müller⁴; Joachim T Haug¹; Marie K Hörnig⁵

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Several predatory insects have convergently evolved raptorial appendages for grasping prey. Amongst them, preying mantises (Mantodea) and raptorial lacewings (Mantispidae) display broadly similar predation strategies and possess similar morphological adaptations. During the Cretaceous, especially around 100 million years ago, lacewings are known to have had remarkably greater disparity in the raptorial appendage, whereas in mantodeans they appear to have diverged only after this period. This raises the question of whether mantodeans have replaced lacewings in certain predatory ecological roles.

Here, we quantified morphology based on the outlines of the raptorial femur, using elliptic Fourier transformation. We combined an existing dataset from literature with 48 previously unexamined Cretaceous Kachin amber fossils from Myanmar (both lacewings and mantodeans), reaching a consequent 96 fossils spreading across the Mesozoic and the Cenozoic. This substantially expands the available fossil record of raptorial insects.

The resulting morphospace comparison indicates a mantodean expansion into regions previously occupied by raptorial lacewings. However, several morphologies in fossil lacewings remain unmatched by present mantodeans, indicating potential loss of ecological function through time. Overall, our results suggest a partial substitution of predatory ecological niches after the Cretaceous, and only a partial occupation of predatory morphospace, formerly represented by raptorial lacewings. Our findings demonstrate that extinction and diversification do not necessarily result in complete replacement of ecological functions.

Molecular methods for understanding lekking behaviour

Rebecca Chen; Carl Soulsbury; Kees van Oers; Joseph Hoffman

Lekking species exhibit one of the most striking mating systems in nature: males aggregate on non-resource territories, engage in intense competition and elaborate displays, show highly skewed reproductive success while providing only indirect genetic benefits to their offspring. For decades, evolutionary biologists have studied lekking systems to understand what factors cause variation in male quality and hence, what processes underpin such extreme reproductive skew.

In this talk, I present an overview of the molecular approaches I use to study lekking behaviour, highlighting the power of integrating genomic and epigenomic tools with long-term ecological data. Drawing on extensive behavioural, fitness, and genetic datasets from black grouse (*Lyrurus tetrix*), my research bridges evolutionary biology, behavioural ecology, and conservation genetics.

I will show how bioinformatic analyses can be used to link lekking behaviour to genetic quality, how molecular changes can reflect the costs of reproductive investment, and how molecular clock approaches can provide insight into variation in life-history strategies. Together, these approaches demonstrate how molecular data can deepen our understanding of the evolutionary dynamics shaping lekking systems.

Temporal niche in *Drosophila melanogaster*: the importance of living a temporally organised life and the role of Hsp83 in temporal niche expansion.

Angelica Coculla¹; Luis Garcia Rodriguez¹; Carlina Feldmann²; Maite Ogueta¹; Sina Mews²; Roland Langrock²; Ralf Stanewsky¹

University of Münster¹; University of Bielefeld²

To adapt and survive in fluctuating environments, organisms have developed various feedback mechanisms that allow them to anticipate regular and unexpected environmental changes. Circadian clocks are highly conserved, self-sustained feedback mechanisms which rely on environmental cues to synchronise their activity to daily environmental fluctuations. Synchronised circadian clocks allow organisms to concentrate their behaviour within their species-specific temporal niches, providing an overall fitness benefit under cyclic environmental conditions. While species tend to occupy a specific temporal niche, the temporal niche of individuals is plastic and can be expanded and even shifted upon the occurrence of environmental stressors. However, the molecular mechanisms that allow the increase of behavioural variability within the population are yet to be understood. The co-chaperone heat shock protein 83 (HSP83) has been suggested as the main behavioural capacitor for temporal niche adherence, but its mechanisms through which it affects the circadian clocks of flies is unknown. This project confirmed the role of Hsp83 as the molecular driver for temporal niche expansion and demonstrated that Hsp83 depletion exacerbates inter-individual behavioural variation, by dysregulating the transcription of the neuropeptide Pigment Dispersing Factor (PDF) in the central clock neurons. Furthermore, this project investigated whether *Drosophila melanogaster* could actively shape their own temporal niches and regimes. To answer this question, a behavioural assay was developed giving flies the possibility to escape an arrhythmic-inducing constant light (LL) condition, by choosing between a lit and dark area (Bunker conditions). Not only are flies able to actively restore their circadian clock and rhythmic behaviour under Bunker conditions, but also maintaining a temporal niche and having a functioning circadian clock proved beneficial for the overall fitness of the fly.

Nautilus sex determination is unique among cephalopods

Hector Torrado; Carlos Leiva; Ana Riesgo; Sarah Lemer; Arthur Perez; Jose Lorente-Sorolla; Bruce Carlson; Marjorie Awai; Gonzalo Giribet; **David Combosch**¹

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Mechanisms for sex determination are highly diverse among animals and can evolve rapidly across taxonomic groups. This fundamental process dictates an animal's sexual fate and ultimately its development. Recent research has suggested that cephalopods follow a ZZ/ZO sex determination (where males are homozygous and females are hemizygous) that originated at least 480 million years ago, making it one of the oldest conserved sex determination systems known for animals. By combining phenotypic sex data with three genomic datasets from the highly divergent cephalopod clade Nautiloidea (including genome-wide datasets for 91 specimen from 6 species across 9 populations), we show that nautiloids follow an XX/XY sex determination system, where females are homogametic and males are heterogametic. We also identified chromosome #4 as the X chromosome rather than the Z chromosome, as previously suggested. 1 Lastly, we identified five scaffolds representing a putative Y chromosome, based on combined evidence from Bayesian analyses, differences in genome coverage across sexes, and extremely low levels of heterozygosity. Our study identified 36 genes on the putative Y scaffolds, 30 of which are known to be linked to male reproductive functions and include sexual markers conserved across bilaterians. Our findings thus add to previous assumptions about sex determination in cephalopods and their common ancestor and illuminate the diversity of sexual systems and their remarkable turnover in animals.

Early-life heat shock tolerance in insects. A case study on select *Drosophila* species

Raimon Cuxart i Erruz; Claudia Fricke

MLU Halle-Wittenberg

Experimental designs that expose insect embryos to different thermal regimes to measure fitness and physiological responses remain under-used, with most studies focusing on adult or juvenile stages. Yet, temperature effects on fitness-related traits are increasingly recognized as life-stage specific and timing-dependent. Therefore, future climate predictions on insect population dynamics may underestimate thermal vulnerability when focusing solely on adult lethal limits. Recent advances in insect thermal biology have addressed this by generating fitness thermal metrics beyond adult survival such as the thermal fertility limit (TFL80), the temperature for which 80% of a population becomes unfertile.

Here, we propose a standardized approach to estimate embryonic and early juvenile thermal viability in response to step-change heat shocks, providing an analogue to adult lethal temperature metrics (LT80) and the recently proposed thermal fertility limit (TFL80) for embryonic and early larvae heat-shock exposure. We exposed 20000 eggs and larvae of three *Drosophila* species (*D. melanogaster*, *D. simulans* and *D. virilis*) to four-hour static heat-shock treatments at 30, 33, 36, 39, and 42 °C, applied at two distinct embryonic time points and immediately after hatching. Heat shocks were conducted closely after egg laying, after 50% embryonic development time; and after egg hatching at the early larval stage. We modelled thermal reaction norms to calculate the critical temperature for which embryo viability was reduced by 80% (ECTL80), and the same for egg-to-adult viability (EACTL80).

Strikingly, thermal vulnerability differed significantly across early-life stages, with early embryonic exposures yielding the lowest ECTL80 and EACTL80 values across all species and stage-specific patterns showing marked interspecific variation. These results highlight the importance of incorporating perspectives that account for differential developmental vulnerability in insect thermal ecology studies, shedding light on the life-stage specific vulnerability of insects to heat waves and its implications for population dynamics in the context of climate change.

Strobilurins fungicides inhibit the mitochondrial metabolism of mussels**Eugénie T. R. DEREUDER**; Inna M. Sokolova

University of Rostock, Institute for Biological Sciences

Worldwide, pesticide use grew steadily in the last decades to increase crop yields and ensure food security. Strobilurins in particular represent about a quarter of fungicide sales. They are quinone outside inhibitors (QoIs) that block the electron transport system and inhibit fungus cellular energy production and development. Although they had been initially categorised as low-risk compounds, recent studies showed that strobilurins are more toxic to aquatic than terrestrial organisms. Contaminated water runoffs may reach key ecosystem species, such as the coastal blue mussel *Mytilus edulis*, a reef-forming species. In this study, we quantified in vitro the relative inhibitive power of three strobilurin fungicides (azoxystrobin, pyraclostrobin and trifloxystrobin) on mussels' mitochondrial respiration (OXPHOS and LEAK). We found an increasing order of mitochondrial toxicity of azoxystrobin < pyraclostrobin < trifloxystrobin, with EC₅₀ of 669, 251 and 84.2 nM for the OXPHOS and 494, 154 and 49.8 nM for the LEAK, respectively. Reactive oxygen species (ROS) production remained stable through increasing concentrations of strobilurins, while oxygen consumption decreased, resulting in an increasing fractional electron leak (FEL). Reduced mitochondrial capacity for aerobic metabolism may threaten the fitness and important ecological roles of mussels. Ongoing experiments are exploring the effect of acute in vivo exposure of mussels to waterborne trifloxystrobin (10 µg/L), with focusing on the mussels' mitochondrial function, energy balance, metabolites and oxidative stress. This study provides valuable information about the mechanisms of toxicity of strobilurin fungicides on non-target species at the cellular and organism level.

The embryotheca of Hydra is a semi-permeable interface allowing embryo communication with the environment and microbiome

Ella Doveton; Francesco Nienhaus; Jörg Wittlieb; Alexander Klimovich

In recent decades, animal development has increasingly been understood as a process in dialogue with the environment rather than an autonomous programme. Yet the mechanisms governing this dialogue, and their evolution, remain largely unknown. Here, we address this gap using embryonic development of the freshwater polyp Hydra. Shortly after fertilization, the embryo forms a chitinous cuticle, or embryotheca, beneath which most of the embryonic development takes place. Previous studies (Martin et al., 1997) suggested that the embryotheca acts as an impermeable protective barrier. However, recent studies (Noack et al., 2025) indicate that environmental factors, including bacteria, impact hydra embryonic development and, in particular, neurogenesis. This challenges the assumption of the embryotheca's impermeability. To resolve this paradox, we monitor the embryotheca formation in real time and describe its morphology at high resolution. Using fluorescent dyes of different molecular weights, we demonstrate that small molecules cross the embryotheca in vivo, whereas passage of larger molecules is attenuated. Thus, the embryotheca represents a selectively permeable interface that enables the embryo's communication with the environment and the microbiome during development. Our study reveals how physical properties of embryonic barriers complement molecular pathways to integrate developmental programmes with environmental cues.

Building a macrogenetics database for arthropods

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Genetic diversity is a fundamental component of biodiversity that contributes to the capacity of populations to cope with environmental change. Understanding the extent to which population genetic processes are consistently associated with environmental factors across species is a powerful way to examine the processes maintaining patterns of biodiversity. The field of macrogenetics addresses these types of questions by synthesizing publicly available data to study population genetics at broad spatial and taxonomic scales. Macrogenetics research predominantly focuses on vertebrates, particularly mammals, and rarely features invertebrates. We therefore know little about the broad scale spatial distribution of arthropod genetic diversity across species or how such patterns covary with drivers of global change, such as urbanization and agriculture.

To address this issue, we are building a macrogenetics database using publicly harvested data from arthropod population genetics studies. Most macrogenetic studies utilize mitochondrial DNA (mtDNA); however, our database is built using nuclear DNA (nuDNA). We selected microsatellites, which are highly polymorphic and neutrally evolving, from population genetics studies. Using a list of over 50,000 arthropod genera and common names, we queried the Dryad repository for microsatellite genetic data. We then selected datasets based on a priori inclusion criteria (e.g., arthropod species, non-laboratory population, diploid, available geographic coordinates.)

This presentation showcases the database building process and provides some preliminary analytical results. Thus far, we compiled data from 64+ studies, featuring 80+ species across 1465+ populations. Using such analyses can elucidate how land use changes impact populations and their genetic diversity, which can in turn be used to inform conservation efforts. As an example, we estimated two measures of genetic diversity (allelic richness and gene diversity) of bumblebees (*Bombus* spp.). We then used mixed effects linear regression models to test the effects of human-driven land use change, such as urbanization and agriculture, on their genetic diversity.

An experimental test on how parasites and individual variation influence predator functional response

Maja Drakula¹; Lena Gerigk; Joachim Kurtz; Jaime Mauricio Anaya-Rojas²

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Parasites can profoundly influence ecosystems by modifying host traits, thereby altering consumer-resource interactions. We used repeated measurements of the same individuals before and after exposure to a trophically transmitted parasite to quantify infection induced changes in functional responses. This allowed us to disentangle infection effects from pre-existing variation among hosts and revealed patterns that would have not been detectable from group- or post-infection measures alone. Infection reduced overall functional response, with the strongest effects occurring at low prey densities through reduced attack rates. Notably, individuals with intrinsically higher foraging rates were more likely to acquire the parasite, linking pre-existing behavioral variation to infection outcomes and post-infection feeding performance. The results demonstrate that parasites can fundamentally alter predator-prey dynamics, and highlight the value of repeated individual measurements for uncovering trait-dependent infection effects. Such parasite-induced changes may have important consequences for food webs and ecosystem stability, offering a foundation for integrating parasite effects into future models of population and community dynamics.

Cuttlefish adapt their camouflage strategies under naturally occurring dynamic lighting

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Many animals avoid detection or recognition using camouflage tailored to the visual features of their environment. However, these features may be difficult to estimate in habitats prone to dynamic lighting, which might alter the features' appearance, or disrupt the capacity of visual systems to resolve those features. Here, we tested whether 'caustics', a common form of underwater dynamic lighting consisting of moving light bands that can create local, dynamic fluctuations in the intensity of light, affect the camouflage of cuttlefish (*Sepia officinalis*). Owing to specialized pigment cells and a muscular system in the skin, these cephalopods can dynamically adjust their body patterns and three-dimensional skin texture in response to visual features. Although cuttlefish resting on plain or patterned backgrounds usually expressed uniform or disruptive body patterns, respectively, exposure to these backgrounds in dynamic lighting induced stronger disruptive patterns regardless of the background type. We established that dynamic lighting provides additional contrast cues, thereby increasing the overall contrast levels of the visual scene, which elicits a stronger expression of disruptive body colouration in cuttlefish. Subsequently, we exposed cuttlefish to rock stimuli varying in their surface texture and colouration in both caustic and non-caustic lighting and scored their skin texture expression. While this expression was strongest when exposed to contrast-rich rock stimuli, cuttlefish also adopted textured skin under caustic lighting in the absence of rock stimuli, demonstrating that dynamic lighting alone can elicit this response. As for the body pattern expression, we established that the increased contrast levels generated by dynamic lighting elicited the adoption of three-dimensionally textured skin in cuttlefish. Together, these findings show that dynamic lighting strongly influences multiple components of cuttlefish camouflage. We discuss whether these responses represent adaptive strategies that reduce detectability in fluctuating visual environments, or instead reflect constraints imposed by visual processing under dynamic illumination.

Motion aftereffects induced by dynamic illumination**Christian Drerup^{1,2}, James E. Herbert-Read², Martin J. How³**

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Motion detection is an elementary aspect of most animal visual systems. However, many environments are prone to background motion, which might disrupt the ability of visual systems to detect relevant motion cues. While in humans, background motion can disrupt the detection of visual cues even after the moving background component has ceased, it remains unknown whether natural forms of background motion might also affect other animal visual systems. Here, we test whether prior exposure to naturally occurring ‘caustics’, a form of dynamically moving light patterns commonly found in shallow aquatic environments, can have a persisting effect on an animal’s motion detection abilities even after the caustic exposure has stopped. To do this, we established the response probability of the shore crab *Carcinus maenas* to computer-generated expanding disc stimuli mimicking an approaching predator after exposure to either static or moving caustic scenes. Prior exposure to moving caustics had a short-term persisting effect on visual perception in *C. maenas*, reducing crabs’ likelihood to respond to an approaching predator for at least 2 s after the moving caustics had ceased. Our study shows that even after an exposure period to background motion has ended, the visual response rates in *C. maenas* can still be reduced for a short period owing to the prior exposure. While this so-called ‘historical effect’ may derive from an adaptation of the crab’s visual system to the caustic background motion, we discuss whether it may have survival consequences for this crustacean species.

Does self-interest limit prosocial behaviour in the prosocial choice test and giving assistance task?**Sacha C. Engelhardt**¹; Carsten K. W. De Dreu²; Peter M. Kappeler¹; Claudia Fichtel³¹ Georg-August-University Göttingen; ² University of Groningen; ³ German Primate Center (DPZ), Leibniz Institute for Primate Research

Both human and non-human animals can be seen to help and benefit others, but when, how and why prosocial choices are made remains poorly understood. We address these questions with phylogenetically-controlled meta-analyses of prosocial decisions made by actors of 10 avian and 23 mammalian species. We examined if animals behaved prosocially in the prosocial choice test and in the giving assistance task. We assessed the cooperative breeding hypothesis and the effects of different experimental designs on prosocial behavior. We conducted meta-regressions comparisons, and our meta-analyses included more than 300 effect sizes from more than 60 studies. Across species, actors in the prosocial choice test appeared to first consider their own payoffs and only then their partner's, and they benefitted their passive partners only when they themselves benefitted. Prosocial behavior was conditional on the presence of a partner in the prosocial choice test. In the giving assistance task, there was no difference in actors' decisions to choose between a prosocial option and not behaving prosocially. Species' allomaternal care and brain size did not significantly influence prosocial behavior in the prosocial choice test, which did not support key predictions of the cooperative breeding hypothesis. Species' allomaternal care and brain size was significantly negatively associated with prosocial behavior in the giving assistance task, which also did not support key predictions of the cooperative breeding hypothesis. With costly helping being the exception rather than rule, we conclude that prosociality in social vertebrates can evolve to the extent that individual self-interest remains preserved.

Six millennia of population genomics and pathogen prevalence from oyster shells

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The past millennia have seen dramatic ecological changes. The long-term effects of these changes on marine species, their population genomics and microbiomes remain poorly understood. European oysters have likely been affected by multiple ecological stressors, both anthropogenic and natural. They are marine key stone organisms with a long history of human consumption. Their shells have been deposited at archeological sites and natural history collections throughout time. In the last decades, several oyster pathogens have been discovered by modern molecular and experimental methods. Using ancient DNA methods, we extracted DNA from oyster shells that were up to 6000 years old and high-throughput sequenced their metagenomic content. We reconstructed oyster genomes and inferred the prevalence of *Vibrio* bacteria to understand population genomic and microbiome changes throughout time.

Too hot to handle: The influence of heat stress on the parental care of burying beetles

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Animals almost continuously interact with a vast diversity of microbes, and some animals can leverage complex social strategies to manage their microbial interaction partners. However, it remains little understood how robust such social strategies of microbial control are to changing environmental conditions, including those expected under rapid anthropogenic climate change. Here, we tackle this question by investigating the influence of heat stress on microbial control in *Nicrophorus vespilloides*. These burying beetles provide parental care to their offspring on small vertebrate carcasses, an ephemeral resource heavily contested by microbes. While heat stress has been shown to reduce larval fitness and impair parental care, it remains unclear whether these negative effects arise from increased microbial competition. To tackle this question, we are assessing larval fitness, parental effort, and the carcass microbial community in a full-factorial experiment. The occurrence of (i) heat stress, (ii) parental care, and (iii) an antimicrobial treatment reducing the density of microbes on the carcass could show a reduced hatching rate at increased temperatures, as well as lower larval weight. If heat stress reduces the efficacy of parental care in microbial control, we expect that reducing the density of microbes on the carcass mitigates at least some of the negative effects of an increased temperature. By unraveling the impact of heat stress on the efficacy of parental care as a strategy of microbial control, our experiment will contribute to a better understanding of the potential effects of climate change on animal-microbe interactions and the fitness effects of social life.

Impacts of Tire Wear Particles and leached heavy metals on *Gammarus pulex***Friederike Gabel¹**; Elena Lepping²; Hedda Lil Müller²; Ben Schlücking²¹ Institut für Landschaftsökologie, Uni Münster; ² Institute of Landscape Ecology, Uni Münster

Microplastics are increasingly recognized as an environmental problem. Vehicle tire wear is one of the main sources of microplastic input into aquatic environments. Tire wear particles contain numerous pollutants, such as heavy metals, that can enter the environment and affect plants and animals. The release of heavy metals from tire wear particles may depend on particle size and aging. We hypothesized that smaller particles, and especially their eluates, affect organisms more than the larger particles themselves.

We investigated the effects of tire wear particles of different sizes ($< 200 \mu\text{m}$ and $< 630 \mu\text{m}$) at a concentration of 10 g/L on lifespan, activity, feeding rate, and pleopod movement of *Gammarus pulex*. Individuals of *Gammarus pulex* were exposed to fresh tire wear particles, eluates obtained after four weeks of exposure, leached tire wear particles, and a control without tire wear. Heavy metal concentrations in the respective treatments were determined using ICP-OES.

Zinc concentrations were significantly elevated in the eluates. In the eluates, lifespan was significantly shorter (90% reduction), and pleopod movements as well as feeding rates were significantly reduced compared to the control. The activity of the gammarids was significantly lower in the eluate of the smaller particles. In contrast, fresh smaller tire wear particles only affected pleopod movement, while aged tire wear particles and larger particles showed no effects during the experimental period. Thus, the eluates of tire wear particles in particular have effects on gammarids, which may (also) be attributed to the elevated zinc concentrations. Tire wear particles have the potential to reduce the survival of key species in aquatic habitats, thereby disrupting food webs.

Cleared tissue light sheet microscopy reveals cardiac morphology in millimeter-scale crustaceans

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While light sheet fluorescence microscopy has been a cornerstone in developmental biology for years, its application in morphology has not yet been established. With recent advances in tissue clearing and the development of specialized optical technology, light sheet microscopy now allows for multiscale imaging of larger samples. This bridges the gap between established methods, such as confocal microscopy and micro-CT.

The hearts of crustaceans provide a challenging use case for assessing the value of light sheet imaging for comparative morphology. Therefore, heart morphology is visualized for millimeter-scale representatives of different crustacean taxa that are too large for whole-mount imaging in confocal microscopes. Different clearing protocols will be compared, as well as different structural insights via specific fluorescence labelling vs. autofluorescence imaging. It will be shown that large field-of-view setups allow for fast and simple overall morphology, even of delicate cardiac structures, while high-end setups provide unprecedented detail at isotropic submicron resolution. This shows the value of light sheet imaging for comparative morphological studies in non-model organisms and how it can complement the morphologist's toolkit.

The main obstacle to the implementation of light sheet microscopy in morphology is its accessibility. With the Flamingo project, we have made customizable, state-of-the-art light sheet microscopy available to researchers worldwide. In a newly launched pilot project, we specifically aim to make light sheet imaging accessible to the German morphology community.

Colonisation on novel diets: Behavioural and physiological responses of wild house mice during early colonisation stages in new environments with different diets.

Ekaterina Gorshkova

Environmental changes and/or dispersal events lead to animals colonising novel habitats, where rapid behavioural and physiological adjustments are crucial for successful population establishment. As energy consumption is crucial for reproduction and survival, diet is considered one of the key factors influencing both behavioural and reproductive traits. In our study, we investigated the effects of changes in diet composition on behaviour, reproduction, and survival across four generations of wild house mice. Individuals originating from a single population were divided into four groups: a control group (no changes) and three groups with different diet compositions (whole seeds, smashed seeds, vegetable-based), whilst maintaining the same caloric intake. Stress-coping behaviour, sperm count, age at first reproduction and survival rate were measured across generations. No consistent differences in behaviour were observed between groups with different diets or across generations. In contrast, the reproductive traits showed response to environmental change. The F0 generation exhibited a higher sperm count than subsequent generations, indicating higher energy allocation to reproduction during colonisation. Survival rates remained relatively stable in the “whole seeds” and “smashed seeds” diet groups, but declined in the “vegetable-based” diet group over generations. Overall, our results suggest that early responses to novel environmental conditions are primarily driven by life-history adjustment and phenotypic plasticity rather than behavioural changes, highlighting that, at least within the first generations, adaptation has not yet taken place.

When environment gets to your bones: Morphological responses of wild house mice during early colonisation stages in new environments with different diets.

Ekaterina Gorshkova

Anthropogenic influence results in animals constantly facing changes in their habitats. These changes may cause animals to relocate to novel environments, and, in these environments, they often must adjust to new dietary conditions. However, phenotypic plasticity of other body regions is less understood. Here, we assess how vertebral morphology and growth rates change during the early stages of colonisation of novel habitats (semi-natural environments) under a novel dietary regime. Individuals originating from a single population were divided into four groups: a control group (no changes) and three groups with different diet compositions (whole seeds, smashed seeds, vegetable-based), whilst maintaining the same caloric intake. We measured vertebral count, vertebral length and growth rate across four generations (F0–F3). The number of vertebrae up to the caudal region showed no significant differences between groups. Significant differences were found in the number of caudal vertebrae, however, these results may have been due to male aggression. Measurements of individual vertebral lengths (C2, L1, and Ca1) revealed significant morphological differences between groups and generations. F1 mice in all groups on the new diets differed from both the control mice and other generations within the same group. The lumbar vertebra (L1) showed significant differences between generations within each group. Growth rate analysis revealed that F0 mice had significantly lower body weight than controls. However, these differences disappeared in F1 mice. F2 mice on “whole seeds” and “smashed seed” diets were similar to controls, however, those on the “vegetable-based” diet exhibited reduced growth rates. This suggests that vertebral morphology and growth rate can respond flexibly to environmental changes during early stages of population establishment and may also reflect stress-related trade-offs from the parental generation.

52 weeks later: assessing the status of a European fire salamander population one year after the outbreak of Bsal**Sean Gwydion Grond¹**; Lars Poorthuis²; Max Mühlenhaupt¹; Barbara A. Caspers¹¹ Bielefeld University; ² University of Münster

Amphibian populations are on the decline. Habitat loss, climate change and the spread of invasive species make populations dwindle. Among the most critical drivers of the decline observed currently are invasive pathogenic fungi, namely *Batrachochytrium dendrobatidis* (Bd) and *Batrachochytrium salamandrivorans* (Bsal). In amphibians, they cause chytridiomycosis; the disease is known for high mortality. Of the two pathogens, Bsal mostly threatens caudate species. The introduction of Bsal in Western Europe in the early 2000s has led to collapses of European fire salamander (*Salamandra salamandra*) populations ever since and is also threatening other species, such as Crested newts (*Triturus cristatus*). However, scientists observe diverse responses on the population level. As of now, disease dynamics are poorly understood. Since 2022, we study a fire salamander population in Western Germany, that initially was not infected with Bsal. We conduct non-invasive population monitoring, utilising machine learning and pattern recognition, to obtain individual-based activity data. In summer 2025 a Bsal outbreak occurred in this population. Comparing data from 3 years before the epidemic and a year after, we aim to reconstruct spatial and temporal patterns of the Bsal spread in this population; we also address behavioural responses of the fire salamanders by considering diel activity patterns. Our study aims to shine light on possible future perspectives for this population and to draw conclusions for fire salamander conservation in general.

Prenatal maternal effects buffer offspring against reduced post-hatching care in a burying beetle

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University of Bayreuth

Offspring dependency and parental care are tightly interconnected traits that co-evolve across species, yet within species the reliability and quality of care often vary with environmental conditions, social context, and parental state. Such variation creates heterogeneous developmental environments, which can shape how strongly offspring rely on parental care. Maternal effects provide a potential mechanism to cope with this variability, allowing mothers to adjust offspring phenotype or the developmental environment in anticipation of future care conditions. We tested whether mothers modulate prenatal investment in response to expected post-hatching care in the burying beetle *Nicrophorus vespilloides*, a species in which parental care is facultative and highly variable. Using two factorial experiments, we manipulated cues of anticipated care through variation of social context and maternal age and disentangled prenatal maternal effects from post-hatching care by assessing larval performance in its absence. Our results demonstrate that females influence offspring dependency through two distinct pathways: behavioral modifications of the larval environment and direct physiological effects on offspring phenotype. We found that uniparental females facilitate larval access to resources by accelerating carcass preparation, while older mothers produce higher-quality offspring through increased physiological investment in eggs. These findings provide evidence that maternal effects are not merely fixed responses to condition; rather, they are flexible, context-dependent strategies, that allow females to adjust pre-hatching investment in response to cues predicting future care availability. This plasticity ensures that offspring developmental requirements are matched to the specific care regime they will likely encounter, enabling offspring to cope with predictable variation in parental care.

