HUMBOLDT-UNIVERSITÄT ZU BERLIN

German Zoological Society

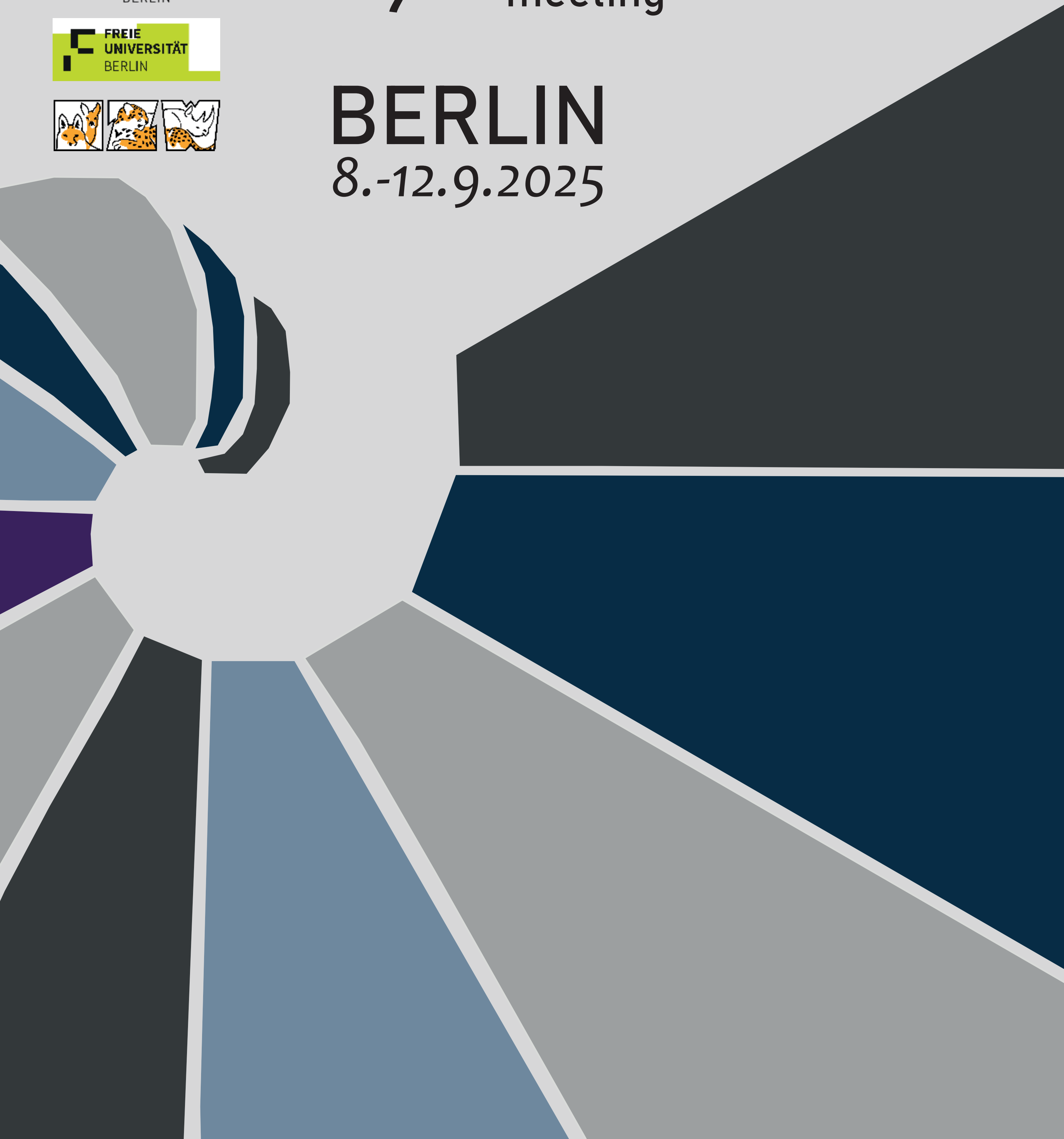
117th annual meeting

MUSEUM FÜR NATURKUNDE
BERLIN

FREIE UNIVERSITÄT
BERLIN

BERLIN

8.-12.9.2025



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Grußwort / Welcome

Grußwort zur 117. Jahrestagung der Deutschen Zoologischen Gesellschaft

Sehr geehrte Damen und Herren,
liebe Zologinnen und Zoologen,

Wir heißen Sie herzlich zur 117. Jahrestagung der Deutschen Zoologischen Gesellschaft in Berlin willkommen. Es ist uns eine besondere Freude, Sie in der Hauptstadt begrüßen zu dürfen – und das aus gutem Grund: Erstmals seit 2003 und insgesamt zum sechsten Mal findet die DZG-Tagung wieder in Berlin statt. Mit rund 350 Teilnehmenden verzeichnen wir zugleich eine der größten Jahrestagungen der Gesellschaft in jüngerer Zeit.

Die diesjährige Tagung ist das Ergebnis der Zusammenarbeit eines Organisationsteams, bestehend aus Forschenden der Humboldt-Universität zu Berlin, dem Museum für Naturkunde, der Freien Universität Berlin sowie dem Leibniz-Institut für Zoo- und Wildtierforschung. Gemeinsam – und vor allem durch die Beiträge der Mitglieder unserer Gesellschaft – ist ein wissenschaftlich anspruchsvolles und zugleich vielfältiges Programm entstanden, das die Breite und Tiefe der zoologischen Forschung eindrucksvoll widerspiegelt.

Freuen Sie sich auf Plenarvorträge führender Wissenschaftlerinnen, einen speziellen Vortrag zur frühen Geschichte der DZG sowie die feierliche Verleihung der renommierten Forschungspreise „Werner Rathmayer“, „Horst Wiehe“ und „Walther-Arndt“. Ein besonderes Highlight bildet der Ice-Breaker-Event im spektakulären Sauriersaal des berühmten Museums für Naturkunde – ein Ort, der Wissenschaft und Geschichte auf einzigartige Weise verbindet.

Darüber hinaus laden wir Sie herzlich zur öffentlichen Vorlesung zur Ökologie von Tieren in der Stadt sowie zum geselligen Konferenzdinner ein, das Gelegenheit für vertiefte Gespräche und kollegialen Austausch bietet.

Wir wünschen Ihnen eine erkenntnisreiche, inspirierende und angenehme Zeit in Berlin sowie eine erfolgreiche Teilnahme an der Jahrestagung.

Mit herzlichen Grüßen
Das Organisationsteam der 117. DZG-Jahrestagung

Heribert Hofer (Institut für Zoo- und Wildtierkunde), Kristin Jütz (Humboldt-Universität),
Brandon Kilbourne (Museum für Naturkunde), Gerlind Lehmann (Humboldt-Universität),
Maria Liedtke (Museum für Naturkunde), Rudolf Meier (Museum für Naturkunde),
Dirk Mikolajewski (Freie Universität), John A. Nyakatura (Humboldt-Universität),
Jens Rolff (Freie Universität), Thomas Stach (Humboldt-Universität),
Lauren Sumner-Rooney (Museum für Naturkunde), Jan Wölfer (Humboldt-Universität)

Grußwort / Welcome

Welcome Address for the 117th Annual Meeting of the German Zoological Society

Dear Ladies and Gentlemen,
Esteemed Colleagues in Zoology,

We warmly welcome you to the 117th Annual Meeting of the German Zoological Society in Berlin. It is a particular pleasure to host you in the capital—and for good reason: For the first time since 2003, and for the sixth time overall, the DZG meeting returns to Berlin. With approximately 350 participants, we are proud to host one of the largest annual meetings of the Society in recent years.

This year's conference is the result of a collaborative effort by researchers from the Humboldt University of Berlin, the Museum für Naturkunde, the Free University of Berlin, and the Leibniz Institute for Zoo and Wildlife Research. Together—and above all thanks to the contributions of our society's members—we have created a scientifically rigorous and diverse program that reflects the breadth and depth of zoological research.

Highlights include plenary lectures by leading scientists, a special talk on the early history of the DZG, and the ceremonial presentation of the prestigious research awards: the Werner Rathmayer, Horst Wiehe, and Walther Arndt prizes. A particular highlight is the ice-breaker event in the spectacular dinosaur hall of the renowned Museum für Naturkunde—a venue that uniquely combines science and history.

We also warmly invite you to attend the public lecture on urban animal ecology, as well as the conference dinner, which offers a wonderful opportunity for in-depth conversations and collegial exchange.

We wish you an insightful, inspiring, and thoroughly enjoyable time in Berlin, and a successful participation in this special annual meeting.

With warm regards
The Organizing Committee of the 117th DZG Annual Meeting

Heribert Hofer (Institut für Zoo- und Wildtierkunde), Kristin Jütz (Humboldt-Universität),
Brandon Kilbourne (Museum für Naturkunde), Gerlind Lehmann (Humboldt-Universität),
Maria Liedtke (Museum für Naturkunde), Rudolf Meier (Museum für Naturkunde),
Dirk Mikolajewski (Freie Universität), John A. Nyakatura (Humboldt-Universität),
Jens Rolff (Freie Universität), Thomas Stach (Humboldt-Universität),
Lauren Sumner-Rooney (Museum für Naturkunde), Jan Wölfer (Humboldt-Universität)

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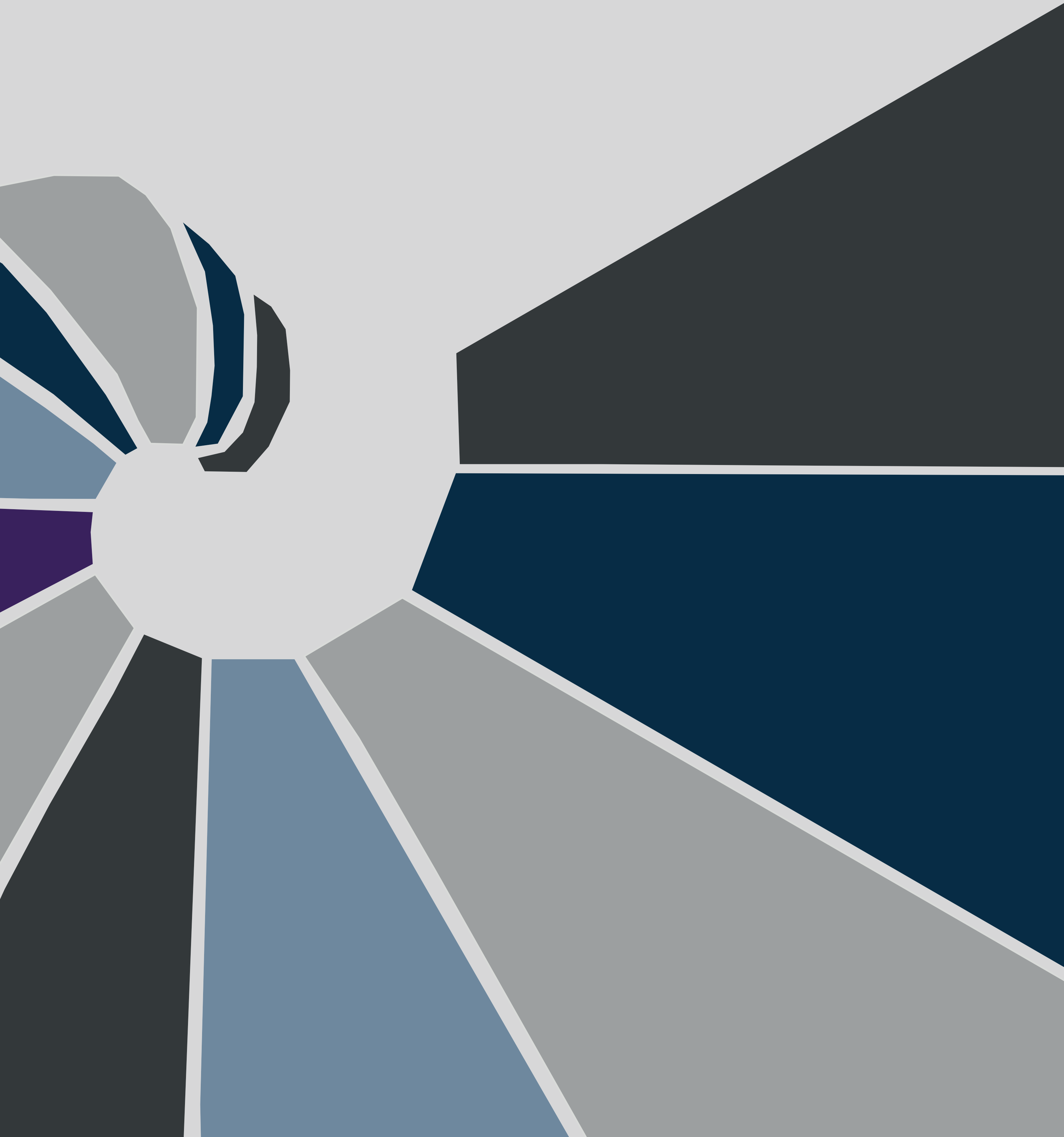
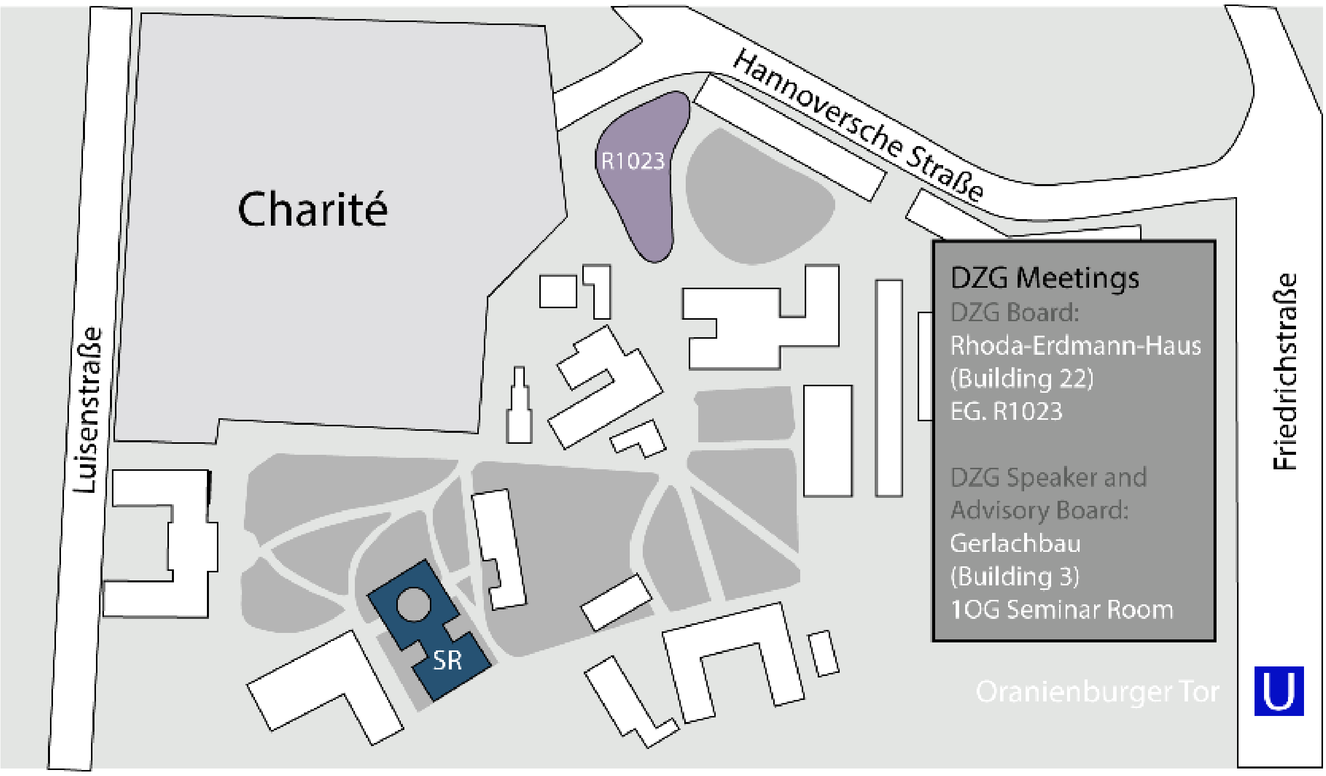


VENUE

The 2025 DZG Meeting will take place in **4 locations**.