Evolution of Beetle Leg Joints Revealed by Synchrotron X-ray Microtomography

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Beetle legs contain a wide range of biomechanical adaptations, yet the evolution of their internal joint structures remains poorly understood. A striking example is the screw-and-nut joint found in some weevils, in which rotation and axial displacement are mechanically coupled.

Using synchrotron X-ray microtomography, three-dimensional morphometrics and phylogenetic comparative methods, we investigated variation in the mesocoxa-trochanteral joint across major weevil lineages. Our results show that screw joints are not simply separated from other joint types by overall morphology. Instead, continuous variation in joint shape is combined with a limited set of mechanically viable structural configurations. This suggests that complex biomechanical systems may evolve through the gradual modification and recombination of individual components rather than through a single transition between distinct functional types.

Building on this case study, we are extending the analysis across the beetle tree of life. By combining high-throughput imaging with quantitative morphology, phylogeny and ecological data, we aim to identify general patterns in the origin and diversification of beetle leg joints.

Genital damage as a means of avoiding sperm competition: the case of orb-weaving spiders

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In polygamous species, males benefit from adaptations that reduce sperm competition by monopolizing females. Strategies against sperm competition can be physiological, behavioural or morphological. Therefore, studying the interactions between male and female genitalia beyond sperm transfer is essential for understanding these adaptations.

Spiders are perfect study organisms, because of their complex, and diverse genitalia. Males utilize modified legs (pedipalps) for copulation, whilst females possess an intricate structured genital region (epigyne). In orb-weaving spiders (Araneae), the epigyne typically features a structure called the scapus, which is crucial for interlocking. As previously demonstrated in *Larinia jeskovi*, females of *Larinioides cornutus* may also lack the scapus, suggesting an alternative strategy against sperm competition. In *L. jeskovi*, females that lack the scapus are mechanically unable to mate again. To investigate the mechanisms of female genital damage in *L. cornutus* and compare them with those in *L. jeskovi*, we conducted laboratory observations of mating behaviour and high-resolution imaging (SEM and μ CT) of cryofixed pairs during copulation.

Controlled observations of matings confirmed that males were responsible for female genital damage in *L. cornutus*. Using scanning electron microscopy (SEM), the intact epigyne of virgin females was compared with that of mated females. Using μ CT reconstruction, we elucidated the mechanical complexity of genital interlocking and identified the male structures causing genital damage. The mechanism of scapus removal differs between *L. cornutus* and *L. jeskovi*. Behavioural observations showed that female *L. cornutus* that have lost their scapus do not mate again. This is not due to a mechanical conflict, but rather to a reduction in the females' willingness to mate.

Our study demonstrates that genital damage is an effective strategy for preventing sperm competition. Furthermore, damage mechanisms in Araneidae have likely evolved multiple times, as both the mechanisms and effects on mating behaviour differ between the two species observed.

How variable is the morphology of the crustacean olfactory lobe? A comparison of isogenic and genetically diverse *Procambarus* crayfish

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Olfactory lobes of aquatic crustaceans are the primary centers for olfactory processing. They are bilaterally paired neuropils in the deutocerebrum of the central brain and comprise numerous olfactory glomeruli, subunits with a high synaptic density that receive and process olfactory input. Variation in olfactory lobe morphology may therefore reflect differences in glomerular spatial organization. Whether such differences are related to glomerular number or other aspects of glomerular arrangement remains unknown. Moreover, there is little information on stability versus variability of glomerular numbers in crustaceans, an important aspect for any consideration of olfactory coding strategies in these animals. In crayfish, olfactory lobes are commonly described as spherical neuropils. However, this assumption is largely based on two-dimensional anatomical descriptions. Here, we investigated the three-dimensional (3D) morphology of the olfactory lobes and whether differences in glomerular numbers and organization are reflected in olfactory lobe shape. Additionally, to assess the potential influence of genetic diversity, we compared the parthenogenetic *Procambarus virginalis* Lyko, 2017 with its congeneric, sexually reproducing species, *Procambarus alleni* (Faxon, 1884).

3D-reconstructions were generated from micro-CT data using 3D-Slicer with manual segmentation of each olfactory lobe. 3D-reconstructions revealed an overall kidney-like shape of the olfactory lobe. Intraspecific variations of olfactory lobes morphologies were not species-specific and not related to differences in glomerular numbers, suggesting that remaining variation may reflect structural and spatial differences among individual glomeruli. Together with the observed variability in glomerular numbers in both the parthenogenetic and sexually reproducing species, indicating that glomerular numbers are not genetically fixed, these findings support growing evidence that olfactory lobe organization in crustaceans may rely less on the formation of additional glomeruli and more on structural flexibility within the existing glomerular system, implying a different olfactory coding strategy than we find in insects. This study was supported by DFG Project Ha 2540/19-1.

Interplay of body size, behaviour and predation strategy in *Daphnia* inducible defences**Martin Horstmann**; Johanna Knupfer; Linda Weiss; Ralph Tollrian

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Daphnia are well known for their ability to protect themselves against predators through the development of inducible morphological, behavioural, and life-history defences. The interplay of body size and behavioural defences, however, has rarely been investigated, although it may be a decisive trait for the evolution of defensive strategies. Therefore, we investigated the behavioural response of the relatively small species *D. barbata* and the two relatively large species *D. longicephala* and *D. magna* in the presence of the heteropteran backswimmer *Notonecta*, an ambush predator, and the tadpole shrimp *Triops*, a cruising predator. We hypothesised that, in addition to prey body size, predator hunting strategy is a relevant factor for the evolution of defensive strategies. We found that the small species *D. barbata* responded with distinct behavioural alterations in depth selection, swimming velocity and swarming behaviour to *Triops* and *Notonecta* presence, whereas the large species *D. longicephala* adjusted only swimming velocity and depth selection. Large *D. magna* showed no behavioural response at all. In general, daphniids appeared to demonstrate a more pronounced response in the presence of the ambush predator *Notonecta* compared to the cruising predator *Triops*. Based on these observations, we identified an interplay pattern between prey body size, predator hunting type, and resulting behavioural response, which may also apply to other species.

Better Together – How Offspring Cooperation Shapes Benefits across Family Contexts

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Relationships within families are among the most essential forms of social interactions. Social isolation experiments in a variety of different animals highlighted their importance for well-being and longevity. Thereby, parental care is traditionally considered the primary interaction among families. Nevertheless, family groups entail much more multifaceted interactions between their members. Offspring interactions, for example, range from fierce competition to cooperation and offspring cooperation is indeed a key feature of eusociality. Accordingly, recently emerging views hypothesize that offspring cooperation might have been a key driver in the early evolution of social life. Through the advantages retrieved from staying together as an offspring group, offspring interactions may have been an initial step in the formation of family groups. Using a variety of social isolation experiments in the subsocial burying beetle *Nicrophorus vespilloides*, we were able to highlight that offspring cooperation indeed provides fitness benefits for the offspring, across different social constellations, not only in the absence of parental care but even in its presence, though they manifested differently. Without parents, offspring interactions were able to buffer the missing care, whereas in their presence, they increased brood value, thereby increasing parental investment. Our results further suggest that offspring cooperation can enhance buffering capacities of parental care against harsh environments, such as fluctuations in temperature. We also find that greater relatedness enhances the benefits of offspring cooperation, whereas lower relatedness, through increased genetic diversity, promotes social immunity and improves survival. These opposing effects highlight a crucial evolutionary trade-off for kinship in the early evolution of social life, but also suggest that grouping benefits among offspring are not exclusively tied to indirect fitness gains. Overall, our results support the idea that offspring interactions might have been particularly important in early family groups, where parental care was optional rather than obligatory.

Eight legs, eight glands, endless possibilities: rethinking spider silk use

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The silk glands in spider facilitate a wide range of behaviours, including prey capture, web construction, reproduction, locomotion, and dispersal. The silk glands differ across various spider lineages in terms of morphology, number, and silk usage patterns. Most species have several silk glands (from 2 to 8 distinct kinds), yet our understanding of how multiple silk glands coordinate during specific behaviours remains limited. To address this gap, our research addresses two key questions: 1) How does a single species utilize its complete multi-silk gland repertoire across various behaviours, and 2) whether patterns of silk gland use are conserved or diverge across spider lineages performing the same behaviour. To investigate this, we combined high-speed videography, laboratory and field behavioural observations, snap-freezing of spiders mid-behaviour, diverse microscopy techniques, and comparative phylogenetic analysis. Our results demonstrate that individual species often deploy multiple silk glands simultaneously during different behaviours, indicating a complex and heterogeneous use of the silk system. Comparative analysis across lineages reveals that, despite certain behaviours evolving convergently multiple times across the spider phylogeny, silk gland usage remains remarkably consistent. Those glands that are typically associated with different behavioural contexts like locomotion, web building, and dispersal are frequently deployed together for a single behaviour as well. These findings challenged the prevailing "one gland, one behaviour" view of silk biology, suggesting that multi-gland deployment is a widespread strategy in various behaviours in spider silk biology. This study provides a new perspective on the relationship between silk gland evolution and behavioural diversification in spiders.

Temperature-independent motion processing in the central brain of bumblebees

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Insects experience substantial seasonal and daily fluctuations in ambient temperature. The body temperature of bumblebees is influenced by ambient conditions, but they can regulate it within certain limits using behavioral and physiological mechanisms. However, their body temperature cannot be held constant when ambient temperatures exceed 25 °C. Most neuronal responses and underlying biochemical processes in insect sensory systems are known to depend on temperature. Yet, behaviors such as distance estimation require a reliable encoding of information. This suggests that the underlying neuronal processes may be temperature-independent. TN-neurons provide input to the noduli of the central complex and encode translational optic flow. They are therefore strong candidates for providing optic-flow information to the insect odometer. Here we investigated the effect of temperature on the tuning of wide-field motion-sensitive neurons that exhibited physiological characteristics consistent with TN-neurons. We used multi-unit recordings from within or around the noduli to examine responses to gratings with different velocities (range: 112° s⁻¹ to 2705° s⁻¹) under different temperature conditions (range: 23 °C to 34 °C). Our preliminary data show that preferred velocity was unaffected by temperature in 8 out of 9 cases. Additionally, overall spiking was unaffected in most TN2-like neurons (4 out of 5) that were excited by front-to-back motion (i.e. simulated forward flight). Among TN2-like neurons that were excited by back-to-front motion (i.e. simulated backward flight), this effect was observed in 1 out of 4 recordings. These findings suggest that the velocity tuning of TN-like neurons is largely temperature-independent and may provide temperature-compensated optic-flow information to the odometer.

Are trap-jaw mandibles morphologically adapted to mechanical resistance? The case of *Strumigenys* ants

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Within the ant genus *Strumigenys*, we observe recurrent evolution of power-amplification mechanisms that increase mandible-closure speed, resulting in a trap-jaw mechanism. Its species can be split into three groups: long-mandibulated trap-jaws (LTRAP), short-mandibulated trap-jaws (STRAP), and short-mandibulated with gripping mandibles (GRP). The gains and losses of this mechanism involved modifications in mandible and head morphology, but little is known about its functional consequences for the distinct mechanical demands associated with those groups. To test the hypothesis that trap-jaw mandible groups exhibit morphological adaptations to deal with higher mechanical demands than the gripping species, we generated 3D digital models of mandibles from 44 *Strumigenys* species spanning the three groups and measured traits associated with the mandible resistance to bite-loading, namely cuticle thickness, mechanical advantage (MA), and second moment of area (I). Additionally, we used the finite element method to estimate stress under bite loading. Then, we employed PCA to summarise the morphological information and test whether mandible groups occupy distinct regions of the multivariate space. To test which morphological traits better predict stress variation in a comparative phylogenetic framework, we fit PGLS models with mandible stress as the response variable, morphological traits and mandible group as predictors. We found that LTRAP mandibles consistently differ morphologically from the other groups, whereas STRAP and GRP differed only marginally, mainly due to slight variation in mandible thickness and I. These variables were also the main predictors of stress variation, with *Strumigenys* trap-jaw groups showing consistently higher stress levels than GRP mandibles. Our results demonstrate that the distinct functional strategies exhibited by *Strumigenys* mandibles are accompanied by morphological changes with relevant functional consequences, although distinct from our expectation that trap-jaw mandibles would be morphologically adapted to reduce stress levels in strike biting.

The functional morphology of cuttlefish tentacles and implications for controlling strikes

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Cuttlefish and squid (Cephalopoda: Decapodiformes) are versatile predators that can grasp prey within milliseconds using two extensible tentacles. Each tentacle consists of an extensible stalk and a terminal club, which is equipped with suction cups for attachment. In under 40 milliseconds, the tentacle clubs have to be accelerated, rotated to expose suckers and properly aligned with the prey to make contact. The mechanism for tentacle club orientation and positioning in the last phase of the strike is so far unknown. In this study we combine micro computed tomography and histology with 3D highspeed video and computational fluid mechanics (CFD) to investigate how the dwarf cuttlefish *Ascarosepion bandense* controls its tentacles before capturing prey. Our results show that tentacle clubs are capable of rapid turns (exceeding 5000°/s) and decelerate with up to 20 G's before contact. The last phase of the strike is likely dominated by hydrodynamic forces, thus requiring a switch from a low-drag to a high-drag configuration of the tentacle clubs. This could be facilitated by rapid extension of a lateral fin on the club, in which we found cross-striated muscles, a rare muscle type in cephalopods, associated with rapid movements. Furthermore, the muscle arrangement in the club more closely resembles arm musculature, suggesting the clubs are well capable of bending. Finally, we use CFD simulations to investigate whether club deformations based on morphology can reproduce the kinematics observed in actual strikes. Our results help to understand cephalopod hunting and could inform the design of fast, soft gripping devices.

Identifying the genetic underpinnings of repeated behavioral evolution**Johanna Kowalko**

Lehigh University

Adaptation to similar environments frequently results in the repeated evolution of similar traits. For example, species and populations of animals which are adapted to survive and thrive in caves have repeatedly evolved similar morphological, physiological and behavioral traits, providing a powerful opportunity to study the molecular mechanisms underlying repeated trait evolution. To investigate the mechanisms contributing to the repeated evolution of behavioral traits, we utilize the Mexican tetra *Astyanax mexicanus*. *A. mexicanus* is a small, freshwater fish with populations of riverine surface fish and over 35 populations of cavefish. In addition to many common cave-adapted traits like eye degeneration and albinism, multiple *A. mexicanus* populations have evolved changes to behavior, including a reduced response to stressors. We quantified stress-associated behaviors and a suite of other traits in cave-surface F2 hybrids derived from multiple populations of cavefish and performed correlations between traits, demonstrating that multiple traits co-vary in crosses of cavefish from independent populations. Moreover, through quantitative trait loci mapping, we identified the genetic architecture underlying the evolved reductions in stress response in multiple *A. mexicanus* cave populations, and found evidence that at least some of the same genetic loci underlie reductions in stress-associated behaviors in independently evolved cave populations. Further, we have characterized the changes in gene expression associated with stressful stimuli in surface fish and multiple populations of cavefish from this species. Together, these experiments increase our understanding of how complex traits repeatedly evolve, as well as the mechanisms contributing to natural variation in response to stress.

HotSecretions: Effects of heat stress on antimicrobial secretions and fitness in an insect with biparental careCamila Zenobi; Charlotte Wallis; Maja Fluch; **Jos Kramer**

University of Bayreuth

Heat stress can impair fitness by disrupting physiological and behavioral processes and is increasing in frequency and intensity in a rapidly warming world. Species that provide parental care may be especially vulnerable to such stress, because elevated temperatures could simultaneously increase offspring need and impair the expression of parental behaviors. However, how heat stress affects specific components of care and thereby translates into negative fitness consequences is still poorly understood. Here, we address this issue by examining the effects of heat stress on antimicrobial secretions and associated fitness effects in *Nicrophorus vespilloides*. In this burying beetle, parental secretions play a key role in preserving the breeding carcass and might be especially important when elevated temperatures speed up carcass decay. We repeatedly collected anal secretions from breeding pairs maintained under elevated or control temperatures and then linked the amount and antimicrobial activity of those secretions to performance traits of adults and offspring. We found that higher secretion production was associated with higher offspring survival and quality under heat stress. However, even high levels of secretion production could not fully mitigate the negative effects of elevated temperatures on offspring performance, and parents did not increase their secretion production under heat stress. Taken together, these results suggest that physiological constraints may prevent parents from upregulating secretion production under heat stress despite its benefits to offspring. More generally, our results highlight that the capacity of parental care to buffer against environmental stress may be limited where parents cannot flexibly adjust their investment into crucial components of care.

Elemental reshaping of gastropod radular teeth during functional use

Wencke Krings¹; Stanislav N. Gorb²

¹ Leipzig University; ² Christian-Albrechts-Universität zu Kiel

Radular teeth are continuously produced and replaced, but during their functional lifetime they are exposed to repeated mechanical abrasion and to the chemical environment of the buccal cavity. While many studies have addressed compositional changes during tooth formation and maturation, it remains unclear whether mature teeth remain chemically static after entering the working zone. Here, we experimentally tested, whether wear and subsequent removal of an abrasive substrate affect the elemental composition of radular teeth in the freshwater gastropod *Planorbella duryi*. Snails were exposed either to abrasive sandpaper, to abrasive sandpaper followed by a post-abrasion phase without abrasive substrate, or to non-abrasive control conditions. Radulae were analyzed by scanning electron microscopy and energy-dispersive X-ray spectroscopy across defined radular regions representing different stages of functional exposure.

The experimental sequence revealed a radular replacement rate of approximately two tooth rows per day. Continuous abrasion caused pronounced wear and region-specific changes in elemental composition. Calcium and fluorine were reduced in regions associated with intense substrate contact, indicating strong initial modification by combined mechanical and chemical wear. In contrast, individuals subjected to a post-abrasion phase showed partially increased calcium and fluorine values in later functional regions. Elemental analyses of buccal secretions further suggest that saliva through the strong presence of calcium may contribute to surface-level compositional modification, although the underlying binding state remains unresolved.

Our results indicate that radular teeth are not chemically fixed after maturation, but dynamically modified during functional use by tooth age, substrate contact, wear and the buccal chemical environment.

Temporal niche partitioning in a global lizard radiation

Yasemin Kukla; Jendrian Riedel; James T. Stroud; Dennis Rödder

Understanding why some lineages diversify extensively while others remain species-poor is a central challenge in evolutionary biology. Key innovations are often proposed to promote diversification by enabling access to ecological opportunity, yet their evolutionary significance depends strongly on environmental and biogeographic context. Geckos are an ideal system for evaluating these concepts since they are globally distributed, exceptionally species-rich, and display extensive ecological and functional diversity.

Previous work on adhesive toepad evolution across ~80% of the known gecko diversity demonstrated repeated independent origins of adhesive morphologies associated with structurally complex habitats worldwide. Rather than facilitating expansion into novel climatic regimes, adhesive toepads appear to promote ecological specialization within existing environments, emphasizing that key innovations may refine ecological performance to generate novel niche space.

Here, we extend this framework beyond morphology by examining diversification along the temporal niche axis. In contrast to most other lizards, geckos are largely nocturnal, raising questions about how activity time structures ecological interactions. Using global distribution data and comparative analyses of activity patterns, we quantified geographic overlap among geckos. Additionally, we include non-gekkonid lizards within the gecko size range (over 3000 species) to evaluate whether temporal differentiation may reduce competitive interactions. Preliminary analyses reveal geographically structured activity patterns and activity-dependent patterns of species overlap, with evidence for both clustering and avoidance among geckos and non-gekkonid lizards.

Our research highlights how diversification may emerge through multiple ecological dimensions. Together, these results frame geckos as a model for understanding how key innovations interact with ecological opportunity across space, structure, and time.



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Sophie Leonie Kunde¹; Dr. Christoph Mayer²

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Following DNA sequencing and assembly, genome annotation is a fundamental step in the interpretation of genomic information. We present novel neural network architectures for the annotation of diverse genomic elements. Across multiple annotation tasks, our models achieve accuracies comparable to or exceeding those of established methods while substantially reducing computational requirements. We demonstrate the applicability and scalability of the approach in two large-scale case studies involving mitochondrial genome annotation and the annotation of transposable elements in nuclear genomes.

A dark blue silhouette of the Münster city skyline, featuring various church spires, domes, and a tall tower on the right. The text 'Münster 2026' is centered over the skyline.

Münster 2026

Evolutionary genital morphology of caecilian amphibians updated

Susanne Kuehnel¹; Adriano Maciel²; Sonja Herberhold³; Marcelo Sturaro⁴; Felix Beckmann⁵; Ana Prudente²; **Alexander Kupfer⁶**

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Sex is the motor of organismal evolution! Caecilian amphibians are a unique group of tropical vertebrates well adapted to lead a subterranean life. Among the evolutionary key innovations are genitalia such as the male phallodeum, a unique copulatory organ which is everted and safeguards internal fertilization. Since the caecilian cloaca is ontogenetically a part of the digestive system it is not a separate structure exclusively dedicated for reproduction such as the squamate hemipenis. Nevertheless, complex and diverse morphologies have evolved in all caecilian families that include different patterns of longitudinal ridges, tuberosities or crests, but also various forms of paired blind sacs. Here we present a comparative overview of the overwhelming diversity of caecilian genitalia, both for females and males. Using specimens housed in natural history museum collections around the globe we explored the cloacal anatomy of both sexes of several taxa representing the major clades and reproductive modes via classic dissections and conventional histology combined with state of art soft tissue μ CT-scans. We interpreted our results within an evolutionary framework based on most recent phylogenetic hypothesis, to check (1) for gains and losses of specific genital morphologies and (2) for sexual selection issues but also (3) if morphological patterns are linked to the highly variable reproductive modes present in caecilian amphibians. In summary our comparative integrative approach into the complex reproductive morphology of caecilian amphibians offers prime potential for our understanding of the evolution of vertebrate reproduction.

Cellular signatures of immune manipulation in a classic model of host–parasite coevolution at single-cell resolution

Joachim Kurtz ; Gero Heidtmann; Robert Peuß

University of Münster

Parasites are major drivers of natural selection and have shaped the evolution of complex host immune systems as well as sophisticated mechanisms of immune evasion and manipulation. The interaction between the cestode *Schistocephalus solidus* and the three-spined stickleback (*Gasterosteus aculeatus*) has become a key model for studying host–parasite coevolution and the evolutionary arms race predicted by the Red Queen hypothesis. While previous studies of immunity in this system have largely relied on bulk transcriptomics, these approaches could only capture average gene expression across heterogeneous tissues and therefore lacked cellular resolution.

We here apply single-cell RNA sequencing (scRNA-seq) to the *Schistocephalus*–stickleback model to characterise the immune response at the level of individual cell populations. By analysing the head kidney, trunk kidney, and spleen 30 days after parasite exposure, we investigated changes in immune cell composition, proliferation, and differentiation, complemented by cell cycle and pseudotime analyses.

Our results reveal a pronounced shift towards myeloid cell populations in infected fish, whereas exposed but uninfected individuals retain a more balanced contribution of myeloid and lymphoid cells, underlining the importance of both innate and adaptive immunity for resistance against helminth infection. Beyond refining our understanding of immune cell dynamics, the single-cell approach uncovers previously hidden patterns of proliferation and differentiation that could not be resolved by bulk transcriptomic methods.

Importantly, our findings challenge the prevailing view that next to the spleen, the head kidney is the sole immunologically relevant primary lymphoid organ in teleosts. While the head kidney displayed the strongest proliferative activity, the trunk kidney also exhibited substantial immune activity and shared differentiation trajectories, highlighting an underappreciated role in teleost immunity. This methodological advance not only provides new insights into immune manipulation by *S. solidus* but also establishes a more comprehensive framework for future studies of host–parasite coevolution and fish immunology.

The structural diversity of mollusk shells during Cambrian radiation

Luoyang Li

Ocean University of China

The evolutionary success of mollusks is closely linked to the acquisition of highly mineralized shells during the Cambrian explosion (~560–520 Ma), when most modern animal phyla first emerged and biomineralization became widespread. Mollusks construct complex shells composed of >95 wt% calcium carbonate (CaCO_3 ; mainly aragonite and calcite) crystals embedded within a three-dimensional organic matrix that typically accounts for less than 5 wt% of shell mass, and their multiscale hierarchical architectures confer exceptional mechanical properties far exceeding those of non-biogenic carbonates. The molluscan fossil record extends back to the early Cambrian, when they underwent an explosive radiation and are commonly recovered as millimetre-scale ‘micromollusks’ from globally distributed Small Shelly or Small Skeletal fauna (SSF). Soft-bodied anatomies of Cambrian mollusks are largely unknown; nevertheless, widespread phosphogenesis across the Precambrian–Cambrian transition, caused by global transgression onto epicontinental seas, enabled exceptional preservation of shell microstructures at micrometre to sub-micrometre scales. These shell microstructures are preserved on the surfaces of phosphatic steinkerns. Available evidence suggests that early mollusks may have initially produced relatively simple laminar fibrous microstructures derived from ancestral organic scaffolds, followed by the evolution of increasingly complex and highly organized shell architectures. Multiple modern-type microstructures, including foliated aragonite, fibrous, prismatic, and crossed-lamellar forms, are already present in early Cambrian taxa, indicating a rapid diversification of shell structure and progressive increase in biological control over biomineralization during early molluscan evolution.

Evolutionary Dynamics of Sex Biased Gene Expression in Sexually Dimorphic Fireflies**Nicolas Lichilin**¹; Du Haoqing¹; Stepan Saenko²; Sebastian Höhna¹; Ana Catalán¹¹ LMU; ² University of Greifswald

Sexual dimorphism varies widely across species and often reflects distinct selection pressures acting on males and females. Sex-biased gene (SBG) expression is a key mechanism for resolving sexual conflict, yet the evolutionary forces shaping SBG expression remain unclear for most taxa. Fireflies (Lampyridae), with an evolutionary history spanning ~150 million years, display a remarkable diversity in sexual dimorphism, with species ranging from an unnoticeable sexual dimorphism to females retaining neotenic/immature traits, making them an ideal system to study the evolution of SBG expression. Yet, only recently has sexual dimorphism in fireflies begun to be studied.

To address this, we leveraged a newly consolidated firefly phylogeny and analyzed RNA-seq data from 21 globally distributed species. Reference genomes were generated, annotated, and aligned using STAR. Differential expression was modeled using DESeq2 ($|\log_2FC| > 1.5$, $p\text{-adj} < 0.05$), combined with macro-evolutionary phylogenetic comparative methods in R. We used FANTASIA to assign functional annotations, and orthology assessment was performed with OrthoFinder, followed by 1:1 orthologue relationship refinement with Possvm.

Our results reveal a substantially higher abundance of SBGs in firefly bodies (abdomens) compared to heads. Interestingly, bodies exhibited a significantly male-biased gene pattern, while heads tend to show a female-biased pattern. Across the phylogeny, the subfamily Lamprohizinae displayed the highest number of head-specific SBGs. These striking tissue and lineage-specific patterns suggest that divergent selective pressures are associated with unique life-history traits such as female flightlessness and bioluminescent signaling, that strongly shape regulatory evolution.

By integrating comparative genomics and SBG expression in fireflies, we show that SBG expression is lineage-specific, influenced by a combination of stabilizing, directional selection, genetic drift and life history traits of each firefly species. These findings deepen our understanding of how sex-specific selection and regulatory evolution contribute to the emergence of morphological and behavioral dimorphism, with broader implications for evolutionary biology.

Tiny but Mighty – An Integrative Taxonomic Revision of Huttoniidae (Araneae), an Endemic New Zealand Spider Family**Mattes Linde**; Hannah Wood; Cor Vink; Martín Ramírez; Peter Michalik

The monotypic palpimanoid spider family Huttoniidae, endemic to New Zealand, represents a unique lineage within the spider tree of life. Owing to their cryptic lifestyle, apparent rarity, and limited availability of specimens, huttoniids have received little scientific attention, and their diversity and evolutionary relationships have remained largely unexplored. Here, we present the first comprehensive assessment of the diversity and phylogenetic relationships of Huttoniidae using an integrative taxonomic approach combining detailed morphological examinations with molecular phylogenetic analyses. Our study reveals that huttoniid spiders are far more diverse than previously recognized. We describe six new genera and 20 new species, substantially increasing the known diversity of this group and providing the first robust taxonomic framework for this family. Phylogenetic analyses support the monophyly of Huttoniidae as well as provide a robust framework for the establishment of the new genera. Huttoniids are distributed across much of New Zealand, although many species appear to exhibit a high degree of local endemism. Given the cryptic nature of these spiders and the limited sampling coverage available for many regions, additional undescribed species are likely to exist. Further research is needed to clarify distribution patterns, evolutionary history, population structure and potential conservation status, particularly as many species are associated with native habitats that are increasingly affected by habitat degradation and environmental change.

An interdisciplinary approach for monitoring ground beetle community health in salt marshes**Anne Mack**¹; Michael Kuhlmann ¹; Christine Ewers ²¹ Christian Albrechts Universität zu Kiel, Zoologisches Institut; ² Leibniz Institut zur Analyse des Biodiversitätswandels

Salt marshes are highly dynamic coastal ecosystems that are shaped by natural processes and anthropogenic influences. Natural, tide-influenced sites supported distinct species communities, whereas anthropogenically transformed areas may differ markedly in community composition. However, long-term monitoring to understand the consequences of these influences on community health are lacking. Here, we investigated the potential of integrating contemporary population genetic analyses with historical biodiversity and morphological data to assess long-term changes in ground beetle populations along the Wadden Sea coast of Schleswig-Holstein. Morphometric analyses revealed changes in body size and pronotum shape over a period of approximately 40 years, while fluctuating asymmetry remained largely stable. Population genetic analyses indicated low mitochondrial diversity and weak genetic structuring, suggesting dynamic demographic processes. Overall, we demonstrate that different biological levels respond to environmental change to varying degrees and that species lists alone are insufficient to fully capture long-term ecological dynamics. The combination of historical datasets, morphometric approaches, and population genetic data offer great potential for future long-term monitoring programs in salt marsh ecosystems.

Absence of the Earth's magnetic field induces stress in a mammal

Li Zhang; Billy Lam; Alireza Saeedi; Leoni-Marie Webb; Sabine Begall; Christin Osadnik; Alessandro Felder; Adam Tyson; Georgina Fenton; **Pascal Malkemper**¹

¹ Max Planck Institute for Neurobiology of Behavior - caesar

The Earth's magnetic field is a constantly available cue for animals with a magnetic sense. Among mammals, the magnetic sense is most thoroughly studied in African mole-rats of the genus *Fukomys*, subterranean mammals that navigate in dark tunnel systems. Their magnetic sense was discovered more than 30 years ago, but our understanding of the neural pathways involved remains incomplete.

Here, we present a novel pipeline that combines c-Fos immunolabeling, tissue clearing, lightsheet microscopy, and a new 3D brain atlas integrated into the BrainGlobe environment to map global brain activity in mole-rats, which we call MoBI-DiSC (Mole-rat Brain Imaging with iDISCO and ClearMap). We exposed Ansell's mole-rats to a changing magnetic field and compared their brain activity to that of control animals exposed to a near-zero magnetic field using MoBI-DiSC. To our surprise, we find evidence of activation of stress-related pathways following exposure to near-zero magnetic field conditions. Using closed-loop magnetic-field control in a place-preference test, we demonstrate that mole-rats actively avoid near-zero magnetic fields, indicating that such conditions are not neutral for these animals.

Our results demonstrate that a zero magnetic field constitutes a biologically relevant stressor that alters both brain activity and behavior in a magnetosensitive mammal. We suggest that the use of zero-field conditions as experimental controls in magnetoreception research should be reconsidered. More broadly, our findings underscore the importance of the Earth's magnetic field as a permanent and ecologically relevant sensory cue, whose continuous availability may be actively monitored by animals rather than serving solely as a source of directional information during navigation.

Same City, Same Microbes? Repeatability of the urbanisation-driven microbiome alterations

Öncü Maraci¹; Lena Fus; Marta Szulkin²; Barbara A. Caspers¹

¹ Bielefeld University; ² Institute of Genetics and Biotechnology, Faculty of Biology, University of Warsaw

Urbanisation is one of the most pervasive forms of environmental change, rapidly altering multiple ecological conditions across landscapes. Although several studies have shown that urbanisation can influence the assembly of the animal gut microbiome, it remains unclear whether these patterns are consistent across species, years, and cities. To fill this gap, first, we characterised the gut microbiome of juvenile great tits (*Parus major*) reared in nest boxes distributed across an urban mosaic in 2018. Microbial alpha diversity was negatively associated with the amount of impervious surface surrounding breeding sites, and community composition differed significantly between urban and non-urban locations. Second, we examined the repeatability of these patterns across species and time by characterising the gut microbiome of blue tit (*Cyanistes caeruleus*) nestlings reared in the same locations in 2018 and 2019. The reduction in alpha diversity and shifts in community composition observed in urban environments were consistent across both species in 2018. However, these urbanisation effects were not detected in samples collected in 2019, a year characterised by lower temperatures, reduced rainfall, and decreased food availability during the breeding season.

Overall, our findings reveal a substantial but year-dependent effect of urbanisation on the avian gut microbiome. These results underscore the importance of replication across years and highlight the need for long-term studies in multiple cities to better understand the ecological drivers of microbiome variation in changing environments.

Unraveling lateral line contributions to escape decisions

Benedikt Maric; Stefan Schuster; Peter Machnik

Universität Bayreuth

The Mauthner neurons are crucial for triggering the fastest escape C-starts of fish. They determine when an escape response is initiated and whether it turns the fish towards the left or to the right. This makes the Mauthner neuron an ideal system for investigating, at cellular resolution, how a survival-relevant decision is made. By performing in vivo intracellular recordings of postsynaptic potentials in the Mauthner neurons, it is possible to examine precisely how different sensory inputs contribute to the timing and directionality of escape initiation. Previously, only sensory input from the auditory system could be studied. In our laboratory, we have discovered anesthetics that additionally allow visual inputs to be studied. This revealed surprising coordination effects between sensory channels that highlight the Mauthner neurons as a powerful model for studying multisensory integration. Because the lateral line is important in fish, it should also influence the Mauthner neurons and influence both start and directionality of escape responses. However, despite its importance, it has previously not been possible to study lateral line input to the Mauthner neurons in anesthetized animals.

Here, we overcome this limitation for the first time. By establishing conditions that allow intracellular recordings from the Mauthner neurons while preserving lateral line function, we are now able to analyze hydrodynamic input to the escape-initiation network with high spatial and temporal resolution. Our recordings demonstrate how lateral line information is represented in the Mauthner neurons and how it contributes to the perception of the environment in an escape-response context. This approach enables, for the first time, a detailed analysis of how spatially and temporally precise multisensory information is integrated at the cellular level to guide a life-saving behavioral decision: when to initiate the fastest possible escape and whether to start the movement to the left or to the right.

Cities are changing the social lives of animals

Avery Maune; Barbara Caspers; Isabel Damas Moreira

Bielefeld University

Urbanisation is a major driver of rapid environmental change, exposing animals to novel stressors and reshaping the social environments in which they live. Because social behaviour is central to survival and reproduction, understanding these changes is crucial for anticipating species' responses to increasingly urbanized landscapes. We conducted a systematic review examining how urbanization influences animal social behaviour. We analysed its impact on all four components of animal social systems: social organization, social structure, mating systems and care systems. Our literature search identified 227 studies covering (i) the effects of urban stressors on social behaviour (N=170), (ii) social system responses to urban environments (N=75), and (iii) the impact of urbanisation on interspecific interactions (N=12).

Overall, 92% of studies reported significant urban effects, highlighting the pervasive impact cities can have on social systems. While animals exhibit diverse responses shaped by species-specific traits and life histories, our synthesis indicates that the rapid pace of environmental change and the combination of multiple stressors in cities often destabilise complex social groups, instead favouring loosely structured aggregations with dynamic membership. Species unable to disperse outside urban areas may experience higher encounter rates that promote social tolerance and altered selection pressures may drive alternative mating strategies. However, major taxonomic and thematic biases limit broader inference: 62% of studies focused on birds, and 85% of stressor-based studies examined anthropogenic noise, leaving large gaps regarding other taxa and urban stressors.

Our review reveals the profound ways urbanization is reshaping social life. This synthesis is central beyond the scope of urban ecology, providing a crucial foundation for predicting species' responses to rapidly changing environments and for informing conservation efforts in an increasingly urbanized world.



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Machine Learning Methods for Biological Inference and Discovery

Christoph Mayer

LIB-Leibniz Institute for the Analysis of Biodiversity Change, Zoological Research Museum A. Koenig

Machine learning is rapidly reshaping biological research, enabling new ways to analyze complex datasets from genomes to ecosystems. This talk highlights recent developments in machine learning and their application to diverse biological questions, with a particular focus on ecological and environmental data. Case studies from my own research will cover sequence analysis, phylogenetics, ecological monitoring, and species interactions, illustrating how modern machine learning methods support discovery across biological scales.

Modelling active sensing collectives- Can bats tracking consistency avoid jamming cost in groups?

Aditya Moger¹; Thejasvi Beleyur²

¹ University of Konstanz; ² University of Konstanz

Active-sensing animals, such as bats, probe their environment by emitting probes of energy and analysing the returning probes. Even a solitary bat's call generates a cascade of echoes from multiple objects, which the auditory system must segregate into one spatial scene. The problem of spatial scene reconstruction is exaggerated in social groups, where an individual must also discriminate its own echoes from the calls and echoes of conspecifics to prevent constant collisions. How, then, do bats navigate dense collectives without colliding even when facing intense jamming?

We developed a biologically-parameterised dynamic model of active-sensing agents. We create an agent-based model and explicitly model bat behaviour and sound propagation. Inspired by the idea of optic and echo-acoustic flow, we propose that bats may detect their own echoes in large swarms using spatio-temporal consistency. The generated by obstacles around a bat are temporally locked to the bat's call emission. Hence, sounds that are consistent in terms of direction of arrival and post-call delay are more likely to be self-generated echoes.

We demonstrate a dramatic reduction in group collision rates when individuals integrate information over larger time windows. Collision rates decrease by approximately 30% when bats utilise consistency as compared with the negative sensorimotor controllers simulated (non-echolocating agents). Also, agents utilising spatio-temporal consistency avoid negative effects of jamming across an order of magnitude of group sizes (from 5-100 individuals). The collision rates of agents utilising consistency-based controllers and agents with artificially perfect self-generated echo detection are statistically indifferent. The behavioural similarity between the sensorimotor model utilizing consistency and artificially perfect echolocators supports the idea that tracking consistent sounds in both directions of arrival and time delay improves echolocation under masking conditions. The modelling approach lays the groundwork for understanding how multiple echolocators can exhibit collective behaviour despite the complex landscape groups present.

Neuronal contributions to thermal adaptation across timescales in a cnidarian nerve net

Roberto Montanari¹; Aybike Nazli Boldemir¹; Ling Wang²; Amelie Luise Wetzling¹; Robert Prevedel²; Suat Özbek³; Alexander Klimovich⁴; Jan Erik Siemens¹

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Heat stress can be avoided through thermoregulatory behaviours or tolerated through long-term physiological adaptations, referred to as heat acclimation. In animals with centralised nervous systems, neurons are well known to drive thermoregulatory behaviours, and have been implicated in heat acclimation, but whether diffuse nerve nets support similar responses in cnidarians, an early-branching sister lineage to bilaterians, remains unknown. Here, we investigated responses to acute and persistent heat exposure in the freshwater cnidarian *Hydra vulgaris*. Acute heat exposure induces escape through substrate detachment followed by sinking. We show that this behaviour is controlled by thermosensitive motor neurons at the base of the polyp and that is dependent on the molecular heat sensor Trpa1. Persistent heat exposure induces an acclimated phenotype characterised by reduced body size and increased heat tolerance. Acclimated polyps require an intact nervous system to endure in the hot environment. Together, these findings suggest that the capacity of nervous systems to support organismal responses across timescales—from rapid behavioural escape to sustained survival under prolonged environmental stress—may have arisen before the evolution of centralised nervous systems.

Sex smells: Early-life consequences and sexual differences in the chemical phenotype of fire salamanders explored in a mate choice context**Max Mühlenhaupt** .; Pia Oswald; Jeanne Friedrichs; Caroline Müller; Barbara Caspers

Bielefeld University

Chemical cues play an important but often underappreciated role in the communication of animals. Fire salamanders (*Salamandra salamandra*) have a well-developed sense of smell. Typical for amphibians, they display a biphasic lifestyle, beginning their life as aquatic larvae and becoming fully terrestrial after metamorphosis. Previous research has shown that in this species, olfactory cues play an important role in mate choice and that larvae carry habitat-specific chemical fingerprints. However, whether information about the larval habitat persists even after metamorphosis and whether sex-specific differences exist in the chemical phenotype of adult fire salamanders is unknown. In our six-year-study, we first conducted a reciprocal transfer experiment in two contrasting habitats: streams and ponds. Larvae from streams were transferred to ponds and vice versa, with control groups for each habitat. Following the reciprocal transfer experiment, the larvae were housed individually under controlled conditions until adulthood. Towards the end of the experiment, the volatile and skin surface chemical fingerprints of each fire salamander were analyzed. Additionally, during a mate preference trial, each female was presented with olfactory cues of two males that had contrasting transfer habitats as larvae. During this talk, we explore sex-specific differences and the impact of the larval habitat on the chemical phenotype of adult fire salamanders. Furthermore, we shed light on reproductive consequences of these differences in a mate choice context. Our study provides insights into the chemical communication of amphibians and highlights long-term consequences of early-life environments during mate choice.

Invasive clam *Corbicula* sp. as a bioindicator for microplastic concentrations in the final effluents of wastewater treatment plants

Hedda Lil Müller; Friederike Gabel

Institute of Landscape Ecology, Uni Münster

In the context of ongoing plastic production, microplastic pollution in freshwater ecosystems has become an increasing concern. Wastewater treatment plants discharge treated water directly into water bodies and can therefore act both as a barrier and a pathway for microplastics. As many facilities are installing advanced treatment methods to enhance the removal of micropollutants, it is suggested that microplastic concentrations can be reduced as well. However, removal efficiency is assumed to vary between methods, and direct microplastic quantification is time-consuming. Filter-feeding clams could serve as an active bioindicator to assess microplastic pollution over time, but their use in the final effluents of wastewater treatment plants has not been systematically evaluated. To address this gap, we conducted an in-situ exposure experiment and compared the microplastic concentrations in the treated wastewater with those in the clam tissue.

We placed individuals of the clam *Corbicula* sp. in the final effluents of four municipal wastewater treatment plants for two weeks. Two of these facilities implement an advanced treatment level, one oxidative and the other adsorptive. We digested the clams with 10% KOH and analysed the absorbed polymers via μ FTIR spectrometry. Additionally, the microplastic particles in the final effluent were sampled with a drift net and characterised via FTIR spectrometry.

Initial results showed that the effluent of the adsorptive treatment contained the lowest microplastic concentration (2.91 ± 1.66 items/m³), presumably due to particle retention by the cloth filter following the adsorptive treatment. On the other hand, the oxidative treatment was not complemented by additional filtering and demonstrated similar or higher concentrations than the conventional treatment (41.38 ± 52.37 items/m³). While different polymers were confirmed in the clam tissue, concentrations did not reflect those in the treated wastewater. It is possible that microplastic uptake was limited by filtering capacity, selective feeding or stress induced by relocation.

Challenging Upbringing – Quality of Parental Care influences early Offspring Development in a Facultatively Caring Beetle

Leon Müller; Marie Rosenthal; Annika Leimenstoll; Lara Simon; Samuel Wallner; Sandra Steiger ; Maximilian Körner

University of Bayreuth

As parents take over energy-consuming tasks such as food provisioning and predator protection for the offspring's benefit during parental care, they also protect their off-spring from infectious diseases through the exhibition of social immunity. But how the evolution of offspring dependency on parental care has been shaped by this parental pathogen protection remains poorly understood. To address this question, we took advantage of *Nicrophorus* burying beetles, who exhibit intensive parental care and social immunity but greatly vary in their offspring dependency. We simultaneously manipulated the carcass microbial environment as well as the quality of parental care by providing breeding pairs of *Nicrophorus* with either a fresh or an old carcass, and by injecting females with immune elicitors. We investigated consequences of changes in social and carcass environment quality by measuring the immunity of *Nicrophorus* females and their larvae. We find that during the time of parental care, females of more dependent larvae change their investment based on their own health but not necessarily based on the carcass environment, while *Nicrophorus* larvae of the three species react differently to both the quality of parental care and carcass quality. Our findings emphasize that during parent-offspring-coadaptation, the evolutionary process can affect offsprings' ability to react to changing environmental conditions, providing novel insights into the evolution and maintenance of offspring dependence on parental care.

Profile of chemical alarm cues in freshwater gastropods: Integrating GC-MS, behavioural responses, and morphological adaptations.**Nhamo Mutingwende**¹; Denis Meuthen²¹ Bielefeld University; ² Bielefeld University,

Damage-released alarm cues that are passively released from injured conspecifics are a valuable source of information regarding local predation risk. They have been documented to induce antipredator defenses across many aquatic taxa. However, attempts to elucidate their chemical composition have primarily focused on teleost fish. In contrast, the identity and properties of these chemical alarm cues in aquatic invertebrates such as molluscs remain largely underexplored. Thus, we are lacking knowledge on whether the composition of these alarm cues are taxon-specific or whether our knowledge about fish alarm cue composition can be generalized to other taxa. In our study, we profile the chemical alarm cues of *Physella acuta*, a freshwater gastropod that is a classic model system for alarm cue-induced antipredator plasticity, to identify key compounds associated with the perception of predation risk. We begin by extracting alarm cues from *P. acuta*, followed by profiling the specific chemical compounds present in these cues using gas chromatography-mass spectrometry (GC-MS). We then employ a calibration curve quantitative analysis method to determine the biological concentration levels of these profiled compounds. Using pure compounds at assessed ecologically relevant concentrations, we examine their capacity to induce alarm responses in conspecifics, assessed through behavioural responses and morphological adaptations. Our findings may provide valuable insights into the chemical communication system of gastropods. Furthermore, identifying whether alarm cue composition is shared across aquatic taxa or emerges through convergent evolution could enhance our understanding on the evolution of chemical communication in aquatic environments.

Comeback of the Red Kite in East Westphalia**Chantal Oliver¹**; Jörg Westphal²; Nayden Chakarov¹; Oliver Krüger¹¹ University of Bielefeld; ² Kreis Lippe

The Red Kite (*Milvus milvus*) is showing a gradual recovery in Central Europe. Its occurrence is closely associated with suitable habitat conditions, sufficient food availability, and relatively low levels of disturbance. In East Westphalia, recent breeding records indicate a local return of the species, highlighting the region's potential to support viable populations. However, evidence from across Germany suggests that this recovery remains fragile. Agricultural intensification, the loss of habitat quality, and additional mortality risks, particularly collisions with wind turbines, continue to affect survival and reproductive success. East Westphalia therefore represents an example of regional population growth that should not be considered permanently secure. Continued conservation efforts will be essential to maintain and strengthen current population trends in the future.

The early social environment influences fitness in a colonial-breeding seabird**Cagla Onsal¹**; Sandra Bouwhuis²; Maria Moiron¹¹ Bielefeld University; ² Institute of Avian Research

Early-life conditions can have short and long-lasting effects on offspring fitness and, ultimately, predict adult performance. An important component of early life is the social environment, but its long-term consequences are still relatively unknown. Using long-term data from a free-living common tern (*Sterna hirundo*) colony, we analyzed the effect of natal density, measured as the number of direct neighbors or the distance to the closest neighbor, on a suite of early- and late-life fitness proxies. These proxies include hatching success, chick age at death, fledging mass and probability, probability and age of returning to the colony, recruitment probability and age, lifespan, and lifetime reproductive success. We expected an effect of early social conditions on fitness, but for this effect to gradually decrease over the lifespan. Our analyses revealed a negative effect of the number of neighbors on all early-life fitness proxies, but no effect of either density measure on any post-fledging fitness proxies. Overall, these results confirm that individual fitness can be shaped by the early social environment. How such fitness effects influence population dynamics remains to be explored.

Local ant fauna recovery following control of *Linepithema humile*, but no additional benefit of behavior-manipulation approaches**Lina Pedraza**¹; Tiago Fernandes²; Silvia Abril³; Tomer Czaczkes⁴¹ Freie Universität Berlin; ² Freie Universität Berlin; ³ University of Girona; ⁴ Freie Universität Berlin

The Argentine ant *Linepithema humile* (Mayr, 1868) is amongst the world's most damaging invasive species, causing substantial ecological disruption and economic losses. Conventional insecticide-based control methods often show limited long-term effectiveness and can harm non-target organisms and disrupt the treated ecosystems. To overcome these limitations, we evaluated a novel management strategy combining a sustainable baiting system with a behavioral intervention aimed at modifying ant cognition and collective behavior.

The baiting system consisted of a biodegradable alginate hydrogel that provides an environmentally friendly delivery method for attractive resources, with a toxicant (Spinosad). In parallel, we applied a cognitive intervention based on caffeine and artificial odor cues, which have previously been shown to affect ant learning and foraging behavior under laboratory conditions. Four treatments were deployed across twenty 10 x 10 m plots within an invaded area in Spain. Ant communities were surveyed before treatment and monitored on nine occasions over two consecutive years.

Plots treated with toxicant and caffeine, either alone or in combination with odor cues, exhibited a nearly 60% reduction in *L. humile* abundance within four months compared with the negative (no toxicant) control. However, these reductions were similar to those achieved by the positive control containing only the toxicant. Following the application of the treatment, native ant species, including *Crematogaster scutellaris* and *Pheidole pallidula*, reappeared at monitoring stations.

Although the intervention did not completely suppress Argentine ant populations, the recovery of native species suggests control efforts reduced invasion pressure and potentially caused shifts in community dynamics. These findings highlight the value of invasive ant control efforts and the behavioral research into sustainable, low-impact yet effective control techniques that must continue.

Phylogenomics and morphometrics reveal new species and signals of an adaptive radiation in Vanuatuan *Strumigenys* trap-jaw ants (Hymenoptera: Formicidae)

Tobias G. Pfeifer; Kyle W. Gray; Christian Rabeling

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The South Pacific region harbors thousands of tropical islands and endemic species, making it one of the most geologically complex and biologically unique regions on the planet. Although islands account for only 6.7% of land surface area, they are home to approximately 20% of global biodiversity, ~50% of all endangered species, and 75% of documented extinction events. In light of the current global biodiversity crisis, the systematic documentation of island biodiversity is of central importance for enabling well-founded species conservation measures and understanding the evolutionary processes of these particularly fragile ecosystems. Ants (Hymenoptera: Formicidae), which are highly abundant, diverse, and ecologically dominant insects, are important biodiversity indicators and serve as valuable model systems. Recent advances in biodiversity research in the South Pacific region have revealed the Vanuatuan archipelago as a novel ant biodiversity hotspot with numerous undescribed species, especially in the ant genus *Strumigenys* Smith, 1860. *Strumigenys* ants are one of the most diverse and abundant ant genera worldwide but have not yet been systematically studied in Vanuatu, which hinders a comprehensive understanding of the biogeographic and evolutionary history of *Strumigenys* ants in the South Pacific.

Therefore, we employed an integrative taxonomic framework to formally revise the genus *Strumigenys* in Vanuatu. Specifically, we combined phylogenomics of ultraconserved elements (UCEs), biogeography, qualitative morphology, and quantitative morphometrics to delimit species, infer the evolutionary history, and explore the morphological diversity of *Strumigenys* trap-jaw ants in Vanuatu. This integrative approach revealed the presence of seventeen *Strumigenys* species, ten of which are hypothesized to be endemic to Vanuatu, making *Strumigenys* the most species-rich ant genus in the archipelago.

Moreover, the UCE phylogeny revealed a clade of high elevation endemics that exhibit substantial morphological variation and whose evolutionary history indicates the first potential case of an adaptive radiation in Vanuatuan ants.

Long-term impacts of a single uptake of imidacloprid on brood care and reproduction in ant founding queens

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Ants are key components of most terrestrial habitats and contribute to various ecosystem services. They live in social colonies composed of reproductive (males and queens) and non-reproductive (workers) castes. Most ant colonies are founded independently by a single queen directly after the mating flight. Any pesticide-induced impairment during the critical founding period can have long-lasting consequences for colony establishment and growth, yet empirical data on pesticide effects on colony founding ant queens are absent.

We experimentally addressed this knowledge gap by orally exposing founding queens of the common garden ant, *Lasius niger*, once to the neonicotinoid imidacloprid and quantifying early (3 weeks) and long-term (12 weeks) effects. Queen survival was significantly reduced at high doses. Egg production of surviving queens decreased during the first two weeks, whereas egg size remained unaffected. Sublethal effects persisted, with treated queens showing significantly reduced reproductive output, likely due to impaired brood care behaviour that resulted in inadequate prevention of mite infestation and increased egg and larval mortality.

Our findings demonstrate for the first time, complex long-term effects of a single exposure to imidacloprid on reproduction and brood care behaviour in colony founding *L. niger* queens that standard short-term assessments may fail to detect.

Effects of early-life rearing conditions and supplementary UV-A lighting on laying-hen behaviour

Mr Alfie Prettyman

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UV-A light is visible to hens but is largely absent from conventional indoor poultry lighting. This altered visual environment, compared with that of their natural habitats, may impair conspecific recognition and influence aggression, space use and fearfulness. We investigated whether introducing UV-A light during the laying period changed flock-level crowding, movement, fearfulness and aggression, and whether these responses depended on early-life rearing conditions.

Forty-eight chicks were housed across eight rooms and assigned to one of four early-life rearing treatments: standard industry lighting, intermittent lighting, broody-hen presence or dark brooders. At 33 weeks of age, UV-A lighting was introduced in all rooms, enabling within-room comparisons before and after UV-A supplementation.

Flock movement was recorded continuously during illuminated periods using ceiling-mounted cameras positioned centrally in each room and operating at two frames per second. Automated computer-vision analyses were used to detect and track individual hens and quantify their spatial distribution and aggregation. Grid-based analyses measured patterns of space use, while Gaussian mixture models were used to estimate the number, density and spatial arrangement of hen clusters. Optical flow was used to quantify overall flock-level activity. Fearfulness was assessed using tonic immobility and novel arena tests, while aggression was quantified through behavioural observations on feather pecking. Statistical models looked at the effects of UV-A supplementation, early-life rearing treatment and their interaction.

These preliminary findings suggest that UV-A supplementation did not substantially alter broad flock-level movement or space use, although effects on finer-scale aggregation patterns remain to be established.

Of Bees and BOOMs – The evolution of a nutritional mutualism between Wolbachia and solitary bees

Leopold Preuß¹; Marta Tischer; Anastasia Andrews; Panagiotis Theodorou; Christoph Bleidorn; Stefanos Siozios; Michael Gerth

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The intracellular endosymbiont Wolbachia is found in approximately 40% of arthropod species. It often acts as a reproductive parasite, exerting negative fitness effects on its host, although it can be beneficial in certain host species. A recent analysis of more than 200 Wolbachia genomes revealed the presence of a biotin synthesis operon (BOOM) in 14 strains from different insect hosts. Strikingly, eight of these strains were symbionts of solitary bees. Although solitary bees are a diverse and ecologically important group of insects, the role and evolution of biotin (vitamin B7) supplementation by Wolbachia in bees remains enigmatic. The aim of this study is to investigate the distribution and evolutionary history of BOOM in order to elucidate the potential function of Wolbachia in solitary bees. A screen of over 150 bee species revealed BOOM to be present in 23% of cases. Phylogenetic analysis of newly sequenced Wolbachia genomes showed that BOOM is found strongly enriched in bee infecting Wolbachia strains, where two distinct clades of the BOOM exist. Further, bacteriophages were identified as likely mechanisms for the lateral transfer of BOOM genes between Wolbachia strains. Finally, we find a significant correlation between the host bee diet and the presence of BOOM carrying Wolbachia. Altogether, these findings indicate a dynamic evolutionary history of an intricate association between solitary bees and Wolbachia, suggesting a potential role as a nutritional mutualist.