Humboldt-Universität zu Berlin, Campus Nord

09. September	DZG Board Meetings



Museum für Naturkunde Berlin, Invalidenstraße 42, 10115 Berlin

09. September	Icebreaker

Luise Dahlem, Königin-Luise-Straße 42-44, 14195 Berlin

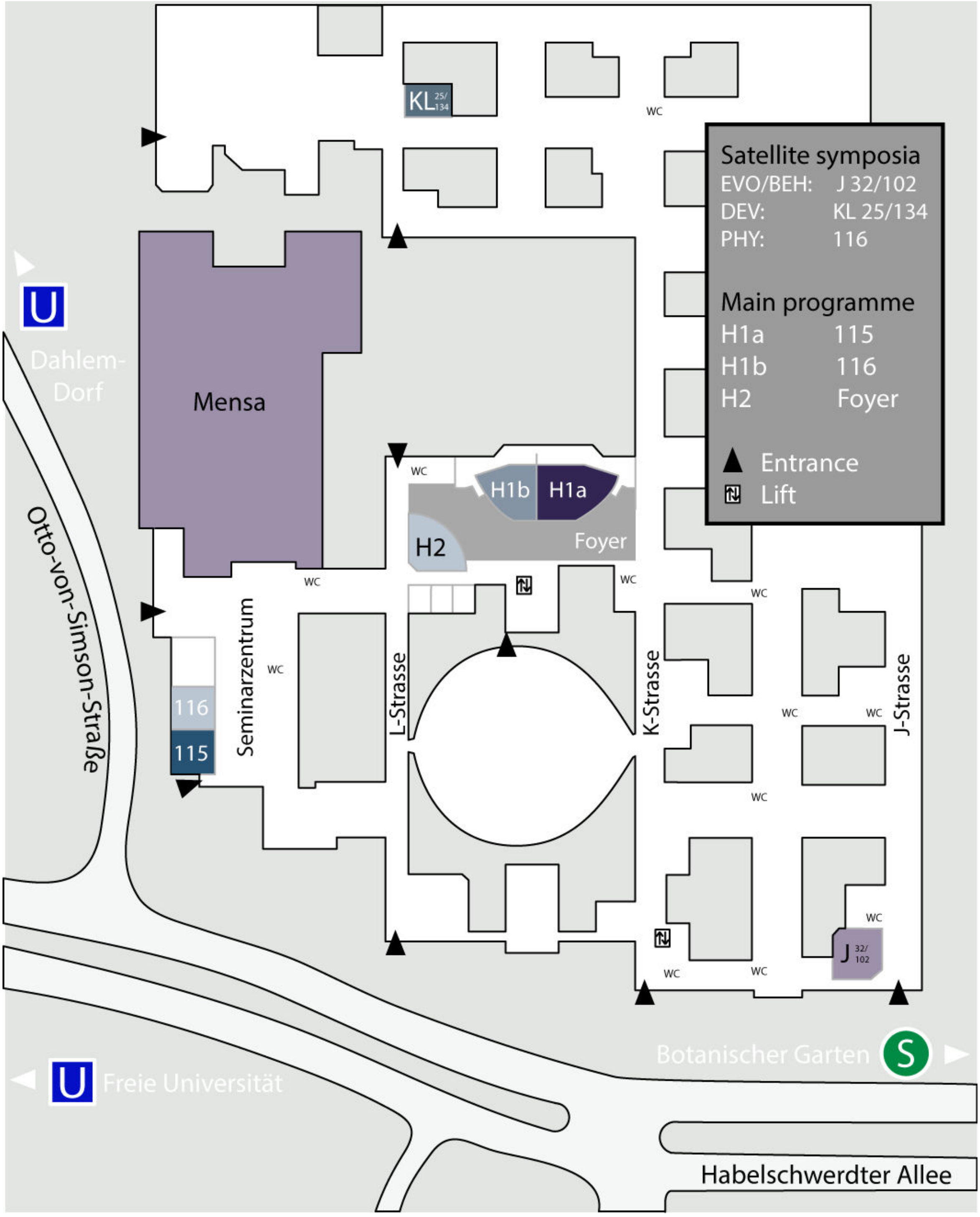
12. September	Conference Dinner

VENUE

Freie Universität Berlin, Rost- und Silberlaube

08. & 09. September Satellite Symposia EVO & BEH DEV PHY

10. - 12. September



VOTING

Student Awards

Vote for the **best Talk** and the **best Poster**.

Student Contributions are marked in the Abstract Booklet

with the following symbol.

🎓

Please put your vote in the provided boxes!

This can be done until Friday 6 pm at the Registration Desk.

Awardees will be announced at the Closing Event.

12. September Luise Dahlem
Königin-Luise-Straße 42-44, 14195 Berlin

About BMKGENE

Biomarker Technologies (BMKGENE), founded in 2009, is a leading genomics service provider with over 16 years of active innovation in high-throughput sequencing and bioinformatics. We deliver comprehensive multi-omics solutions – including genomics, metagenomics, epigenetics, single-cell omics, transcriptomics, and our proprietary BMKMANU S3000 spatial transcriptome technology – complemented by our advanced BMKCloud bioinformatics platform.

Demonstrating a strong commitment to R&D, BMKGENE holds over 60 national invention patents and 200+ software copyrights. Our expertise has underpinned over 5,000 successful projects across diverse research domains, empowering partners to publish hundreds of high-impact papers in top-tier journals such as Nature, Cell, and Science.

We have established long-term collaborations with organizations spanning 84 regions worldwide, providing robust genomic solutions on a global scale.

- 16 Years of Expertise
- Multi-Platform Coverage
- Multi-Omics Integration
- Extensive Experience
- Tumor-Specific Team
- Fast Turnaround Time