The evolution of circadian rhythm strength in locomotor activity of *Tribolium castaneum*

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Circadian rhythms are almost ubiquitous adaptations to diel environmental cycles. Several species exhibit highly robust and strictly timed rhythms, while others seem to display more interindividual variation and weaker rhythms. The evolutionary mechanisms driving these differences in temporal niches remain poorly understood.

To address this question, we use *Tribolium castaneum*, an established model organism, that displays high interindividual variation in its locomotor activity rhythms, which sets it apart from common models in chronobiology. We make use of this variation and the beetle's short generation time to mimic the evolution of stronger versus weaker behavioural rhythms by artificial selection for these traits.

Over seven generations, we selected individuals with strongest or respectively weakest behavioural rhythms in each generation. Activity was monitored using Drosophila Activity Monitors (DAM5H), and rhythmicity assessed by chi-squared periodograms and autocorrelation functions. Although interindividual variation persisted throughout the selection process, the selection regimes started to diverge in both rhythmicity strength and the proportion of rhythmic individuals from the third generation onwards.

Together these findings demonstrate that strength of locomotor activity rhythms is at least partly heritable, while the persistence of variation indicates a complex underlying genetic architecture. Our study represents a rare example for experimental evolution of circadian rhythms and provides evidence that strength of circadian rhythms responds to selection pressure. The resulting beetle lines now bring the potential to study the mechanisms underlying the evolution of rhythmic strength by genome and time-series transcriptome analysis.

Eleven new hymenopteran genomes - A basis for exploring the genomic background of secondary phytophagy

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Phytophagous larval nutrition is well known in several hymenopteran taxa all over the species tree. In contrast to primary phytophagous sawflies, many species have developed secondary phytophagy. During evolution, these species reverted from a parasitoid or zoophagous larval lifestyle back to the development on various plant tissues, including pollen, nectar, seeds and gall tissue. This shift has independently occurred in many different clades, making it a promising system to study parallel evolution. In our project, we are interested in the genomic background and genome dynamics shaping these fascinating lifestyle transitions. To compare the genomes of phytophagous lineages and their close zoophagous relatives, we have selected several species from representative phytophagous taxa within Aculeata and „Parasitica“ that are still lacking genome data. Here, I will present the first eleven genomes of the project. I will also share initial findings on the evolution of gene family sizes in our secondary phytophagous species compared to their zoophagous sister groups. Finally, I will discuss the next steps in the project to address our research questions regarding parallel genome evolution and similar genomic innovations.

Gene conversion empowers natural selection in a clonal fish species

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Sexual reproduction is ancient and ubiquitous despite its obvious disadvantages. Theory predicts that the reassortment of alleles that results from sex is necessary for natural selection to act effectively on individual loci; therefore, a purely clonal organism should rapidly accumulate deleterious mutations and go extinct. Nevertheless, many asexual species have existed for longer than theory predicts is possible, such as the Amazon molly (*Poecilia formosa*), a clonally reproducing fish arising from a single hybridization event more than 100,000 years ago. Here we show that although the Amazon molly has accumulated mutations faster than its sexual progenitor species, this has not led to functional mutational decay, defying theoretical expectations. Instead, gene conversion facilitates both adaptive and purifying selection by generating new clonal lineages in which previous mutations are either reverted or fixed, and by resolving hybrid incompatibilities between the ancestral haplotypes. The transition to clonality altered chromatin structure, but the asexual haplotypes of the Amazon molly nonetheless maintain the divergent mutational landscapes of their progenitor species. Together, these results provide

new insights into long-standing questions about the trade-offs involved in asexual reproduction.

The caput-pronotum joint of the acorn weevil *Curculio glandium* - a self-cleaning ball-and-socket joint

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Successful reproduction in many insects relies on specialised oviposition mechanisms. In weevils, a modified rostrum enables females to excavate channels into host plants, such as oak acorns. The excavation process requires caput rotation within a deep pronotal cavity, forming a ball-and-socket joint (caput-pronotum joint, CPJ). Such joints are rare in insects and expose an enclosed cavity directly to the external environment, making them prone to particle ingress and accumulation. Some species exhibit concentric ridge microstructures on the caput in the CPJ region, leading us to hypothesise a self-cleaning function. We characterised CPJ morphology of the acorn weevil *Curculio glandium* using μ -CT, 3-D segmentation and scanning electron microscopy. The caput sits in a ring-shaped socket and is actuated by two antagonistic muscle pairs (caput flexor and extensor). To test our hypothesis, live adults were coated with spherical copper particles (providing high μ -CT contrast) and particle volume in the joint cavity was measured between 0 and 48 h post-exposure. Additionally, animals were observed for cleaning behaviour. Particle volume declined significantly between 1 and 3 hours post exposure before reaching a stable plateau. This reduction coincided with frequent head rotation and antenna stepping behaviours observed immediately after exposure, which were rare after 48 h. Our results indicate that the CPJ of *C. glandium* is a specialised ball-and-socket joint that remains functional through an active self-cleaning mechanism: repeated head rotations by the ridge-bearing caput expel particles from the joint cavity, providing the first experimental evidence for active self-cleaning in an insect spherical joint.

Heatwave treatment reduces behavioural predictability but preserves individual differences in woodlice

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Extreme climatic events such as heatwaves are increasing in frequency and intensity, yet their effects on animal personality and behavioural plasticity remain poorly understood. Behavioural repeatability reflects the extent to which individuals differ consistently from one another and can be partitioned into among-individual and within-individual sources of variation. We examined whether exposure to a simulated heatwave altered repeatability in multiple behavioural traits of 148 rough woodlice (*Porcellio scaber*). Following initial behavioural tests, we randomly assigned individuals to either a heatwave treatment ($N = 72$) or a control group ($N = 76$). We quantified six behavioural traits - latency to emerge from a dark tube, latency to emerge after a squeeze, number of crossings in an open field, number of crossings after a squeeze, runway time, and righting response - and estimated repeatability. Before treatment, all behaviours showed repeatable individual differences ($R = 0.23$ to 0.49), with activity-related traits exhibiting the highest repeatability. Following treatment, behavioural responses varied among traits. Heatwave exposure did not uniformly reduce among-individual variation, and repeatability remained detectable across all traits. For emergence latency, repeatability increased after heat exposure. In contrast, repeatability for crossings declined, largely because increases in among-individual variation were accompanied by increases in within-individual variation. The most pronounced change occurred for crossings after a squeeze, where repeatability decreased after heat exposure but increased in control animals. This decline was associated with elevated within-individual variance, indicating greater within-individual behavioural variability after thermal stress. Overall, our results suggest that heatwave exposure does not eliminate consistent behavioural differences among woodlice. Instead, thermal stress appears to increase behavioural variability and reduce predictability in certain activity-related traits, highlighting within-individual plasticity as a potentially important response to extreme temperature events.

Transposable element islands at the interface of 3D genome architecture and karyotype evolution**Janina Rinke;** Jürgen Gadau; Lukas Schrader

Universität Münster

Karyotype diversification is a common phenomenon in evolution, yet how the underlying chromosomal rearrangements emerge often remains unclear. Here, we generated chromosome-level assemblies for ten species of *Cardiocondyla* ants and the outgroup *Nesomyrmex wilda* to investigate the genomic basis of karyotype diversification. *Cardiocondyla* species possess the smallest ant genomes reported, yet exhibit extraordinary chromosome number variation ($1n=8-32$). Transposable Elements (TEs) in *Cardiocondyla* genomes are highly compartmentalized into dense TE Islands. These islands coincide with pericentromeric regions, are hotspots of structural variation, and frequently overlap chromosomal breakpoints, implicating them as anchors of Robertsonian translocations and rapid centromere turnover. 3D genome analyses revealed spatial clustering of centromeres embedded in TE Islands, providing a structural context facilitating repeat-mediated chromosomal rearrangements. Our results identify TE Islands as focal regions that both promote and record structural genome evolution, revealing a mechanistic link between TE compartmentalization, 3D genome organization, rapid karyotype diversification and genome compaction.

Different paths to sociality: genomic footprints in weevils

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Eusociality, comprising overlapping generations, alloparental care, and division of reproductive labour, is rare but has evolved convergently in insect orders as diverse as Hymenoptera (ants, bees, wasps), Blattodea (termites), and Coleoptera (weevils). In Hymenoptera, its evolution has been associated with positive selection on specific gene sets, gene family expansions (e.g. related to communication), and genome-wide relaxation of selection with increasing social complexity. Whether these molecular signatures observed in Hymenoptera are shared across independent origins of sociality in insects remains an open question. Weevils (Coleoptera, Curculionidae) offer an excellent opportunity to address this: the entire spectrum of sociality is present within this family, including the only obligately eusocial beetle, *Austroplatypus incompertus*. Here, we use comparative genomics to test whether molecular footprints of sociality in weevils mirror predictions derived from Hymenoptera. We sequenced the genomes of *A. incompertus* and two facultatively eusocial weevil species, and combined these with published genomes of 18 additional weevil species. Together, this dataset covers two independent origins of sociality. We find genome-wide relaxation of selection increasing with social complexity, most pronounced in *A. incompertus*. However, contrary to expectations, we detect significantly more convergent gene family contractions on the branches where sociality evolved, but no excess of expansions. We also find no increase in positive selection with increasing social complexity. These results suggest that sociality in weevils is associated with gene losses and relaxation of selection rather than gene family expansions and positive selection. These patterns are consistent with an important role of sheltering and reduced effective population size not observed previously in other clades.

Environmental Stress Accelerates Airway Aging Through Persistent Innate Immune Activation

Thomas Roeder¹; Ruben Prange; Ann-Cathrin Hofacker; Jörg Hammel; Jörg Hammel; Susanne Krauss-Etschmann; Judith Bossen

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Aging of the respiratory system is a major risk factor for chronic lung disease, yet how environmental stressors influence airway aging trajectories remains poorly understood. Here, we use *Drosophila melanogaster* to investigate how cigarette smoke (CS) exposure affects airway structure, molecular state, and organismal resilience.

Using multi-scale imaging, we show that both aging and chronic CS exposure induce collapse of thoracic air sacs and loss of terminal tracheal branches, indicating progressive deterioration of airway architecture. Transcriptomic analyses revealed a biphasic response to CS exposure. Acute exposure activated adaptive stress, detoxification, tissue remodeling, and neuromodulatory pathways, whereas chronic exposure induced persistent oxidative stress, innate immune activation, and suppression of epithelial maintenance programs. Integration of these datasets with aging-associated transcriptional changes demonstrated that chronic, but not acute, CS exposure shifts airway transcriptomes toward aged molecular states, accompanied by alterations in telomere-associated signatures.

To determine the functional consequences of chronic immune activation, we assessed survival of flies lacking major antimicrobial peptides. While AMP-deficient flies exhibited reduced lifespan under baseline conditions, they survived significantly longer during chronic CS exposure, indicating that sustained innate immune effector activity becomes detrimental under prolonged environmental stress.

Spatial ecology and sex-specific space use in the West African Saber-toothed frog (*Odontobatrachus arndti*)**Sona Saji**; Barbara Caspers; Marvin Schaefer

Bielefeld Universität

Saber-toothed Frogs (Anura: Odontobatrachidae) are the only vertebrate family endemic to West Africa and inhabit fast flowing mountain streams. Owing to the difficult-to-access terrain, their pronounced shyness, and their tendency to retreat into rock crevices when approached, their ecology remains poorly understood. In this study, we combined nocturnal visual encounter surveys with VHF radio telemetry to track individuals of an *Odontobatrachus arndti* population, along a 200 m river section over six weeks. We aimed to quantify movement patterns, space use, and site fidelity to provide the first detailed insights into the species' spatial ecology and to derive implications for the frogs' biology.

We tracked 66 frogs, including 22 individuals fitted with VHF transmitters. Males and females exhibited distinct patterns of space use. Females occupied a broader portion of the stream channel, indicating greater lateral movement, whereas males maintained more spatially restricted ranges closely associated with cascade microhabitats, highlighting their relevance as breeding habitat. Spatial overlap patterns mirrored these differences: overlap among males was low, consistent with territorial behaviour, whereas females showed higher overlap and male–female overlap was intermediate. Gravid females moved significantly greater distances than non-gravid individuals, suggesting increased movements associated with reproduction. Transmitter-tagged individuals provided more relocation data than individuals monitored through visual encounter surveys, enabling detailed analyses of movement behaviour and spatial overlap. Transmitter attachment did not measurably affect movement behaviour.

These findings provide the first quantitative assessment of spatial ecology in *O. arndti* and reveal a previously undescribed social structure linked to access to cascade habitats. Our results demonstrate the suitability of VHF telemetry for studying this elusive stream-dwelling species, overcoming challenges associated with difficult terrain and low detectability. Given increasing mining pressure in the Nimba Mountains, the study establishes an important ecological baseline and highlights key habitats for the conservation of this Near Threatened species.

Subpopulation dynamics in the parasitoid wasp *Nasonia vitripennis* (Walker 1836) are independent of ecology and *Wolbachia*-infection**Benjamin Sampalla¹**; Pawel Malec; Elina Dolanc; Jan Frisenhan; Johannes Steidle¹¹ Universität Hohenheim

To understand which reproductive barriers initiate speciation is a major question in evolutionary research. Therefore, it is important to study the dynamics of population structures over time to capture early processes of separation. We studied potential separation processes in a local, sympatric population of the hymenopterous parasitoid *Nasonia vitripennis* (Walker 1836), belonging to the Chalcidoidea. This super family is characterised by high species numbers and a specific biology including frequent inbreeding, which should enable separation processes. We follow up on a previous investigation of the same population from 2012, which revealed the presence of inbreeding lines, different microsatellite-defined subpopulations, and two ecotypes, one parasitizing fly pupae in bird nests and the other next to carcasses.

The analysis of microsatellite data from wasps collected in 2012 and 2025 revealed the presence of the same three microsatellite-defined subpopulations in both years, but with different frequencies in the two habitats. Genetic clustering was not associated with either bird nest or carrion as microhabitat, the height of the nests in which they were collected, and unidirectional cytoplasmic reproductive isolation (CI) caused by *Wolbachia*-infection. Obviously, additional factors must be responsible for early structuring of the studied population.

Mechanisms of Intestinal Starvation Resilience in the Mexican Cavefish**Ana Santacruz**¹; Chongbei Zhao²; Nicolas Rohner¹¹ University of Münster; ² Stowers Institute for Medical Research

Naturally starvation-resistant species provide a unique opportunity to uncover the evolutionary adaptations that preserve intestinal integrity and absorptive capacity under extreme nutrient limitation. The Mexican cavefish (*Astyanax mexicanus*) is a remarkable model of starvation resilience and metabolic adaptation. Having evolved in nutrient-poor cave environments, cavefish experience unpredictable food availability, resulting in repeated cycles of starvation and refeeding. To investigate how the intestine responds to prolonged nutrient deprivation, we combined detailed morphological analyses with high-resolution single-cell transcriptomic sequencing (scRNA-seq) of laboratory-starved cavefish and their surface-dwelling ancestors. As expected, the intestine functions as both a major metabolic and immune organ, comprising a complex assemblage of cell types, most of which are also found in the mammalian intestine. We identified striking differences in both cellular composition and transcriptional responses between the two ecotypes. Compared with surface fish, cavefish exhibit a greater investment in adaptive immunity, particularly through an expansion of T-cell populations. In contrast, surface fish are enriched in enterocyte populations, consistent with differences in ecological niches and nutrient acquisition strategies between the two ecotypes. During starvation, the cavefish intestine activates regenerative programs involving key cell-survival and cellular recycling pathways while suppressing inflammation, suggesting enhanced mechanisms that preserve intestinal homeostasis, protect against epithelial damage, and maintain barrier function. In contrast, starvation in surface fish results in epithelial injury and impaired barrier integrity, consistent with a leaky gut phenotype. To functionally validate the cellular mechanisms underlying this enhanced barrier resilience, we used intestinal cell lines derived from cavefish and surface fish that retain the starvation-response phenotype of their donors. Overall, our results suggest that the cavefish intestine has evolved adaptive mechanisms that enable repeated cycles of nutrient deprivation while preserving tissue integrity and function.

From Sabre-teeth to self-medication: How a single ecological factor drives outstanding evolutionary innovations in a frog.

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Sabre-toothed frogs (Anura: Odontobatrachidae) are an ancient West African endemic family comprising only five recognized species. Despite an evolutionary history extending at least to the Late Cretaceous, they have retained a remarkably conserved body plan, ecology, and life history. Yet this evolutionarily conservative lineage exhibits an unusual concentration of biological innovations that span multiple levels of organismal biology.

Across all species, distinctive adaptations occur in morphology, physiology, and behavior. Adults of both sexes possess prominent fang-like mandibular projections used in physical combat, while larvae bear specialized oral suckers that allow them to develop in fast-flowing torrents. Their communication system is unusually elaborate for anurans, including female advertisement calls and reciprocal male–female duets. In addition, they employ diverse chemical signaling mechanisms involving novel compounds produced by male breeding glands and specialized mandibular adipose tissues. Most remarkably, they actively consume medicinal plants to combat parasitic infections, providing the first evidence of self-medication in an amniote vertebrate.

We herein propose that all these traits must have been simultaneously driven by the same ecological factor: life in cascading torrents and waterfall habitats. Interestingly, individual elements of this adaptive repertoire are also known from other torrent-dwelling frogs around the world. However, these traits are typically distributed among different lineages rather than concentrated within a single clade. Odontobatrachidae therefore represent an intriguing system for investigating how extreme ecological specialization can generate evolutionary novelty across various biological dimensions still maintaining long-term evolutionary stability.

Impact of conspecifics, prey and predators on the evolution of the hearing range of the smallest terrestrial mammal, the Etruscan shrew

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Hearing is an important sensory modality for the survival of animals, enabling sound localization, intra- and interspecific communication, and recognition of prey and predators. Animal species exhibit species-specific hearing ranges because of physiological constraints and adaptations to their social and environmental niche. This study investigated the impact of miniaturization in body size, intraspecific communication, prey detection, and predator avoidance on the hearing range of the Etruscan shrew, the smallest terrestrial mammal.

Auditory brainstem responses (ABRs) were recorded from 21 adult individuals of both sexes, including young and aged subjects. Additionally, anatomy and histology of the inner ear was assessed to estimate size-related physiological constraints. The vocal range for conspecific, prey (*Gryllus bimaculatus*), and predator (red fox, barn owl) sounds were analysed and compared to the hearing range of the Etruscan shrews.

Etruscan shrews showed an U-shaped audiogram with a hearing range from 9 - 65 kHz at 60dB SPL. An age effect was observed for higher frequencies, corresponding to age-related hearing loss as observed in other mammals. The frequency range of conspecific vocalizations covered a large part of the hearing range. Histology revealed a low number of outer hair cells which may underlie the broadband structure of conspecific vocalizations. Prey signals overlapped the lower to most sensitive frequencies, whereas predator calls were below the hearing range. Notably, conspecific vocalizations were outside the hearing range of aerial predators suggesting predator avoidance. Overall, the auditory system of Etruscan shrews reflects a trade-off between physical constraints, prey detection, predator avoidance, and coevolution with conspecific vocal production and provides insights into the evolution of species-specific hearing ranges.

An accessible molecular approach to tackle the taxonomic urgency

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Biodiversity loss has created an urgent need to document species before they disappear. Taxonomy plays a central role in this effort but is often considered a field in crisis due to limited funding and a shortage of trained personnel. In this race against extinction, molecular approaches have become indispensable tools. While DNA barcoding enables rapid and scalable species identification, the commonly used single-locus approaches provide limited resolution for species discovery. Conversely, genome-scale multilocus methods offer high accuracy but remain costly, labor-intensive, and inaccessible to many taxonomists, particularly in low- and middle-income countries.

As a compromise between accuracy and accessibility, we propose a framework based on standardized sets of 5–20 nuclear markers. This approach maintains a simple, scalable, and affordable workflow while providing greater power for species delimitation and straightforward integration into existing taxonomic practices. To identify suitable marker sets, we developed a bioinformatic pipeline that mines reference genomes for potential marker regions and applied it to spiders as a model system. By combining long markers optimized for fresh material with short markers recoverable from older specimens with degraded DNA, the framework leverages modern third-generation sequencing technologies and enables work with museum collections.

We identified 14 loci that perform reliably across the spider tree of life, recovering a robust phylogeny and successfully delimiting even closely related species. Our results demonstrate that standardized multilocus marker sets can bridge the gap between traditional DNA barcoding and genome-scale approaches, providing a practical and widely accessible tool for accelerating biodiversity discovery.

Transposable Elements in Ant Macroevolution

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Transposable elements (TEs) are key contributors to genome evolution, yet their macroevolutionary role in the adaptive radiation of the ants remains poorly understood. We analyzed 163 ant genomes spanning 12 of 16 extant subfamilies to characterize TE impacts over the past 100 million years. We identify convergent TE bursts in ancestors of the most speciose ant clades, preceding rapid diversification following the Cretaceous–Paleogene extinction event approximately 66 million years ago. We demonstrate that TEs associate with expansions of olfactory receptors and other key gene families, and reveal striking compartmentalization of ant genomes into faster-evolving TE-rich and more conserved TE-poor regions. Our findings demonstrate the broad-scale impact of TEs on ant genome evolution and their particular impact on the diversification of the chemical communication systems.

Water flow analysis reveals hydrodynamic differences between ecological morphs of *Daphnia*

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Daphnia are small crustaceans that inhabit the pelagic zone of limnic ecosystems. They are a well known example for phenotypic plasticity in the presence of predators. Their common name, “water fleas”, derives from their characteristic hop-and-sink locomotion. The upward movement is generated by a powerful downstroke of their second antennae, the subsequent sinking is caused by their negative buoyancy. *Daphnia* are assigned to an intermediate hydrodynamic regime in which both, inertial and viscous forces, are important, thus making them an interesting system at the interface of fluid mechanical research and ecology. We investigated the water flow surrounding *Daphnia longicephala* in its typical and its defended morph, which is expressed in response to the predatory backswimmer *Notonecta*. We recorded multiple individuals performing their natural hop-and-sink movements with Particle Image Velocimetry (PIV). PIV computes the water flow from the motion of suspended tracer particles. By synchronizing, averaging, and statistically comparing flow fields around multiple individuals, we quantified hydrodynamic differences between the two ecological morphs. We found reduced water velocities around head and body alongside increased water velocities in the region of the second antennae of defended animals. These alterations indicate that predator-induced morphological defences modify the hydrodynamic interaction between animal and environment. Our findings therefore provide new insights into the ecological consequences of inducible defences in *Daphnia* concerning predator–prey interactions and defence costs.

Bidirectional interactions between circadian rhythms and immunity in *Tribolium castaneum***Nora Schulz**; Tobias Prüser; Johannes Grüneberg; Joachim Kurtz

University of Münster

Circadian rhythms coordinate daily oscillations in behaviour and physiology and may help organisms align immune activity with predictable variation in infection risk. At the same time, immune activation or infection can disrupt circadian behaviour. In insects, the interaction between circadian rhythms and immune responses remains poorly understood.

Here, we investigated bidirectional links between circadian rhythms and immunity in the red flour beetle *Tribolium castaneum*. We tested whether the time of day at which immune treatment is administered influences immune gene expression and examined whether wounding or pathogen exposure alters locomotor activity and rhythmicity.

Expression of immune response-related genes varied significantly with time of day, and responses were more pronounced when animals were treated in the relative morning compared to the relative evening. This suggests circadian modulation of immune responses. Conversely, wounding and pathogen exposure significantly altered locomotor activity in females, indicating that immune activation can affect behavioural rhythms. Together, our results show that circadian rhythms and immunity interact bidirectionally in *T. castaneum*: the time of day shapes immune gene expression, while immune activation can alter behavioural rhythms.

The Scent of Growing Up: Dynamic Larval Profiles During Family Life in Burying Beetles

Meryellen Silvania Cavalcanti; Jacqueline Sahm ; Catherine Watson; Johannes Stökl ; Sandra Steiger

University of Bayreuth

Chemical communication plays an important role in social interactions among insects, but most research has focused on adult insects. This gap is particularly relevant in species that exhibit parental care, where parental behavior can be influenced by chemical signals emitted by the larvae. Previous studies in other insect species have suggested that maternal feeding responses may be modulated by the odor of the larvae, but the chemical identity of these signals remains largely unknown. In this study, we investigated the chemical profiles of *Nicrophorus* larvae, a genus of burying beetles characterized by complex biparental care. Larvae of different species and developmental stages vary in their dependence on parental provisioning. We collected first-, second-, and third-instar larvae and performed hexane extractions of their surfaces to obtain cuticular compounds. Using gas chromatography coupled with mass spectrometry (GC-MS), we detected various compounds on their surfaces. We observed differences among all species, indicating changes in chemical profiles. These results provide evidence that *Nicrophorus* larvae produce chemical mixtures that change over the course of their development, supporting the hypothesis that these signals may influence interactions between the larvae and their parents. Our study contributes to a broader understanding of the role of larval chemical communication in the evolution of insects from subsocial to social forms and highlights the importance of analyzing multiple life-cycle stages to understand the dynamics of parent-offspring interactions.

Functional ecology of Steninae (Coleoptera: Staphylinidae) in Northeast India

Simon Sommerfeld

Universität Tübingen

The south-eastern slopes of the Himalayas represent one of the global biodiversity hotspots, yet this region remains comparatively understudied. The hyperdiverse genus *Stenus* is distributed worldwide, with one of its major radiations, the former genus *Dianous*, likely originating in this area. Therefore, Northeast India provides an ideal region to investigate the ecological diversification of this group.

During a four-month field study, beetles were collected along two elevational gradients ranging from 150 to 2700 m above sea level. I investigated patterns of diversity and species composition across elevation and combined ecological field data with experimental approaches examining microhabitat preferences and tarsal attachment forces.

Species diversity showed a hump-shaped pattern along the elevational gradient. In addition, the probability of encountering *Stenus* in waterfall habitats strongly decreased with increasing altitude, whereas occurrences in detritus habitats increased. This pattern was mainly driven by a decline in the former *Dianous* lineage, which showed a strong preference for waterfall habitats. Furthermore, we found significantly lower tarsal attachment forces in *Dianous* compared to other *Stenus* species. Higher tarsal attachment forces were associated with a preference for vegetation habitats under natural conditions and for vertical microhabitats in experimental settings.

These results highlight the role of habitat specialization and functional traits in shaping the diversification of Steninae along environmental gradients and reveal ecological differences between *Stenus* and the former *Dianous* lineage.

A Cross-Species Comparison of Behavioural Welfare Indicators Among Guinea Pig, Rat, and Chinchilla Caretakers in Austria and Germany

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Small companion mammals such as guinea pigs, chinchillas, and rats are widely kept but far less researched than dogs and cats, and species-specific welfare guidelines have only recently been tested empirically. We synthesised large online surveys of German-speaking caretakers (1,181 guinea pig, 978 rat, and 336 chinchilla respondents), combining previously published studies with newly analysed data. Behaviour was summarised by principal component analysis and linked to husbandry and human–animal interactions through regression models; healthy and sick guinea pigs were compared using non-parametric tests.

Two factors consistently emerged. First, husbandry: species-appropriate housing (e.g., adequate hiding spots), social companionship, and enrichment shape welfare indicators. Guinea pigs showed more affiliative and play behaviours when caretakers frequently offered food enrichment, and rats showed more social behaviour with enrichment and proper social housing. Most chinchillas received key resources (companions, dust baths, elevated areas, hay, water), but insufficient enclosure size and individual housing remained common. Second, the human–animal relationship mattered across species: caretakers who felt more comfortable with and bonded to their animals provided more enrichment, hand-feeding, gentle handling, and health checks, and in guinea pigs more positive interactions correlated with increased affiliative behaviours, indicating good welfare.