MGI
DNBSEQ T7


Illumina
Nova X Plus


PacBio
Revio

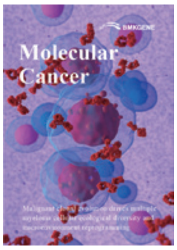

Nanopore
PromethION

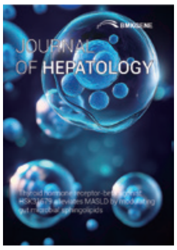

AB SCIEX
QTRAP™6500+

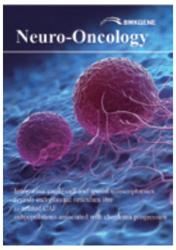

Waters
QTOF

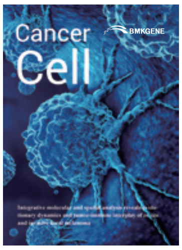

BMKMANU
S3000

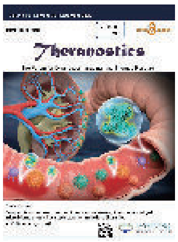
10X
Genomics

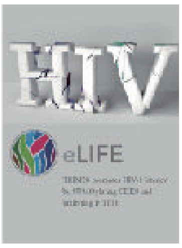












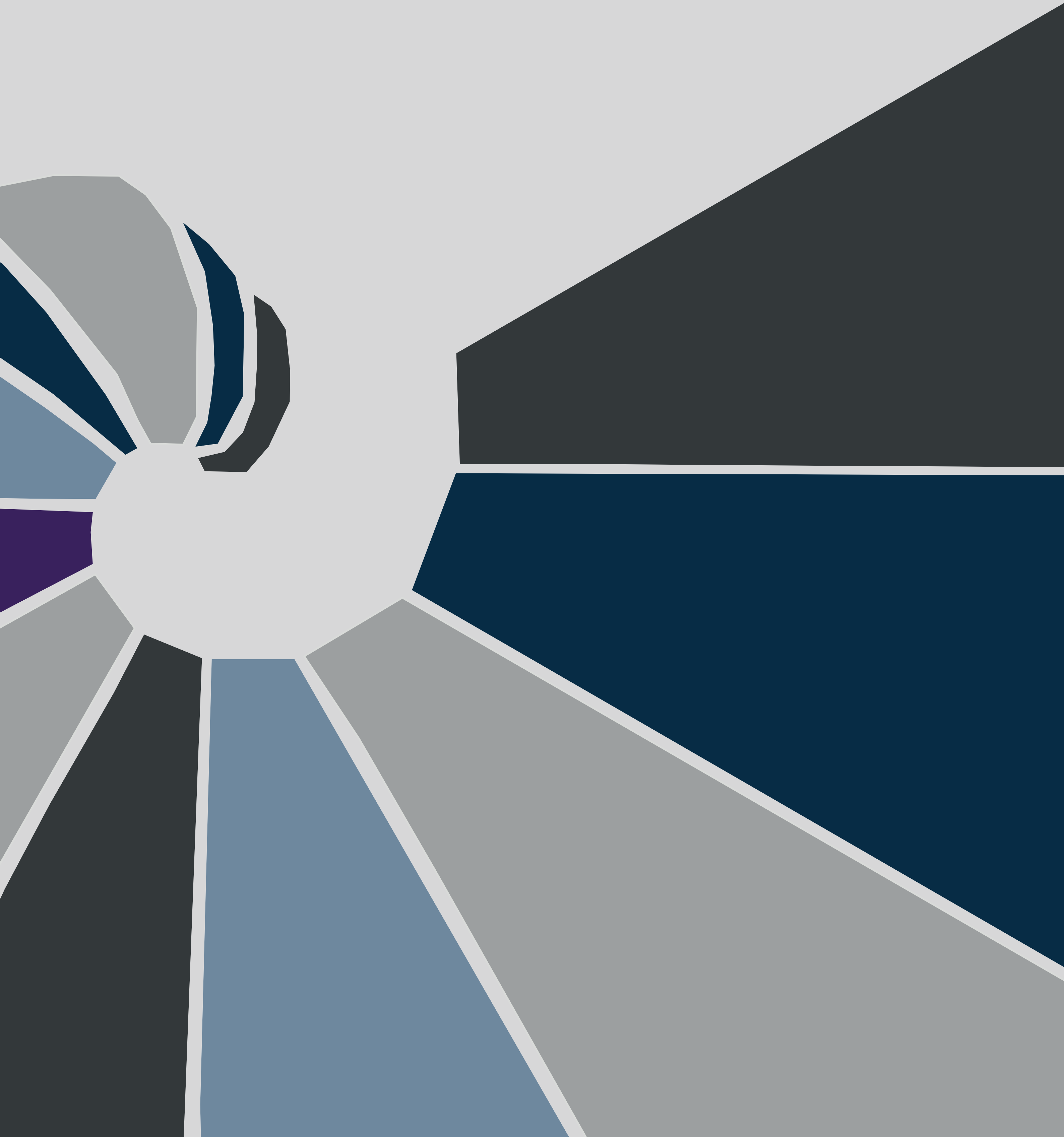
Biomarker Technologies (BMKGENE)

✉ info@bmkgene.com 🌐 www.bmkgene.com

Global Locations

Germany | United Kingdom | United States | China

Invited Plenaries



The Role of the Microbiome in Eco-Evolutionary Interactions

Ellen Decaestecker

Katholiek Universiteit Leuven

Prof. Ellen Decaestecker’s research group, the MicrobiomeEcoEvo group hosted at the KU Leuven Interdisciplinary Research Facility Life Sciences, investigates host-microbiome interactions in different model systems ranging from invertebrates (water fleas, freshwater snails and spider mites) up to (marine) mammals and primates (lemurs and humans). Within the One Health framework of the role of environmental change in disease emergence and control, we study host-microbiome interactions to gain insight into the processes that control the dynamics of these interactions. Via a combination of in situ field surveys and in vivo experiments using germ-free host organisms and microbiome transplants and via next generation sequencing (metabarcoding and metagenomics), we investigate the effect of anthropogenic induced environmental disturbance on the community composition and functionality of the microbiomes. We study whether adapted microbiomes can modify host phenotypes that affect ecosystem level processes resulting in microbiome mediated hierarchical eco-evolutionary dynamics.

Ecological and Genetic Factors Driving Antipredator Defense Strategies in Lepidoptera

Johanna Mappes

University of Helsinki

Natural selection has repeatedly driven the evolution of two contrasting antipredator defense strategies—camouflage, to avoid detection, and aposematism, to advertise unprofitability. But what determines when and why these strategies are favored? In this talk, I will explore the theoretical foundations and present recent findings from studies on my model species, the wood tiger moth (*Arctia plantaginis*), as well as insights from global experiments investigating the ecological and selective forces shaping these strategies.

Anthropocene Biology in Eastern Europe and Beyond

Marta Szulkin

Anthropocene Biology Lab, Institute of Evolutionary Biology

Berlin is the birthplace of urban ecology, and as such a fitting place to discuss the effects of urbanisation – a flagship symbol on the Anthropocene – on wildlife. Berlin is also a city that uniquely reflects the legacy of politics and war on the urban mosaic and resulting environmental structuring. In my talk, I will first delve into the impact of urbanisation on wildlife, particularly passerine birds, in an understudied region: Eastern Europe. I will further explore the complex ways political systems shape ecological and evolutionary patterns and address the underappreciated effects of armed conflict on evolutionary ecology. Second, I will discuss how urbanisation and climate change often act as compounded stressors on urban wildlife, and highlight the importance of mitigating these processes in our endeavor to build resilient urban communities for the future. Finally, I will end on a lighter note by focusing on the intriguing effects of global plastic pollution – another cornerstone of the Anthropocene – on animal phenotypes. Specifically, I will report on how terrestrial hermit crabs have begun using plastic waste as protective shells—a phenomenon that could shape their evolutionary trajectory in unexpected ways.

PLENARY

The Role of the Microbiome in Eco-Evolutionary Interactions

Mirjam Knörnschild

Museum für Naturkunde Berlin

Bats are a highly interesting taxon for animal communication research. Echolocation, requiring precise and rapid auditory - vocal motor integration, is a preadaptation for complex vocal communication. Moreover, bats have a diverse set of social systems, and phylogenetically controlled analyses suggest a positive feedback loop between social and vocal complexity. In my talk, I highlight the latest results from our team on bat vocal communication, with a special focus on the information content encoded in bat vocalizations and the causes and consequences of vocal production learning. Vocalizing bats reveal a wealth of personal information such as individual ID, motivational status, and regional origin, and playback experiments demonstrate that this information is functionally relevant for conspecifics. In addition, the vocal ontogeny of bats has some interesting parallels to that of other sophisticated communicators, including humans.

Can sponges differentiate between microbial friend or foe?

Ute Hentschel Humeida

Christian-Albrechts-Universität zu Kiel & GEOMAR

The recognition that all higher organisms live in symbiotic association with microorganisms has opened new perspectives in biology. Marine sponges (phylum Porifera) are prominent examples of such host-microbe interactions, because many species harbour enormously dense and diverse symbiotic microbial consortia within their mesohyl matrix. Their characteristic, filter-feeding lifestyle poses the need for sponges to distinguish between three categories of bacteria: food to digest, symbionts to incorporate, and pathogens to eliminate. If and how sponges discriminate between these categories is still largely unknown. This presentation will focus on recent functional insights into sponge-microbe cross talk and it will report on our efforts to move sponges from an exploratory science to one where sponges are used as experimental models for marine host-microbe symbioses.

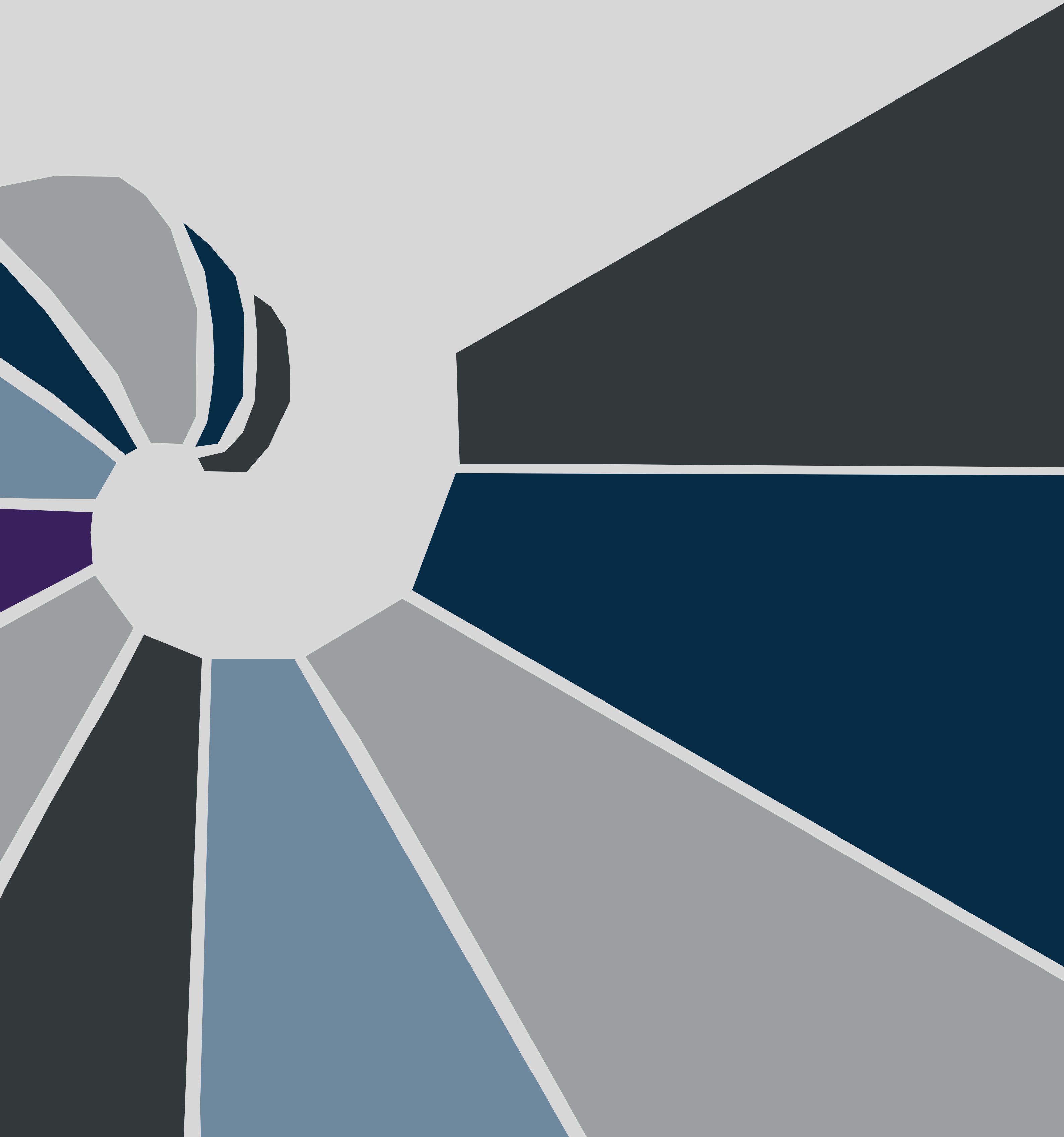
From brain to behavior: the neural basis of insect olfaction

Silke Sachse

Julius-Maximilians-Universität Würzburg

Most animals rely on their olfactory system to accomplish behavioral tasks that guarantee their survival and reproduction. Since the odor space consists of an enormous, nearly infinite number of possible stimuli, olfactory systems require special strategies to perceive, identify and evaluate the highly diverse odor information from the environment. The vinegar fly *Drosophila melanogaster* represents a premier model system for studying olfactory processing mechanisms since it exhibits a stereotyped architecture which is similar to its mammalian counterpart, but is less complex and highly tractable as well as susceptible to genetic manipulations. By exploiting these genetic techniques and linking them to neurophysiological, molecular and behavioral methods, my lab is dissecting the neural circuits that are involved in coding, processing and perception of odors. We identified and dissected the neuronal correlates to specific behavioral outputs resulting from the perception of odor mixtures, we demonstrated that the neural composition of every olfactory glomerulus is unique and correlated to its functional relevance, and we were able to show that higher brain centers decode the behavioral value of an odor. We are currently examining whether the olfactory circuitry is hardwired or can be modulated by previous experience. We are also studying the olfactory code in non-model organisms such as sister species of *D. melanogaster* exploiting different ecological niches as well as the migratory locust. Furthermore, we are interested in multimodal sensory processing and integration. The lecture will summarize our recent insights into the coding strategies and plastic components of the olfactory circuitry of insects.

Invited Talks



Opening Lecture

From Fossils to Flies - Evolutionary Biology Research at the Museum für Naturkunde

Icebreaker

Nadia Fröbisch

Museum für Naturkunde Berlin

With over 30 Million objects, the Museum für Naturkunde (MfN) houses one of the largest natural history collections in the world, which forms the foundation of research of the in-house scientists as well as for scientist visiting from all around the world. (Paleo)zoology of invertebrates and vertebrates is a strong research focus at the MfN and covers various fields including paleontology, functional morphology, diversity patterns in modern environments and deep time, biodiversity discovery and evolutionary developmental biology. The strong interaction and collaboration of scientists fosters a research environment that aims towards a modern natural science, which allows for disciplinary projects as well as for a broader perspective and interdisciplinary research.

Von Füchsen und Menschen: Rotfüchse in urbanen Lebensräumen

Fri, 18:15

Sophia Kimmig

Verhaltensökologin

Asphaltwüste Stadt versus naturnahes Land – diese Klischeevorstellung hält sich hartnäckig, entspricht jedoch nicht der Realität. Längst sind unsere Städte zu Oasen der Artenvielfalt in einer Wüste von land- und forstwirtschaftlich geprägtem Offenland geworden. Städte bieten vielen Wildtieren auf Grund ihrer strukturellen Vielfalt das, was ihnen in ihren Ursprungslebensräumen genommen wurde: Nahrung, Nistplätze, Verstecke. Gleichzeitig bringt das Leben in der Stadt auch viele Risiken für Wildtiere mit sich und nicht jede Art kann dort bestehen. Manche Wildtiere sind dagegen zu echten Stadtbewohnern geworden, darunter auch der Fuchs, der in Städten sogar deutlich höhere Populationsdichten erreicht als auf dem Land. Füchse werden zwar häufig im Stadtgebiet gesichtet, allerdings findet der Großteil ihres Lebens außerhalb der menschlichen Wahrnehmung statt. Ihre Erforschung verschafft uns Einblicke in dieses heimliche Leben. In meinem Vortrag gehe ich vor allem darauf ein, wie der städtische Lebensraum das Verhalten der Füchse bestimmt, wie er beeinflusst, wohin die Tiere abwandern, wovon sie sich ernähren, mit wem sie sich paaren, und wie ihnen das Zusammenleben mit ihrem Erzfeind, dem Menschen, gelingt.