Guinea pigs with a veterinary diagnosis showed reduced social play and resting with peers, decreased locomotor play (popcorning), and increased discomfort behaviours such as teeth grinding and chattering. These signs could help caretakers and veterinarians detect illness earlier in a species that conceals symptoms.

Overall, relationship quality, not just housing, appears to influence welfare, as it does for dogs and cats. Recognising species-specific behavioural signs lets veterinarians better advise on enrichment, social housing, gentle handling, and early disease detection. Future work should move from caretaker-reported data toward observational, long-term validation and integrate these indicators into practical welfare-assessment tools for species that currently lack them.

Mitochondrial redox buffering as a conceptual paradigm enabling animal-algal photosymbiosis**Patrick R. H. Steinmetz**

Michael Sars Centre / University of Bergen

Photosymbiosis provides some animals with access to photosynthetically derived metabolites, including sugars, amino acids, and fatty acids. Despite enabling animals to grow and survive in nutrient-poor environments, photosymbiosis remains restricted to relatively few animal lineages and often exhibits environmental instability, most prominently exemplified by coral bleaching. Although ecological and physiological aspects of animal–photosymbiont interactions have been extensively studied, particularly in corals and sea anemones, the cellular mechanisms underlying their maintenance and stress-induced breakdown remain poorly understood.

Here, I present a conceptual synthesis of published physiological, metabolic, ecological, and transcriptomic observations that identifies host mitochondrial redox homeostasis as a central, previously underappreciated constraint on photosymbiotic stability. Photosymbiosis drives predictable diel fluctuations in oxygen and metabolite availability within host cells, generating recurrent hypoxia–reoxygenation dynamics with parallels to ischemia–reperfusion injury in humans, where rapid reoxygenation promotes oxidative damage. Alternative respiratory pathways, which function as redox buffers in plants and are present in all known photosymbiotic animal lineages, are identified as key mechanisms for maintaining electron flux and redox balance in host mitochondria. Reinterpreting existing evidence, particularly from corals, suggests that diverse bleaching-associated stressors (including thermal stress or oxygen fluctuations) converge on host mitochondrial electron transport systems. Furthermore, the cumulative and synergistic effects of these stressors are expected to increase the likelihood of oxidative damage and bleaching. Together, these observations identify failure of mitochondrial redox buffering as a major and previously underappreciated driver of photosymbiotic instability. Positioning host mitochondria as central integrators of bleaching-associated stress generates testable predictions regarding differences in bleaching susceptibility among host genotypes, symbiont species and strains, and associated microbial communities.

Promises and challenges of macrosynteny as a phylogenetic marker considering robusticity**Torsten Struck**¹; James Fleming²¹ Natural History Museum, University of Oslo; ² University of Barcelona

In the last decade, macrosynteny gains increasing consideration as a phylogenetic marker. Macrosynteny investigates genome architectures with respect to genic composition of chromosomes detecting conserved synteny groups called ancestral linkage groups (ALGs). While such groups generally lack collinearity, they are often stable over long evolutionary times. Large changes in ALGs can happen due to fissions or fusions, recognizing three fusion forms. In the first one, Robertsonian translocation, two or more ALGs merge without exchanging genes. In the second one, a ALG is inserted into another one without mixing their genes. Finally, in the third one, fusion-with-mixing, ALGs fuse and mix their genes. While the other two events are possibly reversible, the last one is supposedly irreversible, comparable to Shannon entropy. Due to its irreversibility, this last event is therefore considered a very strong phylogenetic character. It is therefore increasingly exploited in answering challenging phylogenetic questions such as the first phylum to branch off within animals. In this presentation, it will show the potential of macrosynteny as a phylogenetic marker, but also show the challenges and problems associated with this approach. Using the phylogeny of Lophotrochozoa, I will show the remaining problems of the approach. First, a detailed analysis of possible macrosynteny events shows that convergent evolution of fusion-with-mixing events are rampant in the genomic evolution of Lophotrochozoa and convergent evolution is much more common than unique evolutionary events. Second, I will show that the detection of ALGs in the first place is affected by the large (N) problem in statistics. This means significant results are detected but are biological meaningless. I will present a new jackknifing procedure allowing to assess the robusticity of the detection of ALGs complementing the significance test. In combination, they allow for a more conservative but robust detection of ALGs.

From traits to processes: An integrative perspective on inbreeding using a cichlid fish model

Timo Thünken

University of Bonn - Bonn Institute of Organismic Biology (BIOB)

Recent integrative research has challenged the traditional view of inbreeding as uniformly detrimental, highlighting that the costs of inbreeding are often highly context-dependent, e.g. shaped by environmental conditions and population history, and can be balanced by inclusive fitness benefits. While most studies on this topic focus on fitness-related outcomes, much less is known about how inbreeding affects the processes that generate phenotypic variation.

Using *Pelvicachromis taeniatus*, an African cichlid fish with pronounced kin mating preferences as model system, I examine how inbreeding shapes the mechanisms underlying kin preference, sexual signaling, and cognition. First, I show that kin preferences are not fixed but vary with inbreeding level. While kin recognition remains intact, mating preferences shift from kin preference in moderately inbred fish to kin avoidance in highly inbred fish, whereas in hybrids produced by crossing inbred lines they revert to kin preference. These findings suggest that inbreeding influences how kin-related information is evaluated during mate choice.

Second, I demonstrate that the effects of inbreeding on sexual signaling are context-dependent. In males, differences in coloration between inbred and outbred individuals emerge primarily under competitive conditions, with inbred males displaying less intense coloration. In females, a positive correlation between colour intensity and body condition was observed only in outbred individuals, but not in inbred individuals, suggesting that inbreeding can alter the function and reliability of colour signals.

Finally, I demonstrate that inbred, outbred, and hybrid fish exhibit similar learning performance despite differences in brain size and decision-making processes, suggesting that cognitive pathways may differ with genetic background.

Together, these findings highlight that the consequences of inbreeding cannot be fully understood from trait-based measures alone. Instead, I propose that understanding how inbreeding shapes behavioural, cognitive, and developmental processes underlying phenotypic variation provides a more comprehensive view of its evolutionary consequences.

Metabolic costs of winter warming in a spider.

Carolina Ortiz Movliav¹; Lilly Steglich¹; Ebbe Nürnberg¹; Louisa Trieglaff¹; Thomas van de Kamp²; Philipp Lehmann¹; Alexander Wacker¹; **Gabriele Uhl**¹

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Winter warming disrupts metabolic processes and energy balance in ectotherms, affecting performance and survival. The wasp spider *Argiope bruennichi* overwinters as first-instar juveniles (spiderlings) inside an egg sac, unable to respond to temperature changes by moving elsewhere, making it ideal for studying temperature effects on overwintering physiology. We examined how warmer winters affect *A. bruennichi* in Southern France by exposing offspring to three winter temperature treatments: a control representing current conditions and two increased temperatures of +3.7 °C and +4.8 °C based on IPCC projections (SSP3-7.0 and SSP5-8.5). We hypothesized that warmer winters increase metabolic activity, altering metabolism-related traits and survival. Spiderlings in warmer treatments showed higher metabolic activity, accumulated more nitrogenous waste, had lower fatty acid reserves, lower body condition, and higher mortality than the control, indicating substantial physiological costs of winter warming. Species distribution modeling projects a contraction of climatically suitable habitat by 2081–2100 under both scenarios at the core of the distribution, with a northward shift of the suitable habitat. Given the pronounced physiological costs of warm winters demonstrated by our study, an even more substantial impact of climate change on the species' distribution is to be expected.

Weismannian insulation of the superorganismal germline

Esther van den Bos¹; Lena Wiegert¹; Joshua Grebe¹; Kerstin Becker²; Jürgen Gadau¹; Jacobus Boomsma³; Lukas Schrader¹

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Major transitions in evolution have repeatedly shifted selection from lower-level entities to higher-level organisms and, in some lineages, to colonial superorganisms. Within these “fraternal” transitions, multicellular organisms and insect superorganisms are nested yet analogous cases, both built on high relatedness, irreversible division of labor, and integrated development that aligns fitness interests across levels. We tested whether superorganismal colonies truly parallel multicellular bodies by building on Weismann’s germ-plasm theory, which separates a protected germline from a more expendable soma. In turn, queens (as the colony’s germline) should be more robust to perturbation than workers (as the colony’s soma) during development, reflecting stronger protection of the hereditary lineage. Waddington’s canalization concept, with Hsp90 as a key molecular buffer, offers a concrete mechanistic link between germ-plasm theory and measurable developmental robustness. Using the ant *Cardiocondyla obscurior*, which has irreversibly sterile workers and reproductively specialized queens, we inhibited Hsp90-mediated buffering during late larval development and quantified caste-specific changes in morphology and gene expression. Our results show that queens proved more developmentally canalized and less responsive to perturbation than workers, supporting an extension of Weismannian germline insulation to the colony level within the major-transitions framework.

Identifying the function of the enigmatic body in cuttlefish and squid suckers

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Decapodiformes cephalopods, like squid and cuttlefish, have stalked suckers lining their arms and tentacle clubs that allow them to capture prey effectively. Right below where the stalk connects to the sucker, lies a structure encapsulated in connective tissue, called the enigmatic body. For over a century, there has been much debate about whether this structure serves as a ganglion, secretory gland or regenerative tissue, but its purpose remains unclear. In this project we aim to understand what tissue types comprise the enigmatic body.

To answer this question we analyzed arm and tentacle suckers of *Sepia officinalis* and *Loligo forbesii*. We used histology and Transmission Electron Microscopy (TEM) to study the general, intracellular, morphology of the enigmatic body, make a comparison between arm and tentacle suckers, and stain for the presence of mucus. Immunohistochemistry and 3D X-ray scans were used to identify whether the enigmatic body is connected to the nervous system. Suckers were torn from the arm *ex vivo*, to test whether the enigmatic body contributes to regeneration. Based on our current findings we suspect the enigmatic body has a role in secretion, but to this day it remains an enigma.

A Host–Symbiont Association as a Synapomorphy Within the Taxonomic Conundrum of the Haplosclerida (Phylum Porifera)

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The morphological systematics of sponges is often hindered by the simplicity and plasticity of their characters, which are frequently homoplastic and conflict with molecular phylogenies. Independent characters are thus needed to test and interpret molecular hypotheses, and functional and ecological characteristics, including an organism's biotic associations, can provide more evidence. One such association involves the branching worm *Ramisyllis*, a sponge macrosymbiont that spends its entire life inside a single sponge, with its body branching throughout the host's canal system. Recognising its host sponges has long been difficult, because the host genus *Petrosia*, like most families and genera within the demosponge order Haplosclerida, is paraphyletic or polyphyletic under morphology-based classification. Using target capture enrichment with a haplosclerid-specific bait set, we recovered 428 exon loci from museum specimens of *Petrosia* currently placed within the provisionally designated Clade A of the Haplosclerida, and reconstructed a robust phylogeny. Where morphology distinguishes no clear groups, all *Ramisyllis*-hosting sponges form a single, well-supported clade that spans nearly the entire Indo-Pacific and separates into an Indian Ocean and a West Pacific lineage. This consistency suggests that the hosts may share a functional architecture that provides the niche the worm occupies. A coherent host lineage allows further traits that characterise it to be examined, such as those shaping filtration and the microbial environment, which may in turn clarify how this intimate relationship functions and is maintained.

The heat of the moment: validating thermal markers of reactivity along coping styles in small mammals

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Acute stress triggers adaptive physiological responses, including changes in body surface temperature and the release of glucocorticoids. According to the coping style hypothesis, proactive individuals with higher risk-taking behaviour show a higher acute reactivity of the sympathetic nervous system and lower hypothalamic-pituitary-adrenal (HPA) reactivity compared to reactive, shyer individuals. Measuring acute physiological state typically requires invasive methods, potentially intensifying stress. High-resolution infrared thermography offers a non-invasive alternative to capture sympathetic reactivity, e.g. as changes in eye region surface temperature in endotherms. However, validation across taxa remains limited. We aimed to both validate the physiological stress response to a standardized behavioural test in small mammals and to quantify among-individual variation along the proactive-reactive personality continuum. We captured 60 common voles (*Microtus arvalis*) from a wild population in Münster, Germany, and assessed boldness (latency to exit a tube) in a dark-light emergence test and activity (distance moved) during a 10-min open-field test (OFT). We measured eye region surface temperature during the exposure in the arena (i.e. OFT) and collected faecal samples over six hours post-OFT to quantify faecal glucocorticoid metabolites (FCMs). The full test battery was repeated after a week. FCM levels increased significantly following the OFT, and individuals showed consistent among-individual differences in FCM levels. We further predict that more proactive individuals will show a stronger and faster eye temperature increase but lower FCM responses than more reactive ones. Together, these findings will help to provide an ecologically and physiologically validated framework for using infrared thermography as a non-invasive biomarker in lab and field settings.

In vivo investigation of vibrations inside the locust ear**Henja-Niniane Wehmann**¹; Marcel van der Heijden²; Manuela Nowotny³¹ Friedrich-Schiller-Universität Jena; ² Erasmus MC Rotterdam; ³ Friedrich-Schiller Universität Jena

Being able to hear and also determine the direction sound comes from allows animals to avoid predators, find prey or communicate with conspecifics. Directional hearing becomes challenging when animals, such as insects, are small with respect to the wavelength of sound. Different insect species have evolved different hearing organs and solve this problem in different ways.

As acridid grasshoppers, desert locusts have tymanal ears on the left and right side of their first abdominal segment. The chordotonal Müller's organ attaches directly to the back of the tympanum and allows the locusts to hear sound frequencies between less than 1 kHz and about 40 kHz (Suga, 1960, Jpn J Physiol 10). For the lower part of this frequency range, the wavelengths are larger than the distance between the ears. Internally, the ears are coupled by air sacs, which is thought to be important for directional hearing at lower sound frequencies (Römer & Schmidt, 2016, Biol Cybern 110) and is not fully understood.

We employ a technique called optical coherence tomography (OCT) to measure the vibration of the desert locust tympanum and parts of the first internal air sac in vivo. By observing the vibration of the ear at low and high frequencies of sound and by impairing tympanal motion of the ipsi- or contralateral ear, we aim to improve our understanding of the coupling of the ears and contribute to the general knowledge on insect ear mechanics.

A conserved syncytial nerve net across major ctenophore lineages**Brian Wehner**¹; Alexandre Jan; Harald Hausen; Maike Kittelmann; Pawel Burkhardt¹ University of Bergen, Bergen, Norway

The organization of ctenophore nervous systems has fascinated biologists since the pioneering studies of Agassiz, Hertwig and Chun. Recent ultrastructural reconstructions of the lobate ctenophore *Mnemiopsis leidyi* revealed that neurons of the subepithelial nerve net (SNN) form a continuous syncytium rather than a network of discrete cells connected by synapses. Whether this unusual architecture is unique to *Mnemiopsis* or represents a general feature of ctenophores has remained unknown. Here, we examine the neuronal ultrastructure of three phylogenetically and ecologically distinct species: the cydippid *Pleurobrachia pileus*, the beroid *Beroe cucumis*, and the early-branching euplokamid *Euplokamis* cf. *dunlapae*. Using volume electron microscopy and three-dimensional reconstructions, we compare the organization of their subepithelial nerve nets across lineages that differ markedly in body plan, prey-capture strategies and locomotory behavior. Despite these differences, all three species exhibit the same fundamental syncytial organization previously described in *Mnemiopsis leidyi*. This suggests that the syncytial SNN is an evolutionarily conserved feature of the phylum rather than a lineage-specific specialization, while also revealing species-specific adaptations. Together, these findings establish the syncytial nerve net as a widespread organizational principle of ctenophore nervous systems and provide new insights into the evolution and diversification of neural architectures in animals.

Evolutionary biomechanics of maximum running speed in spiders (Araneae)

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Maximum running speed is a central performance trait, linking morphology, physiology and behaviour to fitness. It is shaped by physical capacity and ecological selection but may also be constrained by ancestry. To examine how these forces interact across macroevolutionary timescales, we conducted an allometric study in a hyper-diverse arthropod taxon – spiders (Araneae).

Drawing on running performance data for 258 species from 64 of the 139 extant spider families, we integrated phylogenetic comparative methods and biomechanical modelling to disentangle the effects of body size, ancestry, leg morphology, ecological guild and preferred locomotor orientation. Maximum

running speed varied substantially, both across body mass and among species of similar body mass. By accounting for body mass with a recent biomechanical model, we show that size-specific performance carries a strong phylogenetic signal, and that high-performing runners first evolved within the derived infraorder Araneomorphae. Strong running performance, after accounting for both body size and shared ancestry, was associated with relatively longer legs and, to a lesser extent, ecological guild, but not with leg slenderness or a preference for inverted versus upright locomotion.

Macroevolutionary patterns of running performance thus reflect not only variation in body size, but also size-specific leg morphology, ecological differentiation and phylogenetic history. We hope this study contributes to the development of formal evolutionary biomechanics – one that seeks to explain patterns of diversity through the explicit integration of large-scale comparative data, natural history and quantitative models derived from first principles.



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POSTER SESSION



Hidden Mechanics of Pollination: Ecomorphological Interactions between Insects and Petal Landing Platforms

Marielle Arold

Tübingen Universität

Insect-pollinated flowers have evolved a remarkable diversity of surface structures that mediate the physical interaction between petals and visiting pollinators. This thesis investigates petal landing platforms across multiple angiosperm species (including *Salvia officinalis*, *Aconitum lycoctonum*, and *Echium vulgare*) with a focus on the morphological and physicochemical properties of their surfaces and their correspondence to the tarsal morphology of their respective pollinators.

Using a descriptive-comparative field and laboratory approach, landing sequences were recorded at the Botanical Garden of Tübingen to document natural pollinator behaviour and tarsus positioning. Caught pollinators were prepared for scanning electron microscopy (SEM) to characterise tarsal attachment structures, while petal landing surfaces were analysed via cryo-SEM. Surface topography was quantified using optical profilometry on resin casts. The wettability and free surface energy of the petal surfaces were assessed through contact angle measurements, providing insight into the chemical composition and adhesion-relevant properties of the cuticle.

Infrared thermography was additionally employed to test whether the conical epidermal cells characteristic of many bee-attracting flowers produce thermally distinct landing zones that could constitute a heat reward for pollinators in the field.

The study compares generalist and specialist pollination systems to examine whether specialist flower–pollinator pairings exhibit a more pronounced adaptive correspondence at the petal–tarsus interface than generalist interactions, an effect well established in mouthpart coevolution but less explored for tarsal attachment. Results are interpreted within the framework of flower ecology theories, including foraging facilitation and nectar theft prevention, and discussed in terms of functional ecomorphology.

Social and mating preferences in firebugs

Natalia Bauer-Mätzkow; Daniela Rößler; Timo Thünken; Brian Saltin

University of Bonn

In many animal species, social interactions and mate choice are not random but can be influenced by factors such as relatedness or the genetic quality of the partner. The firebug (*Pyrrhocoris apterus*) is a gregarious, non-eusocial insect that forms aggregations and interacts with conspecifics throughout its life. Clustering is an active process guided by contact pheromones and visual cues. Both chemical and visual stimuli play an important role in mate choice.

In this study, we investigate whether firebugs prefer to interact and mate with individuals from their own or from another population. Before the choice experiments, several groups of firebugs from different populations were collected in Bonn. In pre-tests, the behaviour of the groups was compared under standardized laboratory conditions. The results revealed similar activity and locomotor behaviour across populations.

In the choice experiments, each focal individual is presented with two partners of the opposite sex, one originating from the same population and one from a different population. The experimental arena is divided into multiple zones that differ only in the individual presented as a potential partner. Video recordings from above are used to quantify the time that focal individuals spend in the vicinity of one of the partner choices. Prior to the experiments, males and females were kept separately to prevent recent mating. These experiments may provide insights into the social preferences of firebugs, which might play a role in inbreeding avoidance in this species. As all populations used in this study originate from urban habitats within Bonn, future studies could investigate whether individuals show different preferences when presented with mates from geographically more distant populations.

Microstructure and mechanical properties of the phasmid egg shell (Phasmatodea) and its role in ornithochory

Thies H. Büscher; Chuchu Li; Linus M. Reck; Eberhard Haase; Judith Burack; Stanislav N. Gorb

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The eggs of stick insects (Phasmatodea) are an enigmatic example of early life stages of insects that warrant extensive exploration. They show a great variety of adaptations for dispersal and both biotic and abiotic interactions, as well as a unique material composition. They have a hardened mineralised chorion, which provides a high mechanical stability for protection of the embryo. This hardened capsule forms various functional surface structures responsible for numerous functions across phasmids. Previous studies have shown their capability for dispersal mediated by sea water, ants and potentially through the digestive tract of birds. These dispersal routes exert mechanical and/or chemical stress onto the eggs. To understand how the eggs endure such environmental influences, we conducted feeding experiments with pigeons and experiments testing various parameters the eggs need to endure during birds' digestion. Furthermore, we analysed the egg of *Carausius morosus* in detail, including the micromorphology of the egg chorion of this exemplary species using Scanning Electron Microscopy (SEM) and Micro-Computed Tomography (μ CT), the elemental composition using Energy Dispersive X-ray Spectroscopy (EDX) and the mechanical properties using nanoindentation and compression experiments. We corroborate that the outer chorion of the egg consists of three layers. Two of these (the inner- and outermost) layers consist of chitinous material, while the middle layer is enriched in calcium salts, indicating that this layer likely contributes most to the mechanical stability of the egg, but is also most affected by acidic environment during bird digestion. In the laboratory experiments, low pH strongly reduced survival, even though the shells remained largely intact except for partial dissolution of the calcium-rich layer. We demonstrate here that while the mineralized chorion offers substantial mechanical protection, it also imposes vulnerability to acidic conditions, revealing a trade-off that shapes the ecological limits and dispersal potential of phasmid eggs.

Experimental coevolution of social behavior and insect–microbe mutualism

Chung-Fan Chang; Jos Kramer

Animal-microbes interactions are widespread across all lineages and affect the evolution of many species' traits, including social behaviour. To date, most studies have focused on the benefits of these behaviours provided in their interactions with microbes. However, whether environmental microbial stress can in turn act as a selective force driving the evolution of social behaviour has rarely been examined empirically. To address this gap, this study uses the burying beetle *Nicrophorus vespilloides* and employs experimental evolution under two manipulated levels of environmental microbial stress (strong vs weak) to investigate how parental care behaviour and beneficial gut symbionts change in response. We obtain microbial rinsates from decaying carcasses, dilute them to high or low concentrations, and apply them to fresh carcasses to simulate strong and weak environmental microbial stress respectively. At each stress level, we maintain two independent replicate lineages for eight generations to achieve experiment evolution. At the end of the experiment, we quantify parental care behaviour and gut microbiome composition. We predict that under higher microbial selection pressure, burying beetles will form a closer relationship with gut symbionts that help them overcome environmental microbial stress, and will invest more in parental care behaviours that transmit their own symbionts to their offspring, resulting in gut microbiota more similar to those of their ancestors than in low-stress treatment. Because burying beetles are easy to observe and well-studied, combining this system with experimental evolution to simulate realistic evolutionary scenarios will help us better understand the coevolution of microbes and animal social behaviour.

Effects of male age and nutritional state on vibroacoustic signals during courtship in the house cricket (*Acheta domesticus*)

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Vibration or drumming as an integral part of the house cricket courtship communication has long been neglected. Until recently, most of the research focused on the acoustic component of the signal, leaving non-acoustic aspects relatively underexplored. However, even though it seems clear that the male signal is used in female choice, so far no clear correlation between the song alone and condition of the male could be made. In the last five years, several studies (Stritih-Peljhan & Virant-Doberlet, 2021; Stritih-Peljhan & Žunič-Kosi, 2024) have investigated the multimodal nature of cricket courtship, promoting further investigation of this behavior.

It appears that, in cricket courtship, the two different channels – sound and vibration – do not convey different information, nor do both channels convey the same information independently. Instead, the sound and vibration channels seem to combine to form a single functional signal. In this way, the signal would be truly multimodal. By comparing the acoustic and vibrational signals produced by males differing in age and nutritional condition (resulting in different fitness), our study assesses whether signals honestly convey information about individual quality and can therefore be a basis for female choice. Additionally, we aim to show that the presumed integrated signal of sound and vibration exists and is more than the sum of its parts.

Female choice and signal interaction in the complex vibroacoustic courtship of the house cricket (*Acheta domesticus*)

Ana Majcen; Nataša Stritih Peljhan; **Taina Conrad**

National Institute of Biology

Male house crickets (*Acheta domesticus*) simultaneously use three different vibroacoustic signaling mechanisms during courtship (Stritih-Peljhan & Žunič-Kosi, 2024). Their signal consists of stridulation, tremulation and drumming or foot tapping (Stritih-Peljhan & Virant-Doberlet, 2021). The components of this complex vibroacoustic signal are known, but the role of each component in courtship remains a mystery.

The aim of our study is to disentangle how individual signal components influence the female choice, and whether the combined signal exerts additive or interactive effects on female choice. We examined female choice when presented with different manipulated males that either only produce song, only vibrations or both. For the males that can only produce song they were on a non-vibrating stone surface. For the males only producing vibrations, they had the part of their wings with the stridulatory organ cut off. We assessed how selective an individual group of females was based on the percentage of accepted copulations and their latency to mate. We expect that males that emit a signal with all three components (stridulation, tremulation and drumming) will receive the largest percentage of copulations, followed by males that produce only song (stridulation) and lastly males that produce only vibration. Naïve females will be less selective than experienced females.

This study gives us new insights into this complex vibroacoustic signal.

Differences in stridulation signals and chemical profile of Slovenian and German Burying Beetles

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Communication is essential for coordinating social interactions and parental care in many animal species. In the burying beetle *Nicrophorus vespilloides*, both vibrational signals produced by stridulation and chemical cues play important roles during reproduction and brood care. However, little is known about how these communication signals vary among geographically separated populations and how quickly they might evolve.

This study investigates differences in stridulatory signals and chemical profiles between *N. vespilloides* populations from Germany and Slovenia. In addition, the effects of developmental heat stress on communication traits are examined by exposing pupae to a simulated four-day heatwave. Stridulatory signals are recorded from individual beetles and breeding pairs and analysed using Raven Pro 1.6, while chemical profiles are analysed using gas chromatography–mass spectrometry (GC–MS).

We predict significant variation in both acoustic and chemical communication between populations, potentially reflecting geographic isolation by the Alpine mountain range. Furthermore, heat stress may alter signal production and contribute to communication differences among individuals.

Distribution of European Leptodirini (Coleoptera, Leiodidae) with a focus on diversity hotspots and their threats

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The tribe Leptodirini (Leiodidae) is one of the most species-rich subterranean beetle taxa worldwide- the second largest group after the Carabidae Trechini. More than 1000 species in approx. 240 genera are known so far, mostly in the Palearctic Region, with the largest radiations in the Mediterranean basin. All Leptodirini inhabit caves, litter or deep soil layers.

Often restricted to very small areas, or even known from one single locality, Leptodirini species have many narrow endemic species, and for almost all species the limit of their distribution is unknown. This lack of basic knowledge about their distribution makes it difficult to evaluate their vulnerability to direct and indirect human impacts like soil degradation and karst destruction due to quarrying and mining activities.

In our project, we compiled all published Leptodirini sample localities of European species to calculate Hotspot regions of Leptodirini diversity and to address potential conservation issues in those areas.

3D Analysis of Antennal Movements in Honeybees during Differential Olfactory Conditioning

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Bielefeld University

Honeybees rely on their highly developed sense of olfaction in foraging and social behaviours. As their main sensory organs for olfaction, the antennae play a key role in olfactory conditioning, both for receiving the olfactory stimulus and for triggering the unconditioned proboscis extension reflex (PER). To date, the PER serves as the main readout behaviour in the study of associative learning in bees. Recently, a change in antennal movement was shown to occur in association with appetitive or aversive olfactory stimuli, though it remains unclear whether antennal movements may serve as a reporting behaviour in differential conditioning. Moreover, while the honeybee antenna allows independent movement of four degrees of freedom (DOF), it is unknown how these DOF contribute to changes in antennal movement during associative learning.