Special Presentation

The Dream of Knowing Every Species – The DZG and its First Grand Projects

Thu, 17:35

Michael Ohl

Museum für Naturkunde Berlin

At the first annual meeting of the German Zoological Society (DZG) in Leipzig in 1891, a group of founding members proposed two major initiatives for the newly established organization. They advocated for the formation of a commission to develop binding rules of zoological nomenclature and for the compilation of a Species Animalium Recentium—a comprehensive directory of all known animal species on Earth. While the DZG soon became a key platform for the discussion of emerging biological theories and concepts, these two projects remained central to its early activities for many years. In 1894, following the commission's recommendations, the DZG published the first German-language Rules for the Scientific Naming of Animals.

The Species Animalium Recentium project, however, proved far more ambitious and complex. Beginning in 1896, it took shape through the long-running publication series Das Tierreich (The Animal Kingdom), which continued for more than a century. In 1929, Richard Hesse, then editor of the series, published an estimate of the total number of animal species believed to exist worldwide. He concluded that completing an inventory of all species within the animal kingdom would require several centuries.

Hesse's calculation formed part of a broader tradition—dating back to the 18th century—of attempting to quantify the scale of nature and the challenges involved in compiling a complete "catalog of life." In recent decades, the idea of documenting all species on Earth has again gained scientific relevance and urgency.

Invited Subject Group Talks

Sex, reproductive strategy and immune system evolution

DEV

Olivia Roth

Christian-Albrechts-Universität zu Kiel

Reproductive strategies shape sex-specific immunity and contribute to immunological adaptations. Understanding how reproductive strategy shapes immunity, permits to tackle ultimate and proximate drivers of sexual dimorphism and sex roles. Using the unique evolution of male pregnancy in syngnathids (pipefishes and seahorses), we explore how exceptional reproductive strategies are linked to genetic adaption and phenotypic plasticity in development and immunity. Despite conventional sex hormone profiles and variable sex determination, immunological patterns usually associated with the female sex, are in this teleost family consistently linked to the male sex. Syngnathids´ male pregnancy has coevolved with gene rearrangements and regulatory shifts that promote embryo tolerance. This system offers an opportunity to examine how reproductive roles reshape immune function. By translating findings from model systems with exceptional life histories to human health, we support inclusive and personalized approaches in diagnosis and treatment through the integration of sex and gender into public health strategies.

Tracking the deep evolution of animal sensory-motor integration

DEV

Jeffrey Colgren

University of Bergen

Animals move through and interact with their environments in ways unique to life on earth. This is generally facilitated by complex sensory-motor systems built around specialized cells of muscles and neurons, though their evolutionary origins and how they integrated remains unclear. To reconstruct these historical events, we preform comparative studies in choanoflagellates, ctenophores, and sponges; lineages who's branching patterns bracket key transitions in animal evolution. Choanoflagellates, the sister group to animals, have multicellular life-stages that display coordinated behavior, relying on components involved in neuronal signaling. Ctenophores have both muscles and neurons, with a mixture of unique and conserved features, while sponges lack both cell types, but possess much of the molecular and genetic toolkit to build them. This work suggests a stepwise emergence of true muscles and neurons from components that organized and integrated during the time before the first animals and the last common ancestor of extant lineages.

EVO

Evolutionary genomics and conservation of the Yellow Cardinal (*Gubernatrix cristata*)

Marisol Dominguez

Universität Potsdam

The current gene pool of any species is the product of millions of years of evolutionary history. In the absence of knowledge about future selection pressures, preserving genetic diversity helps safeguard adaptive potential in endangered species. In this talk, I present a long-term study of the endangered Yellow Cardinal (*Gubernatrix cristata*), a Neotropical songbird threatened by illegal trade, habitat loss, and potentially also by hybridization with the more abundant Diuca Finch (*Diuca diuca*). We investigated population structure and genetic diversity, developed a SNP panel to trace the origin of confiscated individuals, and assembled the first reference genome which enabled inference of the demographic history. We found genetic evidence of rare, fertile hybrids, suggesting that reproductive barriers are incomplete. Our work illustrates how genomic data can uncover patterns of gene flow, population structure, demographic change, and rare hybridization, all processes that are central to understanding the evolutionary history and conservation needs of the Yellow Cardinal.

EVO

Food, Sex and Death: How Diet Shapes Sex-Specific Life-Histories

Ruth Archer

Universität Ulm

An individual's diet is a key determinant of its fitness because lifespan, reproduction and immunity all depend critically on nutrition. These effects are not just due to energy, instead both the amount and ratio of specific nutrients matters too. High precision dietary manipulation techniques like the Geometric Framework of Nutrition (GFN) let us examine the relationship between diet and phenotype and identify how diet affects the expression of fitness traits and trade-offs between them. Here, I will use insect models to discuss what the GFN has revealed about the role of diet in constraining life histories, how these effects differ across the sexes and the sex-specific costs of reproduction. Collectively, this will demonstrate how dietary manipulation lets us unravel the complex networks of trade-offs that shape individual life-history strategies.

Convergence, Adaptation, and Constraint: Morphological Insights into Human and Mammalian Evolution

MOR

Nicole Grunstra

Universität Wien

Morphological variation in mammals reflects a complex interplay of evolutionary convergence, environmental adaptation, and developmental constraint. In this talk, I explore three case studies that examine these ‘processes’ across different anatomical systems and taxa using 3D geometric morphometrics and a combination of existing and novel multivariate statistics.

First, I examine bony labyrinth (inner ear) morphology across Afrotheria and other mammalian clades. Despite deep phylogenetic divergence, species with similar ecological niches independently evolved similar labyrinth shapes—highlighting convergent evolution shaped by functional demands.

Second, I investigate cranial shape variation in long-tailed macaques (*Macaca fascicularis*) across the Sunda Shelf. Repeated sea level changes and associated fragmentation of Sundaland during the Pleistocene are often invoked as the main drivers of Southeast Asian mammalian differentiation. However, macaque skull shape is better explained by climate than by genetic structure or Quaternary biogeography – indicative of environmental adaptation rather than historical isolation.

Third, I present a quantitative comparison of pelvic sexual dimorphism in humans and chimpanzees. The two species show a near-identical pattern of shape differences between the sexes. This refutes the long-standing assumption that the human pattern evolved recently and de novo in response to the competing demands of bipedalism and obstetrics. However, the magnitude of dimorphism is much greater in humans, likely reflecting an adaptive response along a conserved developmental pathway to meet specific obstetric challenges.

Tough threads, ballistic webs and bungee-jumps: evolutionary biomechanics of spider extended phenotypes

MOR

Jonas Wolff

Universität Greifswald

Spider silk is among the toughest known materials, enabling spiders to construct multi-functional architectures with a minimum of material investment. Spiders use these architectures (threads, webs, retreats and egg cases) as extended interfaces, which may impressively enhance predatory, defensive and locomotor capabilities. Spiders typically produce multiple types of silk secretions in differentiated glandular systems, that are connected to spinnerets – leg-like appendages equipped with various muscles that enable fine-scale movements. In this talk I give an overview about our latest research on how the structure and function of the spider spinning apparatus, silks and silk architectures changed over 400 million years of spider evolution. In particular, I will demonstrate how changes in spinning apparatus morphology enabled the evolution of novel behaviours and tougher silk threads. Further, I will show examples of how spiders may use silk architectures for power amplification, to subdue large prey and for rapid escape manoeuvres. These examples broaden the perspective of functional morphology, which does not only apply to body parts, but also to extended phenotypes, such as architectures formed by secretions.

Neuronal Epigenetic Control of Metabolic Adaptation: A Conserved Role for JMJD-3.1 in Nutrient-Dependent Plasticity

NEU

Merly Vogt

Helmholtz Diabetes Center, München

The ability to adapt metabolic function to fluctuating environmental conditions is a hallmark of organismal fitness. The nervous system is a well-established regulator of organismal metabolism, integrating environmental cues to coordinate systemic physiological responses. Epigenetic mechanisms are increasingly recognized as mediators of neuronal plasticity, yet their specific roles in metabolic adaptation remain incompletely understood.