Here, we analysed antennal movement in relation to acquisition and extinction curves during differential olfactory conditioning with two aggregation pheromones: whereas Citral was used as the rewarded conditioning stimulus (CS+), Geraniol was not rewarded (CS-). Fifty single, restrained honeybees were exposed to a sequence of 2×5 pretest, 2×10 conditioning, 2 memory test, and 9 extinction trials. Animals were filmed with a stereo-camera setup, and 3D postures of both antennae were reconstructed in a head-fixed coordinate system, using DeepLabCut to track 11 features on antennae, mandibles, and proboscis at 50 fps.

In total, 37 bees learned the odour-reward association, and 25 responded with PER selectively to the CS+. On average, these 'learners' responded to the CS+ with a bilateral forward extension of the antennae, thus confirming previous studies that collapsed antennal movement into a 2D plane. Moreover, we observed that antennal movement response to CS+ is distinct from that to CS-, revealing differential conditioning of antennal movement. Furthermore, we show that only a subset of the 4 DOF carry the CS+ response.

Braver in the City? Nest Defence Behaviour in Great Tits and Blue Tits Across an Urbanisation Mosaic**Basak Dincer**¹; Laurie Johnson; Diana S. Vasconcelos; Maria Moiron; Barbara A. Caspers; Öncü Maraci¹ Bielefeld Universität

Urban environments are one of the most altered habitats. Birds breeding in cities encounter frequent human disturbance, altered predator communities, and novel sensory conditions such as anthropogenic noise and artificial light at night. These environmental changes may influence how parents perceive risk and defend their nests. However, urbanisation-related alterations in nest defence behaviour remain poorly studied, and we still know little about whether urbanisation changes the balance between risk-taking, aggression, and reproductive investment at the nest.

In this study, we examine nest defence behaviour in Great Tits (*Parus major*) and Blue Tits (*Cyanistes caeruleus*) across an urbanisation gradient in Bielefeld, Germany. Using a standardised nestbox opening protocol during the incubation period, we quantify several behavioural responses, including whether and when birds leave the nest, hissing behaviour, threat display, alarm calling, and flight distance after disturbance. By testing each nest twice during incubation, we additionally assess the temporal repeatability of defensive responses.

This experimental approach allows us to determine whether nest-defence behaviour varies with the degree of urbanisation, whether species and individuals differ in their defensive strategies, and whether defence intensity is associated with reproductive investment. By focusing on parental decision-making under risk, this study provides new insights into the behavioural mechanisms that enable birds to cope with human-altered environments and contributes to a broader understanding of behavioural adaptation to urbanisation.

snRNAseq analysis reveals muscular adaptations of *Astyanax mexicanus* cavefish**Kelly Dooling**¹; Ana Santacruz²; Edward Ricemeyer; Wesley Warren³; Nicolas Rohner²¹ University of Münster; ² Universität Münster; ³ University of Missouri

Caves are challenging environments in which cave-dwelling organisms have evolved mechanisms to survive in conditions of little to no light, hypoxia, and nutrient deprivation. The Mexican cavefish, *Astyanax mexicanus*, has emerged as a prominent model organism for studying these processes due to their repeated and independent adaptations to cave environments while maintaining reproductive compatibility with their ancestral ecotype, surface fish, which dwells in superficial rivers and lakes. Studies have particularly noted several metabolic adaptations in cavefish, including hyperphagia, insulin resistance, and increased fat storage. One of the most metabolically active areas of the body lies in muscle tissue, making it a promising target for elucidating further metabolic adaptations. Previous research has found that cavefish display markedly reduced muscle mass and contractility yet maintain similar muscular endurance as the surface fish ecotype. To further characterize the changes associated with these phenotypic differences, we performed single nuclei RNA sequencing (snRNAseq) on muscle tissue from cave- and surface fish. We identified more than 10 putative cell types and detected differences in cell type composition between the two ecotypes in clusters related especially to adipocytes, suggesting increased fat storage in cavefish muscle tissue. These findings provide insight into the cellular and molecular muscular adaptations of cavefish, potentially highlighting techniques used to survive extended periods of nutrient deprivation.

The embryotheca of Hydra is a semi-permeable interface allowing embryo communication with the environment and microbiome

Ella Doveton; Francesco Nienhaus; Jörg Wittlieb; Alexander Klimovich

In recent decades, animal development has increasingly been understood as a process in dialogue with the environment rather than an autonomous programme. Yet the mechanisms governing this dialogue, and their evolution, remain largely unknown. Here, we address this gap using embryonic development of the freshwater polyp Hydra. Shortly after fertilisation, the embryo forms a chitinous cuticle, or embryotheca, beneath which most of the embryonic development takes place. Previous studies (Martin et al., 1997) suggested that the embryotheca acts as an impermeable protective barrier. However, recent studies (Noack et al., 2025) indicate that environmental factors, including bacteria, impact hydra embryonic development and, in particular, neurogenesis. This challenges the assumption of the embryotheca's impermeability. To resolve this paradox, we monitor the embryotheca formation in real time and describe its morphology at high resolution. Using fluorescent dyes of different molecular weights, we demonstrate that small molecules cross the embryotheca in vivo, whereas passage of larger molecules is attenuated. Thus, the embryotheca represents a selectively permeable interface that enables the embryo's communication with the environment and the microbiome during development. Our study reveals how physical properties of embryonic barriers complement molecular pathways to integrate developmental programmes with environmental cues.

The role of head movements in visually guided target choice and approach in walking stick insects

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Stick insects reliably approach stationary visual targets with preferences for areas of low luminance or high-contrast edges. Irrespective of visual input, walking stick insects execute oscillatory head yaw movements that are coupled to the rhythm of the step cycle. Moreover, head movements exhibit a bias towards the turning direction, even after blindfolding. Although it is clear that head movements shift the position of visual features within the field of view, it is unknown whether and how head movements vary as a function of visual features such as target position, number, size or contrast. Here, we test this in a set of experiments, in which we video-recorded free-walking stick insects (*Carausius morosus*) in a circular arena surrounded by 360° grayscale images. Visual targets of different width and contrast were tested in an open-field paradigm. In experiments with two targets, the initial walking path was constrained to a narrow walkway that led into the arena centre. Body axis orientation and the midline of the head were tracked using DeepLabCut. As a direct test of the effect of head movements on target choice and approach, we also tested head-fixed animals in a two-target paradigm.

Our results show that the directional bias of rhythmic head movements predicts target choice in two-target paradigms, but the magnitude of the bias does not depend on two-target target separation. Moreover, fixing the head to the prothorax has no effect on overall choice behaviour, nor on the approach of high-contrast visual targets. However, our experiments cannot rule out a potential role of walking-related yaw movements of the prothorax relative to the mesothorax. We conclude that active head movement is not necessary for visual target choice or approach, but head-movement-related changes of the visual scene contribute to target choice.

BuggedBugs – How land use and climate variability impact on hosts and their parasite communities

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Parasites are the most common life strategy on earth, yet parasite biodiversity remains one of the most overlooked axes of ecological research. Healthy, diverse parasite communities are indicators of ecosystem stability, and their disruption may increase the risk of emerging disease. Despite this, we lack a mechanistic understanding of how stressors, particularly land use intensity (LUI) and climate change, shape parasite communities.

Our project "BuggedBugs" addresses this gap using the unique long-term Biodiversity Exploratories (BE) platform. We focus on true bugs (Heteroptera), a speciose and ecologically diverse group that has been sampled, identified to species, and archived across grassland plots in Germany since 2008, providing an 18-year time series spanning a broad gradient of land use intensity and climate variability.

We hypothesize that increasing LUI reduces host richness and abundance, which in turn drives a decline in parasite diversity, while potentially favouring generalist or emerging pathogens. Climate variability may further modulate these effects via impacts on host phenology, body size, and immune function.

To test these predictions, we are currently developing the contemporary pathobiome baseline: collecting and identifying fresh Heteroptera samples from 27 VIP plots (June and August 2026), and sorting archival material for retrospective parasite community analysis via genome skimming. Together, these approaches will allow us to disentangle the direct and indirect pathways through which global change shapes host-parasite communities across time and space.

Germline mutation dynamics in a eusocial ant: extending our view beyond vertebrate models

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Germline mutations are the ultimate source of heritable genetic variation, and the rate at which they arise is a central parameter in population genetics and evolutionary biology. Yet our understanding of their origin, accumulation, transmission, and evolutionary fate is still largely shaped by vertebrate pedigree studies. These studies have revealed parental-age effects and sex-specific mutation biases, but they do not capture key reproductive features of eusocial insects, where reproduction is monopolized by queens, viable sperm can be stored for years, males are haploid, and offspring may develop into sterile or reproductive castes. This leaves an important gap in our understanding of evolutionary mutation dynamics. How does eusocial reproductive division of labour shape the occurrence and transmission of germline mutations in haplodiploid social insects? Here, I present a project using the ant *Cardiocondyla obscurior* as a tractable eusocial model to investigate how maternal age, sperm storage, haplodiploidy, and reproductive division of labour shape de novo mutation dynamics. By bringing social insects into germline mutation research, this project aims to broaden our understanding of the evolutionary dynamics of mutations beyond classical vertebrate systems.

Developmental principles of neural lineage, type and circuit evolution

Max S. Farnworth

Johannes Gutenberg - Universität Mainz

Brains are complex biological systems with thousands to billions of neurons, connected into neural circuits whose evolution is shaped by principles that both constrain and permit variation. My lab's central question is how neural circuits change through the interplay of such principles. We will address this by leveraging two key aspects: first, two insect integration centres — the central complex and the mushroom bodies — show strikingly dissimilar evolutionary trajectories. The mushroom bodies have expanded repeatedly, while the central complex is largely conserved, providing a powerful contrasting setup to examine divergent modes of neural circuit evolution. Second, we map the development of these circuitries by exploiting the instructive nature of insect neural lineages. Insect neural stem cells and their progeny remain clustered and form discrete functional units, meaning developmental relatedness directly informs adult anatomy.

The lab aims to identify disparate patterns of developmental variation in key parts of the central complex and mushroom body circuitries, and to determine the drivers of such variation, across four accessible insect species. We will first generate single-cell transcriptomic atlases to characterise changes, innovation, and variation in key cell types. We will then build anatomical lineage-based atlases to map the basis of evolutionary variation in our focal circuitries. Combining these atlases with in situ labelling will allow us to identify the most variable cell types across both systems. Finally, we will generate synapse-resolution projectomes using tissue expansion and lightsheet microscopy — first of two GABAergic neural lineages identified by immunostaining, and second of a hypervariable cell type and lineage labelled via transgenic approaches — to precisely determine how developmental variation is realised at the circuit level.

Together, this programme will advance our understanding of how key neural circuits evolve, and how development both instructs and constrains the adaptability of insect circuitries.

Feeling blue - blue mussels and blue carbon**Laura I. R. Fuchs**; Michael Zettler

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Oceans play a central role in regulating Earth's climate by absorbing, storing, and redistributing heat and CO₂ through their physical, chemical, and biological processes. Shallow shelf seas differ from the deep ocean because they are highly dynamic environments where currents and waves strongly influence the transport and deposition of organic and inorganic material. Interest in the ocean's role in carbon storage has led to the concept of "blue carbon," defined by the IPCC as biologically driven carbon fluxes and sinks in marine systems that can be managed. "Coastal blue carbon" primarily refers to habitats such as salt marshes, mangroves, and seagrass meadows, which are characterized by long-term carbon storage. Shellfish have long been important to human societies as food, currency, and raw materials. Today, oysters, mussels, and clams are widely farmed in aquaculture. The idea that shellfish could function as carbon sinks because of the carbon stored in their shells has attracted attention, particularly within the aquaculture sector. In the German Baltic Sea, blue mussels cover about 8% of the seabed. Mussels build their shells from calcium carbonate (CaCO₃) using dissolved inorganic carbon, mainly bicarbonate ions (HCO₃⁻), from seawater. However, shell formation releases CO₂ and reduces seawater alkalinity, lowering its capacity to absorb atmospheric CO₂. After mussels die, their shells usually dissolve, increasing alkalinity and promoting CO₂ uptake. Generally, there is a lack of experimental data in the literature. We conducted experiments in the indoor benthocosm facilities at GEOMAR in Kiel. Patches of mussel reef communities were incubated and DIC; TA, ph, DOC and POC were measured, in order to get a comprehensive understanding of the reef communities impact on the carbon cycle. Our results show that while mussel reef communities are a carbon sink, they are also a CO₂ source.

Using ants in Vanuatu for case-based teaching of integrative taxonomy

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The accelerating loss of species and ecosystem function worldwide has intensified the global biodiversity crisis, necessitating urgent and coordinated conservation action. To inform conservation priorities, there is a need for taxonomic efforts to describe and catalogue Earth's vanishing biodiversity as well as to better understand its evolutionary history. However, there is a dwindling number of trained taxonomists and resources for taxonomy across the globe, which has been referred to as the "taxonomic impediment" to biodiversity discovery and conservation. To help address these biodiversity concerns, there has been a renewed interest in teaching taxonomy to students in higher education with an emphasis on going beyond the classic "one-on-one" mentorship model towards a more collaborative model involving an entire classroom of students. Here, we build upon this framework by utilizing a collaborative and case-based learning approach to teach "integrative taxonomy," which combines traditional comparative morphology, molecular phylogenetics, as well as ecological and biogeographic information to resolve species boundaries more accurately. Specifically, we provided case studies based on our own ongoing research of ant biodiversity in the Vanuatuan archipelago and the broader South Pacific region. So far, these integrative taxonomic training courses has resulted in the delimitation and descriptions of new ant species in the genera *Myrmecina*, *Pheidole*, and *Vollenhovia* from Vanuatu as well as provided foundations for future, broader revisions of these groups. Based on student surveys, this teaching approach of integrative taxonomy gave them a deeper understanding and appreciation for the mechanisms generating biodiversity, provided a sense of community, and enhanced their scientific self-efficacy by increasing their confidence in taking on their own taxonomic projects. Together, these outcomes demonstrate that a case-based learning approach to integrative taxonomy is useful for transferring skills in taxonomy, biodiversity science, and conservation to students with little to no previous experience in these fields.

Is paw preference in rats influenced by environmental novelty?

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The phenomenon of hand and paw preferences is an integral part of laterality research. Scientists agree that both genetic and environmental factors contribute to the development of laterality. Whereas early-life factors such as rearing conditions were already found to influence behavioural lateralisation, evidence for an influence of environmental factors later in life is mostly missing. Therefore, this study aims to investigate the effect of environmental novelty during adolescence and adulthood on the paw preference in female rats, *Rattus norvegicus* f. *domestica*. Since novelty is predominantly processed in the right hemisphere of the brain, a prolonged exposure to novel combinations of environmental enrichment items was assumed to elicit a right hemisphere activation, which is reflected in a left paw preference. To assess behavioural lateralisation, three different paw preference tests (food reaching, tool use and climbing) were conducted three times in total. We found that a regular enrichment change did not alter the behavioural lateralisation in rats neither during adolescence nor adulthood. Different explanations for this finding, such as an insufficient level of novelty or a late onset of novelty exposure, are discussed. The direction of lateralisation was found to be stable over time for the two complex tasks, food reaching and tool use. Moreover, a decrease in strength of lateralisation over time was observed, indicating increased flexibility of paw use. In conclusion, the study confirmed previous findings on stable paw preferences in complex test situations in rats. The increased flexibility in paw use over time represents an interesting similarity to humans, as strength of handedness was also found to decrease with age. Therefore, our findings underline the need for further studies on behavioural lateralisation in nonhuman animals.

(Groneberg, E., Richter, S. H., & Kaiser, S. (2025). Is Paw Preference in Rats Influenced by Environmental Novelty? *Ethology*, 131, 77–93. <https://doi.org/10.1111/eth.13580>)

Smoke and Adiposity: Transgenerational Consequences for Respiratory and Systemic Health

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Lifestyle factors such as high-calorie diets and cigarette smoke are major drivers of metabolic and physiological dysfunction, contributing to chronic diseases including respiratory disorders. Yet, their combined impact on organismal physiology and tissue homeostasis remains poorly understood. To address this, we use the fruit fly *Drosophila* as a model to investigate how these lifestyle-related exposures affect system-ic physiology and airway homeostasis.

In intragenerational experiments, flies were exposed to a high-calorie diet and cigarette smoke either individually or in combination. Both interventions significantly shortened lifespan ($p < 0.0001$), with the combination producing the strongest effect ($p < 0.0001$). High-calorie feeding also markedly reduced physical activity and impaired body composition and fitness parameters, effects that were generally exacerbated by cigarette smoke. Notably, flies exposed to both stressors showed increased susceptibility to airborne challenges ($p = 0.0002$), indicating reduced respiratory resilience.

At the tissue level, both interventions increased intestinal stem cell proliferation and compromised gut integrity ($p < 0.001$). We also observed structural abnormalities in the intestinal tracheal network, suggesting that lifestyle-related stressors disrupt local airway organization at the gut-trachea interface. Building on these findings, we are currently analyzing how these exposures affect airway structure and airway progenitor cells. Initial observations further suggest that parental lifestyle may influence respiratory development in the offspring, and ongoing work aims to disentangle the relative contributions of maternal versus paternal exposure to airway development and respiratory homeostasis.

Refining Housing Conditions: Comparison of Enrichment Preferences in Young and Old Laboratory Mice

Linn Nathalie Hoppe; Viktoria Siewert; Helene Richter; Sylvia Kaiser

Animal welfare has become an increasingly important consideration in animal husbandry over recent decades. As legislation incorporates animal welfare and the protection of animals from suffering, including the avoidance of euthanising surplus laboratory animals, many facilities now house animals to advanced ages. This leads to challenges regarding age-related health issues, such as motor impairments and behavioural changes, which raises the question whether housing conditions and enrichment concepts should be adapted to the changing abilities and needs of older animals. We investigated enrichment preferences in female laboratory mice (*Mus musculus*) of the commonly used inbred strain C57BL/6J. During a three-week preference test, mice from three different age groups ($n = 12$ per group) could freely choose between six enrichment elements (rope, running wheel, heating pad, nest puck, tunnel and food ball), presented in separate compartments of a modular cage system for four hours per day. Interaction frequencies and durations revealed a higher use of nest pucks in middle-aged and old mice, whereas young mice showed a stronger preference for physically demanding enrichment items, including rope and running wheel. The remaining objects showed only minor group differences. Health assessments indicated an age-dependent decline in climbing abilities, which likely reflects underlying physiological changes. Overall, these results demonstrate that ageing modifies enrichment preferences and physical capacities in mice. Our findings highlight the importance of refining housing conditions for old laboratory mice to ensure species- and age-appropriate conditions and enhance animal welfare.

A Comparative TE Annotation Framework for Bees

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Transposable elements (TEs) represent a major component of insect genomes and play important roles in shaping genome structure and evolution. However, comparative studies across bees remain limited by inconsistent TE annotation and lack of consistent and standardized approaches for comparative TE analysis across species.

To address this, we developed a unified comparative TE annotation framework for bees (Apoidea) based on de novo TE discovery across the genomes of 250 bee species. Using Earlgrey and MChelper, we performed genome-wide TE identification, clustering, and consensus sequence construction, generating a non-redundant and standardized TE annotation library that enables cross-species comparability of TE content and genome annotation.

We applied this framework to quantify per-genome normalized TE burden across bee species and further integrated these data with gene loss estimates inferred using TOGA2. Our analyses reveal substantial variation in both TE burden and gene loss across bee lineages. We further explore their distribution in a phylogenetic context to assess potential associations across the bee tree of life.

This study establishes a scalable comparative framework for TE annotation in bees and provides a foundation for integrative analyses of genome evolution and repeat dynamics in insects.

Stranger in the nest: Testing the role of kinship in sibling interactions and development in zebra finches - first results

Laurence Jeanjean; Barbara Caspers; Öncü Maraci

Bielefeld University

Cross-fostering experiments in birds have been used for decades to disentangle genetic and environmental effects, or as a convenient way to manipulate brood size or hatching asynchrony. Because fostered chicks are generally accepted by their foster parents, it is often assumed that relatedness differences within broods have no impact on chick performance and family life. However, recent findings from our research group on captive zebra finches showed that females (but not males) fostered as eggs in another zebra finch nest have a shorter lifespan than non-fostered individuals. This suggests that variation in relatedness between nestmates does influence individual fitness. One possible explanation is that the introduction of fostered chicks alters sibling interactions and social dynamics in the nest, inducing early-life stress with long-term consequences.

To investigate whether and how the swapping of single or multiple eggs affects development, we conducted a cross-fostering experiment and compared behaviour, growth rates and early-life stress of chicks from full-sibling broods with those from mixed-broods in domesticated zebra finches (*Taeniopygia castanotis*). This experiment is the first to systematically explore whether and how egg cross-fostering affects not only the exchanged chicks, but also their nestmates and foster parents, and we present here the first results from this experiment.

Juvenile hormone signaling in the *Daphnia longispina* species complex**Maïke Johann**; phil. Vladislav Ivanov; Mathilde Cordellier

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Environmental sex determination enables *Daphnia* populations to adjust offspring sex in response to changing environmental conditions and is regulated by juvenile hormone (JH) signaling. Although JH analogues such as fenoxycarb have been widely used to induce male production in *Daphnia*, most studies have focused on single laboratory clones from either *D. magna* or *D. pulex/pulicaria* species. Although widely spread in Europe, members of the *D. longispina* species complex (DLSC) have seldomly been included in JH signaling studies. Consequently, little is known about intraspecific variation in sensitivity to JH-mediated signaling among genetically distinct *Daphnia* clones from the DLSC, and its genetic basis. To address this knowledge gap, five *Daphnia* clones were exposed to increasing concentration of the JH analogue Fenoxycarb in a 14-day reproduction test. Survival, reproductive performance and offspring sex were assessed to identify clone-specific phenotypic responses. In parallel, quantitative PCR analyses of candidate genes involved in JH signaling are being conducted to investigate the molecular basis of phenotypic variation. Finally, a comparative genomic approach including many of the publicly available genomes for *Daphnia* species allowed to assess variation of genes putatively involved in JH signaling, in particular the sequence and placement of JH response elements. Preliminary analyses indicate pronounced clone-specific differences in reproductive responses to fenoxycarb exposure, whereas no consistent induction of male offspring was observed under the tested conditions. Together, this study provides a framework for linking clone-specific phenotypic variation with endocrine signaling and its underlying molecular mechanisms in the *Daphnia longispina* species complex.

Sex and the city: Reproductive timing and breeding success of blue and great tit along an urbanisation gradient**Laurie Johnson¹**; Barbara Caspers²; Öncü Maracı¹¹ Universität Bielefeld; ² Universität Bielefeld

Cities are expanding globally, influencing wildlife and resulting in changes to their physiology, behaviour, body condition, and breeding success. As urbanisation contributes to biodiversity loss worldwide, research investigating its effects on wildlife has expanded rapidly. The Eurasian blue tit (*Cyanistes caeruleus*) and great tit (*Parus major*) have emerged as key model species in urban ecology due to their widespread distribution across urban and non-urban habitats and their willingness to breed in nest boxes, thus facilitating experimental research. The majority of these studies compare urban and non-urban populations in large cities with limited green space, reporting reduced reproductive success and altered reproductive timing. Large cities represent only a small proportion of urban areas across Europe, therefore testing whether these effects are consistent across differently sized cities with different green-space availability would allow us to draw more ecologically generalisable conclusions about the impacts of urbanisation on birds. To address this knowledge gap, we investigated the reproductive timing, breeding success, and nestling body condition of blue tits and great tits across a gradient of urbanisation in Bielefeld, a medium-sized German city with a substantial amount of managed green spaces.

We measured multiple ecological variables such as human disturbance, sound pollution, and temperature at multiple time points. This was done to quantify local scale heterogeneity across four sites of varying degrees of urbanisation, and to determine how reproductive timing (egg laying date and hatching date) and reproductive success (number of eggs laid vs chicks hatched and fledged, and nestling body condition) of the two species differ in habitats with different levels of urbanisation. Our findings will provide a broader ecological perspective on how urbanisation influences avian reproductive strategies and fitness across heterogeneous urban landscapes, helping to determine whether patterns reported from large metropolitan areas can be generalised to other types of cities.

Identification of the degrees of freedom in insect leg joints using 3D motion tracking

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Due to their remarkable morphological and functional diversity, insect legs are an important subject of comparative, biological studies and serve as an inspiration for bio-inspired robotics. The design of kinematic chains inspired by insect legs often involves simplifying assumptions regarding the degrees of freedom (DOFs) in each joint to ensure smooth technical applicability. However, information on the true number of DOFs required to fully describe the range of motion of insect leg joints is scarce. In the present study, we used 3D motion tracking to investigate the DOFs of the joints in all three leg pairs of the desert locust *Schistocerca gregaria*. For this purpose, markers were glued to individual segments of the legs of deceased animals and tracked during manually induced movement. The resulting trajectories were used to infer whether the joint's movement is dominated by only one rotational DOF or requires more than one DOF to sufficiently describe the movement. Furthermore, the trajectories were used to infer the center of rotation of the joint, which were then compared to anatomically determined ones (selected manually from μ -CT scans), assessing the suitability of such anatomical points for kinematic modeling. Finally, the resulting trajectories were examined for translational DOFs within the joints. Kinematic data like this, accumulated for a variety of insect species, would significantly increase our knowledge of the movement and architecture of arthropod legs for comparative studies and bio-inspired technical applications.

Characterization of the UFMylation Pathway in *C. elegans*

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The covalent attachment of ubiquitin-fold modifier 1 (UFM1) to target proteins serves as a critical post-translational regulator of DNA damage repair, endoplasmic reticulum stress responses and ribosomal homeostasis. Although disruptions of the UFMylation pathway are lethal in mammals, they are tolerated in *Caenorhabditis elegans* providing a powerful model for exploring the systemic physiological functions of this modification. Using CRISPR/Cas9 we generated a *ufm-1* loss-of-function mutant revealing crucial relevance of UFMylation for ER homeostasis, leading to an upregulation of a BiP/GRP78 ortholog. Furthermore, loss of *ufm-1* resulted in reduced reproduction rate, compromised stress response and reduced motility. To further investigate the regulatory mechanisms of UFMylation, specifically the role of UFM-1 maturation, we generated a genomic-level maturation mutant and crossed it with a deletion mutant of the specific protease *ufsp-2*. While loss of *ufsp-2* mirrored the phenotype of the *ufm-1* null mutant, the constitutively matured UFM-1 mutant also exhibited reduced fitness. Notably, the double mutant showed a partial rescue of the phenotype. Our findings suggest that the precise balance of UFM-1 processing is vital for cellular health and physiological function.

Material electron density as a proxy for stiffness: a solution for more reliable Finite Element Analyses?

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Morphologists can test form-function relationships using computational simulations that approximate natural conditions of a behavior. Finite element analysis (FEA) is a numerical method that approximates the mechanical responses of structures to load, estimating stress and strain. FEA can be applied to 3D reconstructions of a structure and demands information on material stiffness (E). Although 3D morphology is increasingly accessible through X-ray microtomography, obtaining E remains laborious because methods such as nanoindentation are time-consuming and permanently damage samples. Synchrotron microtomography (SR- μ CT) can provide voxel-level electron density (ED) measurements (gray intensity) after calibration with a material of known ED. Because higher ED may reflect greater concentrations of heavier elements, which are commonly associated with local changes in E, ED could reveal stiffness gradients suitable for FEA. We tested this hypothesis by measuring cuticle ED with SR- μ CT in the mandibles of 22 *Atta laevigata* ant workers. We used grating-based SR- μ CT at the Petra III P05 Image Beamline from DESY. Voxel gray intensity represents local ED and was calibrated using the ED of polypropylene pipette tips that held the samples during scanning. Mandibles were segmented in 3D Slicer[®] and interpolated in Biomedisa[®] to generate 3D mandible reconstructions. From these files, we sampled 10% of voxels evenly distributed along the mandible's three dimensions and extracted its gray-intensity values and 3D spatial coordinates. ED exhibited higher values at the tips of the mandible's teeth and along the basal margin, reflecting patterns of Zn concentration and higher E from the literature. These specimens will subsequently be used in nanoindentation tests to measure E. Mandible ED and E will then be quantitatively correlated to test whether SR- μ CT alone can provide reliable geometric and material information for FEA, avoiding the need for nanoindentation tests, not suitable when samples cannot be damaged or under cost and time limitations.