Using Caenorhabditis elegans as a model, we identify the conserved histone demethylase JMJD-3.1 as a critical neuronal regulator of metabolic adaptation to a high-fat diet (HFD). Surprisingly, loss of neuronal jmjd-3.1 is sufficient to rescue multiple HFD-induced phenotypes, including excessive fat accumulation, reduced exploration, and shortened lifespan. These findings suggest that JMJD-3.1 acts in neurons to modulate systemic metabolic responses, possibly by influencing neuroendocrine signaling pathways.

To uncover the underlying mechanisms, we are combining transcriptomic and epigenomic profiling of isolated neuronal nuclei to define JMJD-3.1–dependent gene regulatory programs in the context of dietary challenge. Our work supports a model in which conserved neuronal epigenetic pathways serve as hubs for metabolic adaptation, with implications for understanding brain-body communication in metabolic disease.

Neural representation of space: From compass coding to place coding in an insect brain

NEU

Jerome Beetz

Julius-Maximilians-Universität Würzburg

Each moving animal needs a sense of orientation. Whether it is a bat using a biosonar for mid-range orientation or migratory birds that keep their direction for thousands of kilometres, every individual must know its current location relative to the goal. Here, I summarize our recent findings on spatial processing in the insect brain. With brain recordings from tethered flying monarch butterflies that were free to steer with respect to a simulated sun, we showed that compass coding dramatically changed when the butterfly starts to fly. Through explicit perturbation of the compass or the butterflies' goal direction, we characterized goal-direction neurons. While monarch butterflies are ideal organisms to study directional coding, they are less suited to study place coding. To this end, I recently shift my research focus on honeybees that daily forage in the same habitat. With neural recordings from freely walking honeybees, we started to study place coding.

Of honeybees and water fleas: Data-driven approaches to environmental risk assessment

ECO

Magdalena Mair

Universität Bayreuth

Protecting the environment and its organisms from harmful pollutants is challenging, as only a few surrogate species can be tested experimentally. New Approach Methodologies (NAMs), including computational tools and predictive modeling, are becoming increasingly important in ecotoxicological research and regulation. Automated experiments reduce manual workload, while machine learning enhances toxicity predictions for untested chemicals across species. Alongside these advances, a conceptual shift in statistical methods now emphasizes demonstrating the absence of adverse effects, raising new concerns about test reliability and statistical power. Using honeybees and water fleas as surrogate species, I will explore how statistical approaches may affect conclusions, highlight the role of open data and structured databases, demonstrate progress in automatized image-based data acquisition and high(er)-throughput testing, discuss the unique challenges of assessing microplastics, and propose how more flexible predictive frameworks can improve environmental hazard assessments.

Hi Knowledge: network models for ecological synthesis and knowledge transfer

ECO

Jonathan Jeschke

Leibniz-Institut für Gewässerökologie und Binnenfischerei

In the current era, an unprecedented amount of data and information is available to us in principle, yet these data and information are largely disconnected and trapped in silos. This is true among and even within scientific disciplines including ecology, where there is often a disconnect between researchers working empirically in the laboratory or the field versus those working on theory and models. And different ecological research fields focus on different drivers of biodiversity and global change, making integration across fields challenging. In the Hi Knowledge initiative (www.hi-knowledge.org), we have developed and applied approaches to improve synthesis and knowledge transfer. For example, we have created interactive, structured networks of the major hypotheses of invasion biology and urban ecology, and have connected them with empirical studies. I will present these approaches, highlighting their applicability across research fields, and will outline plans for the future including opportunities for collaboration.

Wired for function: engineering structural maturation and electrical coupling in hiPSC- derived cardiomyocytes

PHY

Nina D. Ullrich

Universität Bern

Human induced pluripotent stem cell-derived cardiomyocytes (hiPSC-CM) have emerged as a promising platform for the development of novel cell replacement therapies in cardiac regenerative medicine. However, despite standardized differentiation protocols, hiPSC-CM retain an immature phenotype, exhibiting a substantial functional gap compared to adult cardiomyocytes. This is particularly evident in Ca2+ handling, a key determinant of contractile function and force modulation, where deficits may underlie the spontaneous contractile activity or automaticity, characteristic of immature cells. Our research aims to promote the cardiogenic maturation of hiPSC-CM in vitro. We demonstrate that both environmental culture conditions and targeted structural and molecular remodelling significantly contribute to enhanced intracellular Ca2+ dynamics and more efficient excitation–contraction (EC) coupling. Furthermore, the limited intercellular connectivity typically observed in multicellular hiPSC-CM preparations can be improved through optimization of growth conditions that more closely mimic the physiological cardiac environment. Collectively, we present a range of experimental strategies to promote the maturation of hiPSC-CM toward a phenotype that more closely resembles adult cardiomyocytes. These insights offer a deeper understanding of how environmental and structural factors influence cardiomyocyte biomechanics and may facilitate the clinical translation of hiPSC-CM for use in cardiac cell therapy.

Evolutionary insect venomics

PHY

Andreas Vilcinskas

Justus-Liebig-Universität Giessen

With over a million documented species, insects represent the most successful group of organisms in terms of biodiversity. At least 14 groups have independently evolved the use of venoms, which are poisonous secretions often delivered through specialized piercing mouthparts or stingers. Venoms can be used to immobilize and kill prey or for defense against predators and pathogens. The recent progress in the exploration of insect venoms as a valuable bioresource for toxins with potential for applications in medicine and agriculture was driven by the combined application of genomic, transcriptomic, proteomic and bioinformatic approaches (Venomics). The detailed molecular analysis of venoms even from small insects pathed the way to address evolutionary questions such as the adaptation of the toxins to different preys and ecological niches as well as the reconstruction of their functional shifts. The combination of venomics with modern microscopic and imaging methods facilitated pioneering studies on the evolution of venom glands and venom delivery structures. The presentation highlights current insights into the role of venoms in the evolution of ants, ant lions, true bugs, parasitic wasps and bombardier beetles.

Many branches, one lineage? Diversity and evolution of ramified worms

SYS

Maria Teresa Aguado Molina

Universität Göttingen

Ramified syllids are unique marine annelids with a single head and multiple posterior branches, exemplifying remarkable morphological and ecological specialization. This talk examines the systematics, evolution, and biogeography of these rare worms, focusing on Syllis ramosa from the Indo-Pacific and species of Ramisyllis found, until now, only in Australia and Japan. Using museomics—DNA extraction from historical museum specimens—alongside fieldwork, we have identified new Ramisyllis species and expanded the known range of Syllis ramosa. By integrating molecular, morphological, and ecological data, we explore the phylogenetic placement of branching worms within Syllidae (Annelida) and test whether their body plan reflects convergent evolution or shared ancestry. We also investigate their strong host specificity, particularly their association with sponges, as a driver of diversification and distribution. Our findings reveal surprising evolutionary complexity, shaped by their unusual body structure and symbiotic lifestyle, and underscore the value of museum collections in uncovering hidden marine biodiversity.

Integrative taxonomy reveals Vanuatu as an ant biodiversity hotspot in the South Pacific

SYS

Kyle Gray

Universität Hohenheim

The South Pacific is one of the most geologically complex and biologically unique regions due to the thousands of islands that vary in size, age, topography, and isolation. Despite considerable scientific and conservation interest in the South Pacific, there are groups of islands, i.e., archipelagos, that remain understudied and limit an integrated understanding of the complex processes shaping the regional biota. One of the historically understudied archipelagos is Vanuatu situated between New Caledonia, the Solomon Islands, and Fiji. Using an integrative taxonomic approach and a time-calibrated phylogeny, I present first insights into the biodiversity, biogeography, and evolution of the Vanuatuan ant fauna (Hymenoptera, Formicidae). These initial results establish Vanuatu as a previously unrecognized ant biodiversity hotspot with numerous new species and show that primary forest habitats serve as important refugia for native biodiversity.