All-in or fold? Resource stability shapes a life-history trade-off in beetle mothers

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Life-history theory predicts that organisms balance investment in current reproduction and self-maintenance in order to maximize their fitness, but how resource conditions and stability shape these trade-offs remains unclear. We experimentally manipulated resource availability and predictability during a reproductive bout in the burying beetle *Nicrophorus orbicollis* by altering carcass size relative to expected brood size and measured female immune response and mass change after an immune challenge. We found that low resource predictability, rather than absolute resource level, was associated with elevated phenoloxidase activity and encapsulation, indicating increased investment in a rapid but potentially self-damaging immune defense in line with a terminal investment response, favoring current reproduction. In contrast, lysozyme-like activity was highest under consistently poor resource conditions, indicating more measured, long-term self-maintenance in line with reproductive restraint. Together, our results show that resource predictability is a key determinant of immune allocation, dynamically shifting the threshold between terminal investment and reproductive restraint.

The Fast and the Curious: Woodlouse Drift. Personality and Learning in *Porcellio laevis*

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Animal personality, i.e. behavioural differences between individuals that are consistent across time and contexts, is widespread across taxa. Arthropods have become increasingly popular in this field due to their ease of handling, their relevance for broader evolutionary inferences and their important role in our ecosystem. However, studies on arthropod personality often focus only on a limited number of traits, restricting the possibility of a more comprehensive understanding of personality trait interactions. This study investigated multiple behavioural traits in the swift woodlouse (*Porcellio laevis*) to identify which behaviours reflect personality and whether these traits are associated with learning ability.

To test for personality traits, individuals underwent two behavioural tests, each of which was repeated three times. Their response to threats was examined by applying aversive touches and measuring the type of behavioural response and, in the case of a freezing response, the duration of immobility. Exploratory behaviour was tested in a three-dimensional staircase open-field arena, which the individuals were free to explore for three minutes. To assess learning abilities individuals were tested in a Y-maze over ten trials. A tactile stimulus served as a cue, and a shelter containing moist soil and food was used as reward.

The response to threats and the exploratory behaviour showed significant repeatability, indicating consistent individual differences. Results from the learning experiment did not suggest personality effects on learning success. However, a strong effect of time of day on overall activity patterns could be observed. Overall, the findings provide evidence for animal personality in woodlice and suggest that learning behaviour may be influenced by circadian factors rather than stable personality differences.

The Role of Individuality: Does Personality Influence How Mice Respond to Experimental Treatments?

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Stable inter-individual differences, often referred to as animal personality, have received increasing attention over recent decades. Personality has been shown to influence diverse biological processes, yet its role in shaping responses to experimental treatments remains largely unexplored, despite evidence that inter-individual differences may contribute to unexplained data variability and ongoing discussions in reproducibility research. To extend the limited research on this topic, this study aimed to investigate whether personality modulates behavioural and physiological outcomes in mice exposed to different experimental treatments. Ninety-six female C57BL/6J mice were classified into slow- or fast-exploratory personality types based on their behaviour in a free exploration test and subsequently allocated to one of two experiments (48 mice per experiment), involving either an enrichment removal or food restriction, each with corresponding controls. Spontaneous home-cage behaviour, exploratory and risk-taking behaviour in a novel environment (novel cage test), faecal corticosterone metabolites, and body weight were assessed over four consecutive weeks. Personality type influenced behavioural responses to enrichment removal, particularly during exposure to a novel environment. No personality-dependent effects were detected under food restriction, where treatment-related group differences dominated. Personality type did not shape physiological responses to either treatment. These findings demonstrate that personality can influence treatment outcomes, though effects may depend on the treatment type and intensity. Hence, inter-individual differences may represent a systematic source of variability in experimental outcomes, potentially limiting the reproducibility of experimental findings.

Genomic signatures of inbreeding in a cichlid with kin-mating preferences**Benedikt Kröll¹**; Julia Schwarzer²; Shannon Douglas¹; Timo Thünken¹

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Genomic diversity can provide important insights into population history, inbreeding background and the genetic basis of phenotypic variation. Moreover, due to its influence on fitness-related traits, it may shape mate-choice strategies. In *Pelvicachromis taeniatus*, an African cichlid with biparental care and mutual mate choice, previous research indicated inbreeding in a wild population and demonstrated pronounced kin mating preferences in behavioural experiments. However, recent mate choice trials indicate that mating preferences can switch depending on inbreeding level. Here, we show that lab-bred lines subjected to different breeding regimes, together with specimens from the ancestral wild type population, differ in single nucleotide polymorphism (SNP)-based genome-wide homozygosity and display corresponding biases in mating preferences. We found that kin mating preferences were associated with moderate levels of inbreeding whereas high levels of inbreeding (i.e., increased homozygosity) were associated with kin avoidance, suggesting that fish adjust mating decisions to balance inbreeding benefits and costs. To further investigate the genomic signatures of inbreeding and potential molecular underpinnings of mate choice patterns, we are extending this analysis using runs of homozygosity (ROH), long contiguous homozygous segments of the genome. In particular, ROH lengths and distributions may help to elucidate the demographic history of populations, including variation in effective population size, bottleneck events and kin mating patterns, thereby providing a basis for assessments of deleterious variant enrichment, inbreeding depression and potential genetic purging. Finally, future brain transcriptome analyses may help identify candidate genes and regulatory pathways underlying kin discrimination and inbreeding-dependent mate choice decisions.

Which visual aspects of the environment do bumblebees prioritise in a spatial learning task?

Albert Lechêne; Sonja Eckel; Martin Egelhaaf; Jens Peter Lindemann

Bielefeld University

Finding food requires central place foragers such as bumblebees (*Bombus terrestris*) to learn how to navigate repeatedly between their nest and food sources. Visual cues are especially important: bumblebees have been shown to use the visual features of objects and their distance to a rewarded site when navigating to a learned food location.

We studied how walking bumblebees perform spatial learning in a virtual reality setup, allowing the manipulation of the visual features of objects placed around rewarded locations. In a conditioning paradigm, bees learned to visit rewarded targets surrounded by two rings of objects differing in colour and in distance to the target. In a test situation, when the two object constellations were spatially displaced, bees preferred the constellation that had been closest to the target during training, indicating that they associated the target with the nearest object constellation. However, which visual features of the closer objects were learned by bumblebees remained unclear. A new set of experiments revealed that the bees prioritised the colour of the close objects over the spatial aspects of the object constellation. Finally, we could show that, in experiments in which the colour of closer objects dynamically changed, bees learned the features of the close objects also during the approach and not only at the reward site. Nevertheless, they prioritised the colour seen at the reward site over that seen during the approach.

Thus, these results reveal how learning a food location takes place during the approach of the target. Coming experiments in virtual reality will help to determine the underlying mechanisms.

Master's thesis - Characterization of the microbiome of neotropical *Drosophila***Katherina Löbel¹; Stefanos Siozios²; Wolfgang Miller³; Michael Gerth²**¹ MLU-Halle, Naturwissenschaftliche Fakultät I; ² Martin-Luther-Universität Halle-Wittenberg; ³ Medizinische Universität Wien

Host-associated microbiomes are crucial to insect physiology, ecology, and evolution. While the microbiome of *Drosophila melanogaster* has been previously studied, comparatively little is known about microbiome assembly in wild neotropical drosophilids. In particular, the relative contributions of host species identity, environmental context, and host condition to the microbial community structure remain incompletely understood. In this research it was attempted to characterize, the bacterial communities of multiple neotropical *Drosophila* species and a *Scaptodrosophila* species collected in French Guiana were by sequencing the 16S rRNA gene and the Cytochrome oxidase subunit I to identify the fly species of each individual and determine the associated bacterial taxa. It was investigated whether host species identity, location or the presence of external wounding would affect the community composition of the microbiome. Across individuals, the communities showed some shared families such as Acetobacteriaceae or Lactobacillaceae, however, especially neotropical flies were found to have microbiomes dominated by the endosymbiont *Wolbachia*. Overall, the beta diversity analysis revealed that host species identity had the strongest structuring effect, whereas sampling location had weaker effects. In contrast, alpha diversity did not differ significantly across species, location or wounding status. Additionally, a potentially new symbiont was discovered. Together, these findings provide insight into microbial community assembly and suggest that host specific filtering plays a key role in shaping microbiome composition of neotropical drosophilids.

Olfactory cues elicit visual memory retrieval in walking bumblebees during navigation in virtual reality

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To navigate complex environments and distinguish among ecologically relevant resources, nectar-collecting insects integrate several sensory cues, such as olfaction and vision, with memories formed through prior experience. Goal-finding behaviours provide a framework for understanding how insects integrate multimodal cues when navigating uncertain environments. In this context, we used the buff-tailed bumblebee (*Bombus terrestris*) to explore how olfactory and visual information interact during goal-directed behaviour. Specifically, we used a closed-loop Virtual Reality (VR) trackball system to investigate whether trained walking bumblebees can recall a specific colour target when triggered by a previously associated odour. Colour recall was measured by the frequency of visits and time spent around associated and non-associated targets. Additional behavioural dynamics during recall were assessed using walking speed and the relation between choice accuracy and time to reach targets. Through absolute conditioning, two odours (citral and geraniol) were associated with either green or blue. Our results suggest that walking bumblebees can recall visual memories based on previously associated olfactory signals. Both odours were capable of triggering recall, geraniol at a choice frequency of 87.5%, citral at 70%, $p = 0.011$. Bumblebees also spent significantly more time near associated than non-associated targets ($p \leq 0.0006$). Analysis of locomotor dynamics suggests a weak speed-accuracy trade-off during colour recall, with no significant effects within conditions ($p \geq 0.06$), where higher accuracy was associated with longer search times. Furthermore, walking speed differed between odour presentation and target approach, remaining lower during odour presentation ($p \leq 0.001$), suggesting that bumblebees reduced their locomotor activity in order to sample olfactory information. Together, these results suggest that olfactory signals can trigger the recall of visual memories in walking bumblebees. Moreover, VR environments allow for novel and precise controlled approaches for studying multimodal signal interactions during goal-finding behaviour.

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Sociality of Captive-Bred Fire Salamanders (*Salamandra salamandra*): Peeking into their behavior and sociality.

Bulisa Masiga; Barbara A. Caspers; Sean Gwydion Grond

Bielefeld University

Fire salamanders are highly threatened by climate change and the pathogen *Batrachochytrium salamandrivorans* Bsal. To prevent these animals from going extinct, an increasing number of fire salamanders are being kept ex situ. Thus far, they have mainly been housed in individual enclosures, as the prevailing view is that fire salamanders are non-social, or at least less social, and therefore should be kept individually.

At Bielefeld University, however, fire salamanders are kept in groups, in which individuals display clear social behaviour. This study aimed to quantify and characterise the social behaviour exhibited by fire salamanders in captivity. To this end, we video-recorded the different groups throughout the night and developed an ethogram of the observed behaviours. We then quantified the amount of time fire salamanders spent engaging in each behaviour.

Our analysis showed that fire salamanders are much more active and display considerably more social behaviour than previously anticipated. We discuss our findings in light of animal welfare considerations.

Magnetoreception in planarians

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The geomagnetic field provides spatial information used by various organisms, including vertebrates and invertebrates, for long- and short-distance orientation. However, the underlying principles remain poorly understood, and a magnetoreceptor has not been identified yet. For freshwater planarians (Tricladida), magnetic orientation was first reported in the 1960s. Here, we studied *Girardia dorocephala* to test whether they respond to changes in magnetic fields and could serve as a tractable model system for identifying magnetoreceptor candidates. In a circular arena, individuals showed a significant directional preference in an Earth-strength (49 μ T) magnetic field, which shifted when magnetic north was rotated, and was absent in a near-zero field (< 100 nT). As experiments were performed in darkness, excluding a light-dependent radical pair mechanism, the behavioral data is consistent with a magnetite (Fe₃O₄) based mechanism of magnetoreception. Therefore, we screened for potential magnetite particles via Prussian-blue staining, X-ray-fluorescence microscopy, transmission electron microscopy, and MRI-quantitative susceptibility mapping, which map the iron distribution and magnetic properties of tissues at different scales. These analyses revealed high iron (Fe) concentrations in the epidermis as well as iron particles within the head, which are further investigated. As a well-established and easy to handle invertebrate model-organism with fast asexual reproduction via fission, remarkable regeneration capabilities and the possibility of gene knockdowns, planarians offer great potential to better understand the principles underlying magnetoreception in animals.

Piscicolins - putative anticoagulants of marine and freshwater fish leeches**Christian Müller**

Universität Greifswald, Zoologisches Institut und Museum

The leech family Piscicolidae (Johnston, 1865) comprises about 60 genera and 100 species that occur both in marine and freshwater habitats. All are hematophagous ectoparasites on fishes, and some members even feed on the blood of Chondrichthyes (Huxley, 1880) including sharks and rays. Their repertoire of putative anticoagulants, however, is only poorly analyzed and characterized. Here I describe the molecular identification of piscicolins, a new group of putative anticoagulants that belong to the hirudin superfamily. Piscicolins are monomeric or oligomeric factors that contain at least one piscicolin module, but they may also comprise additional hirudin/ornatin modules. Both the piscicolin and the hirudin/ornatin modules contain six highly conserved cysteine residues, however, their genetic structures differ: whereas the archetype hirudin/ornatin modules are encoded by two exons, the piscicolin module is encoded by three exons, respectively. The functional characterization of Hbru_Pisc1, a monomeric piscicolin of *Heptacyclus brunneus* (Johansson, 1896) revealed a low, but detectable platelet aggregation inhibitory effect.

Farm animal cognition research – diverse and open?**Christian Nawroth**

Research Institute for Farm Animal Biology (FBN)

Farm animals have received relatively limited attention in animal cognition research, despite their numbers and biomass surpassing all other mammalian species, including humans. Nevertheless, studying farm animal cognition can benefit applied research, as understanding how farm animals perceive and interact with their environment helps clarify how cognitive processes develop under different husbandry conditions and, in turn, informs management practices that better align with their abilities and welfare needs. To assess the diversity and openness of the farm animal cognition literature, we conducted a scoping review of the available cognition literature on cattle, pigs, sheep, and goats. In total, 252 papers fulfilled our inclusion criteria. Most studies were conducted on single breeds at single sites, with an overrepresentation of females and young animals, limiting the generalizability of findings and interpretation of fully developed cognitive capacities in these species. Geographically, most studies originated from North America or Europe, restricting international representation and limiting insights into local breeds across the globe. None of the papers published between 2000 and 2014 contained a data availability statement or shared data openly. This changed between 2016 and 2019, when a small number of studies (8 of 62 papers in total) made data openly available. The trend continued from 2020 to 2024 (24 of 61 papers in total). These sample biases and lack of data sharing reduce diversity, compromise generalizability, and constrain opportunities for meta-analyses and cumulative knowledge building. In the long run, it weakens the potential for a broader understanding of farm animal cognition, which is crucial for understanding the impact of domestication on the brain and for improving husbandry practices to meet farm animals' perceptual and cognitive needs. Strategies to achieve more representative study populations are needed, as well as open and well-documented data sets in farm animal cognition.

Thinking beyond vertebrates: Do invertebrates show signs of affective states?

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One central goal of animal welfare science is to assess animals' affective states. Even though traditional approaches such as behavioural tests or physiological measurements are sensitive to arousal, they do not reliably distinguish between positive and negative emotional valence. A promising approach concerning this issue originates from human cognitive psychology, where emotional states are known to influence the interpretation of ambiguous information. In fact, people in negative states tend to expect negative outcomes, whereas those in positive states expect positive ones. This phenomenon, called cognitive bias, is nowadays one of the most commonly used approaches to assess affective state in animals. Although judgement bias tasks have been successfully applied across a range of vertebrate taxa, including mammals, fish, and birds, their use in invertebrates remains limited. To date, no cognitive bias test has been reported in jumping spiders (Salticidae) or woodlice (Oniscidea). Against this background, the present study will address this gap by examining whether jumping spiders and woodlice show signs of affective states. To this end, a suitable experimental design will be developed to investigate judgement biases and anxiety-like behaviour in both species, followed by an assessment of these traits in individual subjects. Using this correlational approach, we predict that judgement bias performance will be associated with responses to novelty. Specifically, individuals that interpret ambiguous cues more optimistically are expected to exhibit less anxiety-like behaviour, whereas individuals showing more pessimistic judgements are expected to display stronger avoidance responses. Demonstrating such a relationship would support the assumption that judgement bias reflects underlying affective states and, more broadly, contribute to our understanding of emotion-like states in invertebrates.

Investigation of Microplastic Uptake by Chironomid Larvae in Freshwater Ecosystems Using Laser Microscopy

Jieun Park

University of Münster

Since the 1950s, global annual plastic production has been on the rise. At the same time, the amount of plastic debris in the environment has been increasing. Plastic debris that enters the environment is broken down chemically, physically, and biologically in nature. When plastic particles are smaller than 5 mm, they are referred to as microplastics. Aquatic organisms in freshwater ecosystems can ingest these particles as food. In 2018, the “MikroPlaTas” project investigated microplastics in water, sediment, and macrozoobenthos of freshwater ecosystems. In my thesis, I analyze microplastics in larvae of the Chironomidae family from three of the project’s study sites. Chironomid larvae are a suitable bioindicator because they are a dominant family in freshwater ecosystems and are not selective feeders.

In my thesis, I aim to analyze the correlation between elevated microplastic levels in one part of the ecosystem and an increase in microplastic particles within the larvae, and to investigate differences in the amount of particles ingested across taxonomic groups. To analyze the microplastics in the chironomid larvae, I conducted a staining test using the two fluorescent dyes Nile Red and Calcofluor White/Evans Blue. A proven problem with Nile Red is that it can stain not only plastic but also biomass. To test this method, I therefore conducted a two-day microplastic feeding experiment on the chironomid larvae using three different types of plastic. After the feeding experiment, the larvae were macerated and stained with Nile Red and Calcofluor White/Evans Blue. I analyzed the larvae stained with fluorescent dyes using a confocal microscope. I applied the same method to the field samples.

From Banana Phenotype to Gene Networks: Decoding Molluscan Shell Coiling

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The coiled shell is a hallmark of the phylum Mollusca, yet the molecular mechanisms controlling shell coiling remain poorly understood. Recent pharmacological studies have implicated steroidogenic enzymes, particularly 5 α -reductase, in shell morphogenesis. Notably, molluscs lack NR3C nuclear receptors, suggesting that steroid metabolites influence shell development through non-canonical pathways. Consistent with this, inhibition of 5 α -reductase by dutasteride induces a characteristic open-coil "banana" phenotype in *Biomphalaria glabrata* and *Physella acuta*.

In this study, we used the freshwater snail *Lymnaea stagnalis* as a tractable model to investigate the role of 5 α -reductase in shell coiling. Leveraging its well-characterized embryology and sensitivity to bioactive compounds, we combined pharmacological inhibition with transcriptomic profiling (RNA-seq) to identify differentially expressed genes and pathways downstream of 5 α -reductase activity. This study aimed to clarify the role of steroid signaling in molluscan shell morphogenesis and to provide new insight into the evolution of developmental mechanisms in lophotrochozoans. Understanding these processes may also help in interpreting how environmental factors shape shell morphology in natural populations.

Anthropogenic Noise as a Multi-Level Stressor: Behavioural, Physiological, and Microbiome Responses in Birds**Ulla Pebesma;** Barbara A. Caspers; Öncü Maracı

Universität Bielefeld

Anthropogenic noise is an omnipresent pollutant and an emerging global threat to biodiversity. Although its effects on acoustic communication are well documented, the broader physiological, behavioural, and molecular consequences for wildlife remain poorly understood. We aim to investigate how chronic exposure to anthropogenic noise influences birds across multiple biological levels, with particular focus on stress physiology, behaviour, gene expression and gut microbiota.

Preliminary work on great tit (*Parus major*) nestlings revealed significant differences in gut microbiome community composition between urban and rural populations, with distance to city center and sound pollution as the strongest predictors of microbial variation. Urban nestlings also showed higher abundances of potentially pathogenic microbial taxa. Microbiome dysbiosis might therefore be linked to urbanisation and possibly chronic noise exposure.

Building on these findings, the project experimentally examines the effects of ecologically realistic urban noise exposure in captive zebra finches (*Taeniopygia guttata*) and wildcaught great tits originating from habitats with contrasting noise levels. We will determine how anthropogenic noise affects stress-related endocrine pathways, feeding and sleeping behaviour. Furthermore, using RNA sequencing and whole-genome shotgun metagenomics, the study will characterise noise-induced changes in gene expression and the functional potential of the gut microbiome.

By integrating behavioural, physiological and molecular approaches, this project will provide a comprehensive understanding of how anthropogenic noise affects organismal health and fitness. The findings will contribute to identifying mechanisms underlying variation in noise tolerance among individuals and species and inform evidence-based mitigation strategies to reduce the impact of anthropogenic noise on wildlife.

Molecular mechanisms underlying plasticity-led evolution: From epigenetic modifications to genetic change

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Bielefeld University

Phenotypic plasticity describes the ability of genotypes to express different phenotypes in response to environmental stimuli. Epigenetic codes are a key mechanism underlying plasticity, as they are able to change within the lifetime of individuals and control genotype expression. In persistently modified environments, the theory of plasticity-led evolution proposes that phenotypic plasticity chaperones the genetic fixation of a fitting phenotype. One well documented type of phenotypic plasticity are alarm cue-induced plastic antipredator defenses. The freshwater snail *Physella acuta* has been established as a model organism to study this mechanism. Within and across generations, we study epigenetic profiles of *P. acuta* that were lifelong exposed either to low or high perceived predation risk alongside long-term genomic changes. In a split-clutch experiment design, siblings are raised until maturation under constant exposure of either conspecific alarm cues or a water control before we sequence both their epigenomes and genomes. Afterwards, replicates originating from these clutches are maintained in the same environments for up to 6 generations before following up with additional sequencing. Here we first report on the epigenetic modifications that arise within the same generation. Second, we will present initial results of how genomic profiles diverge across environments after 6 generations. We may also give first insights into whether similar or different epigenetic modifications arise in the same generation. Our findings may contribute to an improved understanding of the molecular mechanisms underlying plasticity-led evolution.

Morphological comparison of the modified haemolymph pressure pump between juveniles and adults of *Perania nasuta* (Araneae: Pacullidae)**Stefan Reif¹**; Christian Kropf²; Jens Runge¹¹ Albert-Ludwigs-Universität Freiburg; ² Naturhistorisches Museum Basel

In Araneae (spiders), leg extension is caused by an increase in haemolymph pressure, which compensates for the lack of extensor muscles in two key joints. In the ground pattern of Araneae, contraction of prosomal dorso-ventral muscles compresses the prosoma in the region of the flexible pleural membrane. A number of araneae taxa, such as Pacullidae, are characterised by adult stages with fully sclerotised pleurae that connect the tergum and sternum immovably, which renders compression impossible. Adult *Perania nasuta* (Pacullidae) exhibit external modifications in the opisthosoma, including sclerotised dorsal and ventral plates, as well as smaller sclerites within the soft lateral cuticle. Internally, these sclerotised areas are connected by a laterally concentrated and well-developed opisthosomal muscle sac. This suggests that the generation of haemolymph pressure has shifted to the opisthosoma, where it is produced by contraction of the opisthosomal muscle sac.

Juveniles differ from adults in their sclerotisation pattern. Externally, juveniles exhibit less distinct opisthosomal sclerites, and the extension of sclerotisation of the prosomal pleura is incomplete. This raises the question of whether there are differences in muscle composition that account for haemolymph pressure generation between juveniles and adults. We investigated the skeleto-muscular system of juveniles using micro-computed tomography. We provide detailed 3D reconstructions of both tagmata to demonstrate morphological differences between juveniles and adults to draw conclusions on functional consequences.

EntomoStreet: modular multi-view imaging of ethanol-preserved insects**Peter T. Rühr** ; David Ott

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Large amounts of insect specimens, bulk-samples, from monitoring schemes, museum collections, and field surveys require standardized images before they can be measured, identified, linked to molecular data, or listed as digital specimen entries. For ethanol-preserved material, imaging remains difficult because specimens are fragile, wet, three-dimensional, and often need to be photographed from several angles. Low-cost systems such as the Entomoscope 2.0 provide an accessible basis for automated macrophotography, but the imaging process still requires manual handling when many larger specimens must be documented.

Here, we present EntomoStreet, a design concept for a semi-automated, modular processing line for ethanol-preserved insects above approximately 6 mm body length. The system is based on Entomoscope-style camera stations and is intended to acquire focus-stacked images from four lateral perspectives while minimizing direct specimen manipulation. In the workflow, each specimen is placed in alcohol inside a transparent glass chamber made from low-reflection microscope slides. Two camera modules image the chamber simultaneously from perpendicular directions; the camera-lighting assembly then rotates by 90° to capture the remaining two sides. Multiple prepared chambers can be queued in an assembly-line arrangement, allowing the user to load specimens manually while the machine processes them sequentially. Each chamber carries a label that can be photographed as part of the workflow and later used to place the specimen into a vial for long-term storage.

EntomoStreet is planned as a low-cost and expandable platform, depending on the number of installed camera units. By separating manual specimen loading from automated multi-view image acquisition, the system aims to bridge the gap between single-specimen macrophotography and fully robotic sorting. In combination with downstream image processing or ENIMAS 2.0-compatible analysis, the platform could provide a route toward scalable, standardized digitization of larger ethanol-preserved insects.

Effects of oral exposure to glyphosate on behaviour in the two ant species *Camponotus maculatus* and *Cardiocondyla obscurior*

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Pesticides and herbicides are heavily used in agriculture to control pest species but their increased application can impact biodiversity through their effects on non-target organisms. Glyphosate is the most frequently applied broad-spectrum herbicide worldwide and was originally considered environmentally safe, due to its plant-specific mode of action. However, recent studies show that glyphosate-based herbicides affect various non-target organisms, including insects, by influencing behaviour, development, microbiota and overall fitness.

Ants are valuable model organisms for ecotoxicological research because of their ecological importance, high abundances worldwide, complex social structures and sensitivity to environmental changes (Pohl et al., 2024). They are ecosystem engineers and contribute to soil processes, nutrient distribution and interaction with other organisms. Especially their social organisation provides particular opportunities to research sublethal effects at both individual and colony level. Despite their relevance, ants remain neglected in ecotoxicology in general and risk assessments in particular, especially if compared to other insects, such as bees.

I studied the effects of oral glyphosate exposure on the behaviour of two ant species, *Camponotus maculatus* and *Cardiocondyla obscurior*. Previous research has demonstrated lethal and sublethal impacts of glyphosate-based herbicides on ants (Pohl et al., 2026), but caste-specific behavioural effects have so far not been studied. I will present the results of the exposure to different glyphosate concentrations, focusing on behavioural effects and stress response for different ant castes.

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Characterization of glutathione specific γ -glutamylcyclotransferase 1 in *Caenorhabditis elegans*

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CHAC1 is a highly conserved stress-responsive protein induced by the ATF4–CHOP pathway during ER stress and amino acid deprivation. Best known for its role in glutathione degradation and ferroptosis, CHAC1 has been implicated in cancer, neurodegeneration and neuronal injury. However, its physiological function in coordinating organismal stress adaptation remains largely unknown.

We established *Caenorhabditis elegans* as an *in vivo* model for functional characterization of CHAC-1. Using CRISPR/Cas9-mediated genome editing, we generated a *chac-1* deletion mutant and compared its phenotype with transgenic overexpression lines. *chac-1* deletion significantly shortened lifespan, delayed development and reduced reproductive fitness, whereas overexpression primarily impaired fertility. Both loss- and gain-of-function markedly affected locomotion, exploratory behavior and accelerated the age-dependent decline in chemotaxis, highlighting an essential role for balanced CHAC-1 activity in maintaining neuronal function.

Functional stress assays demonstrated that *chac-1* deletion severely impaired survival under heat, oxidative, osmotic, ER and iron-induced stress, identifying CHAC-1 as a critical determinant of stress resilience. Surprisingly, despite their increased stress sensitivity, *chac-1* mutants displayed reduced activation of oxidative stress and mitochondrial stress reporters, while ER stress signaling remained unchanged. Moreover, mutants exhibited elevated basal lipid peroxidation but failed to further increase lipid peroxidation following selenite-induced oxidative stress, suggesting an impaired capacity to mount appropriate oxidative stress responses. Promoter analyses further revealed tissue-specific expression in neurons, intestine, pharynx, and vulval muscles.

Together, our findings identify CHAC-1 as a central regulator of organismal stress homeostasis rather than solely a downstream mediator of ferroptosis. Loss of CHAC-1 uncouples cellular stress signaling from effective stress adaptation, resulting in impaired survival, accelerated functional decline, and altered neuronal performance. This work establishes *C. elegans* as a powerful model to dissect the conserved physiological functions of CHAC1 and provides new insight into its potential contribution to aging and ferroptosis-associated diseases.

Morphological Determinants of Bite Force in Bisexual and Parthenogenetic *Darevskia* Rock Lizards

Nadine Steffenhagen; Natia Barateli; Giorgi Iankoshvili; Davit Tarkhnishvili; Benjamin Wipfler; Mariam Gabelaia

Bite force is a key functional trait associated with feeding, territorial behaviour and mating in lizards. While external head morphology is often correlated with bite performance, bite forces may differ in the lizards even though externally their head shape doesn't show any significant shape differences. The relative contribution of skull shape remains poorly understood, particularly in closely related species with contrasting reproductive modes. The genus *Darevskia* provides an excellent model system because it includes both bisexual and parthenogenetic species that coexist in similar habitats and are similar in size while only the bisexual *Darevskia* show territorial behaviour.

This study compares bite force and skull morphology in four *Darevskia* species from Georgia: the bisexual *D. portschinskii* and *D. valentini*, and the parthenogenetic *D. dahli* and *D. armeniaca*. Maximum bite force was measured using an isometric Kistler force transducer and external head dimensions were recorded for each individual. Micro-computed tomography (μ CT) and landmarking was used to quantify skull morphology. Morphological variables were analysed in relation to bite force to identify the structural differences and to evaluate whether territorial bisexual species exhibit enhanced bite performance compared to the parthenogenetic species.

Effects of simulated heat waves on female reproductive performance and offspring condition in the nursery web spider *Pisaura mirabilis*

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Climate change increases the frequency, intensity, and duration of extreme weather events, with heat waves threatening biodiversity. Traditionally, assessments of thermal vulnerability of a species has focused on critical thermal maxima and lethal temperatures. However, thermal fertility limits, defined as temperatures impairing reproductive performance, provide a more sensitive indicator of a species vulnerability to heat waves.

This study investigated post-copulatory effects of simulated heat waves on re-mating, fertility and offspring condition in the nursery web spider *Pisaura mirabilis*. One day post-mating, females underwent one of three 5-day heat treatments, each with a day-night temperature fluctuation of 8°C. A daytime maximum of 38 °C (n = 21) represented the acute behavioural temperature treatment, since spiders were shown to become restless under this temperature. The elevated treatment was 32 °C (n = 27) and the control treatment 26 °C (n = 22). All females survived the 5-day treatments and were transferred to control conditions. On day-1, females were presented with a male to investigate the effects of heat on the likelihood of re-mating, which is generally high in this species, but could be impacted by heat stress. Oviposition, clutch size, hatching success and offspring mass were recorded as indicators of reproductive success.

The females' motivation to re-mate remained high across all treatments, probably because males of *P. mirabilis* provide nutrient-rich nuptial gifts. Heat exposure did not affect fertility (clutch size or hatching success). Offspring body weight tended to be higher in the acute behavioural temperature treatment.

Our findings show that elevated to acute behavioural temperatures did not impair either survival or oviposition probability of female *P. mirabilis*. The study tentatively suggests that heat stress can lead to greater investment in subsequent egg batch. We hypothesize that larger body mass in offspring could influence their survival probability and performance under repeated heat waves.

For whom does Optimal Foraging Theory hold? Personality-dependent variation in foraging strategies across individualized landscapes of fear

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Foraging requires weighing energetic benefits against predation risk. Although Optimal Foraging Theory (OFT) predicts how individuals should resolve this tradeoff, substantial variation in foraging behaviour and resource exploitation can be observed. While most models implicitly assume that foragers perceive their environment in similar ways, growing evidence from animal personality research suggests a link between consistent among-individual differences in risk-taking behaviour, perceived predation risk and the tradeoff between speed and accuracy in exploration. Whether these differences lead to distinct foraging strategies and contribute to systematic deviations from optimal foraging prediction remains largely unexplored.

Addressing this question, we exposed behaviourally phenotyped wild-caught bank voles (*Myodes glareolus*) to artificial landscapes of perceived risks and diminishing resource returns. We quantified foraging behaviours and resource exploitation of 20 single foragers across day and night in two risk-uniform landscapes differing in perceived risk through ground cover, containing 25 discrete food patches. Using activity, time in patches, number of patch visits, distance moved and giving-up densities (GUDs), we evaluated how individuals adjust foraging decisions to the level of risk in a landscape. We further investigate whether among-individual differences in boldness and information sampling predict foraging decisions that lead to consistent under- or overexploitation of resources and, consequently, variation in individual payoff. Preliminary analyses indicate that bank voles adjusted their foraging behaviour to perceived predation risk. Individuals were more active, moved greater distances, visited patches more frequently, and depleted food resources to lower GUDs in covered landscapes, suggesting that the experimental manipulation created a landscape of fear. Furthermore, several behavioural traits were repeatable across risk conditions and days, indicating consistent among-individual differences in foraging strategies.

By linking individualized landscapes of fear to variation in resource exploitation, this study may help explain not only differences in optimal foraging outcomes but also their potential cascading effects across ecological communities.

Genetic relatedness promotes equal contributions of males and females to brood care in a biparental cichlid fish

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Kin discrimination, i.e. the differential treatment of kin and non-kin, has been studied in a wide range of social contexts because kin selection theory predicts that genetic relatedness among interacting individuals can reduce conflict and promote cooperation. However, the impact of kin discrimination on parental cooperation in biparental systems has so far been largely neglected. Here, we compared the individual contributions of males and females to brood care in kin and non-kin pairs of *Pelvicachromis taeniatus*, a biparental cichlid fish with a pronounced kin-mating preference. The relative contribution of the sexes differed depending on relatedness within a pair. In unrelated pairs, females contributed more than males, whereas the sexes contributed equally in related pairs. Our results indicate that relatedness affects the resolution of sexual conflict. More equal contributions may reflect higher cooperation between the sexes in related pairs. Enhanced parental cooperation may be an important benefit of inbreeding, which may have contributed to the evolution of inbreeding preference in *P. taeniatus*, and may also help explain inbreeding tolerance observed in other biparental systems.

A manipulative parasite's hidden effect: Increased behavioural variability in Gammarus

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The examination of the causes of organismic variation is a central question in evolutionary biology. Manipulative parasites are well known to alter the behaviour of their intermediate hosts, thereby facilitating transmission to their final hosts. However, most studies focus on changes in mean values for infected and uninfected individuals. Relatively little is known about how parasitic infection affects between-individual variation and, especially, within-individual behavioural variation. The acanthocephalan parasite *Polymorphus minutus* manipulates the behaviour of its intermediate host, the freshwater amphipod *Gammarus pulex*, to increase its chances of transmission to its definitive waterfowl hosts.

This study investigated how *P. minutus* infection influences mean activity levels, between-individual variation, and within-individual behavioural consistency in *G. pulex*. Eighty individuals (40 infected, 40 uninfected) were collected and tested across four repeated trials. Two measures of locomotor activity (LMA), reflecting duration of movement and spatial extent, were analysed.

Results showed that infection by *P. minutus* significantly affected LMA in several ways: on average, infected gammarids were less active than uninfected gammarids. In both groups, individuals differed in activity. Between-individual variation was similar in infected and uninfected gammarids. In contrast, within-individual variation differed significantly between groups: infected individuals showed significantly higher within-individual variation than uninfected individuals, indicating more erratic behaviour.

These findings support the hypothesis that *P. minutus* infection reduces overall activity and increases behavioural unpredictability. While this may suggest parasite-induced manipulation, further studies are needed to determine whether such changes enhance transmission by affecting host–predator interactions and underlying mechanisms.

Right-sided hybrids: Genetic background affects behavioural lateralisation in *Pelvicachromis taeniatus*

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Behavioural lateralisation, defined as a preference for using one side of the body, is a widespread phenomenon across the animal kingdom. It has been associated with cognitive advantages such as enhanced decision-making abilities, improved multitasking skills, and increased boldness. Inbreeding is often linked to reduced behavioural performance due to increased homozygosity and decreased genetic diversity. However, the impact of inbreeding on behavioural lateralisation has rarely been examined.

Here, we compared behavioural lateralisation among inbred, outbred, and hybrid fish produced through crosses between inbred lines, using the cichlid fish *Pelvicachromis taeniatus* as a model system. This species exhibits a natural preference for mating with kin. Both female and male *P. taeniatus* were tested. A repeated detour test was conducted over ten consecutive trials, during which the fish had to leave a start compartment and navigate around a transparent barrier. We recorded the time required to leave the compartment, which served as an indicator of boldness, and the direction of the detour around the barrier (left or right).

The results revealed significant differences in lateralisation direction among breeding groups. A significant right-sided bias was observed exclusively in the hybrid group, whereas inbred and outbred individuals showed no preference for either side. The lateralisation pattern observed in hybrids may reflect alterations in neural organisation or hemispheric processing resulting from the disruption of co-adapted gene complexes. No significant effect of sex on lateralisation was detected. The time required to leave the compartment decreased over the course of the trials, indicating increasing familiarity with the experimental setup and improved task performance. Furthermore, females left the compartment faster than males regardless of breeding group, suggesting sex differences in exploratory behaviour and boldness.

Overall, these findings provide new insights into the relationship between genetic background and behavioural lateralisation, an area that has received little attention to date.

Caffeine pollution impairs antipredator behaviour in *Gammarus pulex* similarly to manipulative parasites

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Caffeine is an emerging environmental contaminant in freshwater ecosystems that is primarily introduced through wastewater. Even at low concentrations, caffeine can affect the physiology and behaviour of aquatic organisms. However, its ecological significance remains little understood. Here, we examined the impact of environmentally relevant caffeine concentrations on the anti-predator behaviour of the freshwater amphipod *Gammarus pulex*. Gammarids play a central role in aquatic decomposition processes and are a primary food source for various aquatic predators. We examined the effects of caffeine in relation to a well-documented effect caused by the manipulative parasite *Polymorphus minutus*. This acanthocephalan parasite manipulates the anti-predator behaviour of its intermediate host, the gammarid, by altering its photophobia, thereby increasing its transmission to the final host, water birds. Using a two-choice experimental design, we assessed the phototactic behaviour of *P. minutus*-infected and uninfected *G. pulex* after 20 hours of high and low concentration caffeine exposure. Caffeine exposure significantly increased the activity of exposed individuals and reduced photophobia to a degree comparable to that of a *P. minutus* infection. These results suggest that human-derived chemicals can mimic the effects of natural behavioural modulators, which could increase predation risk and ultimately alter ecosystem dynamics.

ANTIZOONS - Cascading effects of climate-induced forest conversion on zoonotic pathogens in mammals

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Forest ecosystems provide habitat for numerous wildlife reservoirs of zoonotic pathogens and are currently undergoing profound changes: The consequences of climate change—such as droughts, storms, and pest infestations—are causing widespread damage and require large-scale reforestation efforts using tree species that can withstand future climatic conditions. These habitat changes are likely to influence the interaction between environmental conditions, wildlife reservoirs, and zoonotic pathogens to an unprecedented extent.

The aim of the collaborative ANTIZOONS project is to investigate the cascading effects of climate change-induced forest conversion on wildlife reservoirs and zoonotic pathogens. At 21 forest restoration sites in Hesse, Germany, which differ in their tree species composition, the habitat characteristics, the diversity and composition of the mammal community, and their zoonotic pathogens are being studied using an interdisciplinary approach. Changes in the composition of diets and gut microbiomes will be addressed as possible mediating mechanisms between forest conversion, infection status of wildlife and infection risk of the human population. As some of the most important reservoirs for zoonotic pathogens are also major forest pests, the ANTIZOONS project also serves to optimize forest pest management and thus support plant protection efforts as part of the planned large-scale forest conversion measures.

Involvement of a fatty acid binding protein in chitin formation in *T. castaneum*

Kim Venus; Marius Beck; Hans Merzendorfer

The insect cuticle is a chitin-rich extracellular matrix that protects from mechanical damage and other stressors, provides structural support and enables locomotion. Its formation and maturation are tightly regulated and rely largely on the activity of chitin synthase 1 (Chs1) and the production of cuticle proteins. Although lipids are essential for proper function of the cuticle, e.g. by their function in waterproofing, the mechanism linking lipid handling to chitin deposition remains poorly understood. To investigate this relationship, we examined the role of fatty acid binding protein 8 (Fabp8) in the red flour beetle *Tribolium castaneum* using the pupal elytral cuticle as a model. RNAi-mediated knockdown of TcFABP8 resulted in severe cuticle and molting defects, accompanied by weak cuticle pigmentation. Fluorescence microscopy revealed a reduced Chs1 signal intensity and its altered sub-cellular localization, including a loss of apical Chs1 accumulation. In addition, cuticle thickness and chitin deposition were reduced. Similar results were obtained after RNAi-mediated depletion of TcCHS1, supporting a functional connection between TcFabp8 and chitin biosynthesis. As TcCHS1 transcript levels remained unaffected, the observed effects are unlikely to result from transcriptional regulation of TcCHS1 but rather suggest that TcFabp8 may influence Chs1 vesicular transport and stability at a post-transcriptional level. Together, our findings identify TcFabp8 as an important factor required for chitin formation, supporting a functional link between lipid-handling processes cuticle biosynthesis.

Beyond CFTR Rescue: wtCFTR-mRNA Reprograms Airway Epithelial Homeostasis in Cystic Fibrosis

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UKM Muenster

Cystic fibrosis (CF) is a life-limiting genetic disease caused by pathogenic variants in the CFTR gene. While CFTR modulators have transformed patient care, approximately 10–15% of individuals still lack effective treatment options. Replacement of wild-type CFTR mRNA (wtCFTR-mRNA) represents a mutation-independent therapeutic strategy with the potential to benefit all patients. However, the potential of wtCFTR-mRNA delivery to promote broader reprogramming of the diseased airway epithelium beyond the restoration of CFTR-mediated ion transport has not yet been systematically investigated. Primary human nasal epithelial cells from CF patients (F508del/F508del) and healthy controls were differentiated at air–liquid interface. CF cultures were treated apically with chitosan nanoparticle-delivered wtCFTR-mRNA. Transepithelial ion transport was assessed using a modified Multi Transepithelial Current Clamp (MTECC) Ussing chamber system. Apical CFTR localisation was evaluated by immunofluorescence. Bulk RNA sequencing was performed on treated and matched untreated CF cultures to assess therapy-associated transcriptomic changes. cAMP-mediated conductance (ΔG_t) increased from -0.012 ± 0.03 mS/cm² to 0.293 ± 0.038 mS/cm² (N=15), coinciding with the recovery and restoration of apical CFTR localisation. Bulk RNA-seq revealed 5,583 differentially expressed genes with clear separation of treated and untreated samples by principal component analysis. Treatment upregulated ionocyte markers (FOXI1, BSND), ciliogenesis regulators (FOXJ1, DNAH5), and secretory cell genes, while ER stress (HSPA6/7) and NF- κ B-associated inflammatory mediators (CXCL8, TNF, IL1B) were attenuated. No therapy-associated toxicity was detected. Chitosan-mediated wtCFTR-mRNA delivery restores functional CFTR activity and induces broad transcriptomic remodelling of CF airway epithelia, suggesting effects on epithelial homeostasis extending beyond ion transport correction. Single-cell resolution analysis of an expanded cohort is underway.

Effects of photoperiod and clock mutation on the development of *Drosophila*

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How the circadian clock and photoperiod interact to govern developmental processes remains poorly understood. Previous studies in *Drosophila melanogaster* using period alleles had dissected the clock-dependent contributions to development. We are currently investigating the neuroendocrine mechanisms that link the circadian clock, photoperiod, and hormonal signalling pathways and together shape larval developmental progression, metamorphosis timing, and adult body size.

Using a custom automated hatching-box system that enables continuous, non-invasive monitoring of key developmental transitions of pupariation and adult eclosion, we are quantifying developmental timing in clock mutants and wild-type flies under three photoperiodic conditions: LD 12:12, constant light (LL), and constant darkness (DD). Preliminary observations suggest that photoperiod influences developmental rate, with differences emerging across lighting conditions and clock genotypes. Importantly, body weight and wing size appear largely unaffected across conditions, hinting that any photoperiodic effect on timing may be independent of general metabolism.

To identify the potential neuromessengers relaying circadian information to endocrine centres, we performed immunostaining for candidate neuropeptides in larval clock neurons. Of the neuropeptides screened, only AstC was found to localise in DN1 clock neurons. To further map receptor expression in clock neurons, PTTH neurons, and insulin-producing cells (IPCs), we are establishing a dual-reporter system using Clk856-LexA combined with receptor-T2A-LexA lines.

The overall aim is to determine the relative contributions of direct light input and clock-dependent signalling to developmental timing, and to define the neuroendocrine circuit through which the circadian clock exerts its effects.

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Structural and chemical properties of insect's chitin-containing extracellular matrices

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Insect's body barriers rely on specialized extracellular matrices that protect against harmful environmental influences. The outer barrier is the cuticle, which is composed of chitin, cuticle proteins and lipids. The peritrophic matrix (PM) serves as an inner barrier lining the midgut epithelium. It is composed of chitin fibers that are organized by PM proteins. While cuticle and PM proteins have received considerable attention in the past, supramolecular organization and physicochemical properties of the chitin component - particularly of the PM - remain poorly understood. Here, we combine synchrotron-based X-ray diffraction data from the PMs of lepidopteran and coleopteran insects with RNA interference (RNAi), mass spectrometric and histochemical analyses of the PM from *Tribolium castaneum* to determine chitin's allomorphic state and degree of acetylation. The chitin of the PM exhibits signatures characteristic of dihydrate beta-chitin along the entire midgut. In contrast, the cuticle is made of tightly packed alpha-chitin nanofibrils. Mass spectrometry revealed that the PM's chitin is highly acetylated (>95%). RNAi silencing of gut-specific genes encoding chitin deacetylases TcCDA6-9 further increases the degree of acetylation. Histochemical analyses staining chitin with different degrees of acetylation confirm the predominance of highly acetylated chitin in the PM. Notably, the larval cuticle has a layered organization with deacetylated chitin present in exo- and highly acetylated chitin in endocuticles. Depletion of both TcCDA1 or TcCDA2 impairs chitin deacetylation, which indicates that both proteins cooperate in their activity in the integument. These results establish fundamental principles of polysaccharide-based extracellular matrices, with broad implications for insect biology.

Comparative gait analyses in two differently sized drosophilid fly species running on slippery and non-slippery substrates

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The scarcity of species-specific data on insect locomotion hinders the integration of behavioural, ecological and evolutionary knowledge for this highly diverse group of animals. This lack of information contrasts sharply with the growing number of theoretical approaches to animal locomotion, which emphasise the dependency of locomotion traits — such as specific adaptations in dynamics, energetics, and control — on morphological and physiological characteristics. In this study, we examine the locomotion of two drosophilid fly species that differ in size and weight, in order to reconcile model predictions and observations within a rather narrow framework. Following initial comparative morphometric analyses, wild-type specimens of *Drosophila melanogaster* and the twice as large *Drosophila virilis* were encouraged to run on a running track equipped with flooring of different surface structures. To simulate the range of surface conditions that the animals would usually encounter in their natural habitats, the flooring consisted of slippery PTFE, non-slippery paper, and microrough sandpaper. The runs were recorded from above and from the side using a high-speed video system, enabling us to analyse the horizontal and sagittal kinematics and dynamics of the body, as well as the coordination patterns of the legs. This approach allows us to address the question of how the locomotor systems of differently sized drosophilids cope with different substrate properties.

Consequences of allopatry for the CHC profile of & mate recognition in *Tachinaephagus zealandicus*

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Many insect species rely on cuticular hydrocarbons (CHCs) for close-range mate recognition. When populations become geographically isolated, selection and genetic drift result in genetic and phenotypic divergence. This may include CHC profile divergence, potentially affecting communication. Additionally, hybrids of diverging populations may show reduced fitness.

In the parasitoid wasp *Tachinaephagus zealandicus*, males identify mates by their CHC profile, and the species shows a female profile polymorphism with up to three distinct chemotypes. *Tachinaephagus zealandicus* originates from Australia or New Zealand; however, it has been introduced to North America and Europe. These native and introduced populations have been isolated for about 50 years (>500 generations) with possible effects on CHC profile composition, mate recognition, and hybrid fitness.

To study the effects of allopatry on mate recognition, we are conducting mating trials in which we assess female profile attractiveness up to the second generation, comparing allopatric populations, chemotypes, and Australian subpopulations. Preliminary analyses show a trend of reduced attractiveness of one of the three European chemotypes for Australian males. Previous research has shown that this chemotype is the most attractive to European males. However, this female chemotype was not found in Australian populations. The preliminary data suggest that this chemotype and the corresponding male preference may have evolved after the populations split. Further preliminary results do not show a difference in attractiveness when pooling chemotypes, and we do not find differences in female profile attractiveness when comparing Australian subpopulations. Fitness analyses will quantify hybrid offspring numbers and sex ratios, up to the second generation. Analyses of these parameters will reveal whether post-copulatory isolation evolved after approximately 50 years of geographic isolation between European and Australian populations.

BisonID: identifying individual European bison with an AI powered mobile app

Klaudia Witte

University of Siegen

Conservation research and wildlife management often rely on the accurate reidentification of individual animals. The increased use of camera traps and other forms of wildlife photography have revolutionized this process for species with distinct natural markings (e.g., zebra stripes or whale flukes). For species without distinct conspicuous features, such as the European bison (*Bos bonasus*), challenges for individual visual reidentification remain. Identifiers such as ear tags are controversial, difficult to apply and to read from a distance, yet reliable identification is critical for successful management. Thus, management could benefit from a new, non-invasive approach to reidentify individual herd members. Here, we propose such an approach by developing a robust deep learning model for automated individual identification of European bison under diverse field conditions. For use in the field, we aim to integrate this technology into an intuitive mobile application, making it accessible to conservation professionals, citizen scientists and the public. Key ongoing efforts for this include: first, compiling a comprehensive image database of European bison for model training, second, conducting stakeholder needs assessments to align the tool with real-world management requirements, third, app and infrastructure development. Here we present the project's current progress and outline future steps.

Morphological transformations of the abdominal base in ant-like litter beetles (Coleoptera: Staphylinidae: Pselaphinae)**Ben Zechiel;** Margarita Yavorskaya

Universität Tübingen / Institut für Evolution und Ökologie

With around 10,000 described species the cosmopolitan Pselaphinae comprise the second largest subfamily of Staphylinidae. An extreme structural reorganization and variability of all body regions occurs in Pselaphinae, leading to an extraordinary morphological diversity. This fascinating diversity is still scarcely understood. One of the reasons for many morphological transformations in Pselaphinae could be close association with ants, with myrmecophily evolving in multiple pselaphine lineages. Many changes have occurred to the abdominal base (first three abdominal segments) of Pselaphinae, however, this body region remains understudied in Staphylinidae.

The aim of our study was to explore unique morphological transformations in the abdominal base of Pselaphinae. SR μ CT was used to create 3D reconstructions of the abdominal base of five myrmecophile and non-myrmecophile pselaphine species from different lineages and three outgroup species, including the rare representative of the sister group of Pselaphinae, Protopselaphus. Differences between the species in the compactness of the abdominal base were detected. Several external and internal structures were found that show a strong variability in Pselaphinae. Our findings suggest that Pselaphinae have a less flexible and more rigid abdomen than non-pselaphine staphylinids. Furthermore, two apomorphies in the abdominal base of Pselaphinae were detected: the fusion of the median carinae of sternite II and sternite III and the presence of internal dorsolateral processes in sternite III. We also show differences in the structure of sternite III for the examined myrmecophilous species: dorsolateral processes are stronger developed and closer connected to the endoskeletal elements of the tergite, probably to provide additional stability.

Our study shows that multiple structural transformations have occurred to the abdominal base of Pselaphinae, reducing the flexibility and increasing the stability of the abdomen in this remarkable subgroup of rove beetles.

Oxygen transport capacity shapes the thermotolerance of *Daphnia magna*

Bettina Zeis; Melina Ghanbar Moghaddam; Marie Schulte Ghanbar

Universität Münster

Increasing water temperature challenges poikilothermic aquatic animals as oxygen demand is exponentially increased along with the metabolic rate at elevated temperature, while oxygen solubility and thus its availability by the animals' oxygen transport mechanisms declines.

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 and related to the motility at acclimation conditions. Increasing the oxygen content of the water prolonged the animals' motility and increased swimming intensity. The hemoglobin content of the hemolymph was decisive, and enhanced oxygen transport capacity positively affected *Daphnia's* ability to tolerate elevated temperatures. Moreover, perfusion was adjusted to enhanced oxygen demand at higher temperatures by accelerated heart rate.

Accordingly, the results were in line with the oxygen and capacity limited thermo-tolerance hypothesis (Pörtner et al, 2017, J Exp Biol 220, 2685-2696). They reveal the physiological plasticity of parameters related to oxygen transport capacity in response to heat stress. It can be assumed that these mechanisms are also decisive for the distribution of this zooplankton key species in its habitat.

Oasis of Diversity: Biodiversity of Cemeteries

Sofia T. Zeisig; Laura Dobrandt; Annika Göbel, Christin Pfaff Nina Swietkowiak, Antonia Domnik, Jana Schneider; Tina Wiener Elisabeth Köper

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Biodiversity Oasis – Urban Cemeteries as Biotopes and Stepping Stones: Recognizing, Enhancing and Communicating Biodiversity

Are cemeteries biodiverse green urban infrastructure for animals and plants? As green spaces within densely built environments, cemeteries are described as valuable oases – not only for grieving and remembrance, but also as places of recreation and nature experience: They provide critical habitats for a variety of plants, animals and fungi.

Yet, cemeteries are under increasing pressure. Some are being closed, repurposed, built over, or maintained in ways that may not support biodiversity. What kind of maintenance supports ecological value? How should cemeteries evolve from a biological perspective? Should they be managed as natural oases – or be left to fallow – or be build over? And what other factors shape biodiversity in cemeteries – such as size, isolation, urban context, or human presence?

This doctoral project aims to assess the existing biodiversity of urban cemeteries and identify key parameters for enhancing it. It combines ecological field studies with citizen science approaches to monitor various animal taxa, including mammals (like squirrels), arthropods (like groundbeetles), and others. The ultimate goal is to highlight the ecological potential of cemeteries and provide actionable recommendations for their management. Promoting biodiversity in times of global biodiversity loss and climate change is more urgent than ever. Enhancing structural diversity and preserving cemeteries as habitats for animals, plants, and fungi is therefore essential for sustaining urban biodiversity.

CoupleControl: Benefits of biparental care for microbial control**Camila Luciana Zenobi ; Jos Kramer**

Universität Bayreuth

Microbes are integral components of all natural ecosystems and can therefore have profound effects on animal behavior and life-history traits. While the general importance of animal-microbe interactions is well established, their role in driving the evolution of social complexity in animals remains poorly understood. Here, we address this issue in *Nicrophorus vespilloides*, a burying beetle that faces intense competition with microbes while processing small vertebrate carcasses into an edible nursery for their offspring. Taking advantage of the beetles' naturally flexible caring system, we test whether biparental care improves their ability to mitigate the costs of microbial competition over the breeding resource. To this end, we quantify parental effort, offspring fitness, and the composition of the carcass microbial community in a large-scale experiment manipulating the duration and occurrence of biparental versus uniparental care and the intensity of microbial competition. We hypothesize that biparental care provides greater benefits to offspring than uniparental care under conditions of intense microbial competition. At the same time, we predict that biparental care under these conditions entails a higher combined parental effort and induces more pronounced shifts in carcass microbial communities away from an untended state. Altogether, our results will shed light on how animal-microbe interactions and animal social behaviors reciprocally shape one another, providing insight into the microbial drivers of animal social life.



118th
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