Spider sleep – what we know and what we still dream of

BEH

Daniela Rößler

Universität Bonn

Much remains unknown about the diversity and evolution of sleep in invertebrates. Recent findings reveal compelling evidence for REM sleep–like behaviors in jumping spiders, including retinal movements and limb twitches. These behaviors, observed in a visually guided lineage far removed from vertebrates, challenge long-standing assumptions about the uniqueness of REM sleep. Building on these insights, we have begun systematically recording sleep behaviors across the spider tree of life. Our findings suggest that sleep is a universal feature in spiders, marked by distinct and robust behavioral signatures. This opens new avenues to explore the function and evolution of sleep—particularly REM sleep—outside the vertebrate lineage. I will present our latest results on spider sleep and outline key directions for future research, laying the foundation for an unmatched comparative framework in sleep research, with the potential to reshape our understanding of sleep across the animal kingdom.

Evolution of Social Wound Care Behaviours in Ants

BEH

Erik T. Frank

Julius-Maximilians Universität Würzburg

Open wounds represent a significant risk of infection and mortality, driving diverse ant species to evolve sophisticated social wound care strategies. *Megaponera analis* employs therapeutic treatments on infected wounds with antimicrobial secretions from the metapleural gland, dramatically reducing mortality. Chemical analyses of these secretions identified numerous antimicrobial compounds and proteins. Conversely, *Camponotus floridanus*, lacking this gland, perform prophylactic limb amputations to halt infection spread. *Dinoponera grandis* conduct self-wound care using their front legs, while *Eciton burchellii* army ants exhibit “first aid” wound care behaviours near the raiding sites, followed by antimicrobial care inside the bivouac. These wound care behaviours highlight the evolutionary flexibility of cooperative behaviours under pathogenic pressures and the convergent emergence of functionally analogous solutions in response to a shared threat.

Contributed Subject Group Talks

Investigating the molecular mechanisms underlying the open coil ‘Banana’ phenotype in the fresh water gastropod *Lymnaea stagnalis*

DEV
101

Sultana Parvin
Georg August Universität Göttingen

A calcified coiled-shell is a prominent feature of most members of the phylum Mollusca, yet the molecular mechanisms governing the process of shell-coiling remain largely unknown. Recent evidence suggests that steroidogenic enzymes, such as 5α-reductase, play a role in shell morphogenesis. Inhibition of 5α-reductase by the drug Dutasteride disrupts normal shell coiling, leading to an open-coil “banana” phenotype in *Biomphalaria glabrata* and *Physala acuta*. This study will explore the role of 5α-reductase in shell coiling using *Lymnaea stagnalis* as a model system, leveraging its well-characterized development and sensitivity to bioactive compounds. By employing transcriptomic analyses, we aim to identify differentially expressed genes associated with 5α-reductase inhibition, shedding light on potential pathways involved in shell coiling. An understanding of the molecular basis of shell coiling will provide new insight into the developmental regulation of molluscan morphology and contribute to broader discussions on the evolutionary and environmental influences that shape the structure of the molluscan shell.

Heterochrony in orthodenticle expression is associated with ommatidial size variation between *Drosophila* species

DEV
102

Nico Posnien

Georg August Universität Göttingen

Compound eye size in insects, determined by ommatidia number and size, is a key visual adaptation to diverse environments and lifestyles. Despite its ecological importance, the genetic and developmental mechanisms controlling eye size evolution remain poorly understood. We identified an X-linked region contributing to larger eyes in *Drosophila mauritiana* compared to *D. simulans*, primarily due to increased ommatidia size. We combine fine-scale mapping and gene expression analysis to investigate candidate genes within this region. We report earlier expression of the developmental gene orthodenticle (otd) during ommatidial maturation in *D. mauritiana*. Functional analyses in *D. melanogaster* confirm its role in ommatidia size and organization. Furthermore, a species-specific otd eye enhancer recapitulates the observed heterochronic expression shift. Finally, we identify potential downstream targets of otd differentially expressed between *D. mauritiana* and *D. simulans*. Our findings implicate altered otd expression timing in the evolution of compound eye size, providing novel insights into the genetic regulation of visual system adaptation in insects.

ATAC-seq in Emerging Model Organisms: Challenges and Strategies

DEV
103

Duğçar Ebrar Erdoğan[1]; Shadi Karimifard[2]; **Dr. Natascha Turetzek**[3]; Dr. Barbara Feldmeyer[4]; Dr. Nico Posnien[1]

[1] Georg August Universität Göttingen
[2] Senckenberg Biodiversity and Climate Research Centre/ University of Mainz
[3] LMU München
[4] Senckenberg Biodiversity and Climate Research Centre

The assay for Transposase-Accessible Chromatin using sequencing (ATAC-seq) is a widely used technique for identifying regulatory regions, such as promoters and enhancers, across genomes. While successfully applied in many model organisms, adapting ATAC-seq for emerging systems—such as arthropods—presents unique challenges. These include limited tissue availability, species-specific protocol needs, and incomplete genome assemblies or annotations. Based on our experience, we highlight the protocol steps most critical to data quality in such systems: nuclei isolation, Tn5 transposase incubation, and PCR amplification. We also outline key quality control checkpoints in bioinformatic workflows to ensure data integrity and consistency. Since many emerging model organisms are not available from lab cultures, we evaluate the impact of preservation methods on chromatin accessibility. Using examples from a spider and an ant species, we show that sample replication and stringent quality controls throughout the workflow are essential. Our data emphasize the importance of isolating an optimal number of intact nuclei and fine-tuning amplification conditions for high-quality sequencing results. We recommend using fresh tissue whenever possible, as direct cryopreservation can compromise chromatin integrity. However, preserving homogenates in culture medium may mitigate these effects. With careful adaptation, ATAC-seq can be a powerful tool for exploring the regulatory genome in diverse, non-traditional model organisms.

Do larval jaws re-evolve? – A peculiar case of evolutionary loss and regain of feeding tadpole stages in the frog genus *Anomaloglossus* (Dendrobatoidea, Aromobatidae)

DEV 104

Dr. Benjamin Naumann[1]; Benedikt Derfert[1]; Lorenz Guschker[1]; Jörg U. Hammel[2]; Antoine Fouquet[3]; Hendrik Müller[4]

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„Dollo's Law" emphasizes that complex phenotypes are unlikely to be regained once they are lost during evolution. Recent studies have challenged this claim and demonstrated trait re-evolution in a number of different lineages following an earlier loss. Anurans ancestrally exhibit an indirect life cycle, with a free-living, feeding (exotrophic) tadpole stage that metamorphoses into an adult frog. Endotrophy—development without external feeding relying solely on yolk reserves—has evolved independently at least 16 times across different anuran lineages. In many cases, it correlates with an increasingly terrestrialized life cycle including the reduction of many aquatic tadpole features such as gills, a muscularized locomotory tail and keratinized mouth parts. This reduction or loss of key tadpole traits likely imposes evolutionary constraints, making a reversal to an exotrophic state seemingly improbable. Such reversal back to an exotrophic state including tadpole-typical keratinized mouthparts has nonetheless been observed in Hemiphractidae, *Adenomera* and *Anomaloglossus*. This raises the question about the reduction of cranial musculoskeletal features along this evolutionary trajectory. Here we examine the cranial morphology of *Anomaloglossus* tadpoles with different trophic modes using grating-based phase contrast in combination with 3D reconstruction and anatomical network analysis. Our results indicate that exotrophy in this taxon does not represent the re-evolution of a lost phenotype but instead the elaboration of a still existing developmental program.

From mother to Megalopa: ontogeny shapes the microbiome of native and invasive crabs

DEV
105

Dr. Gabriela Torres PhD[1]; Dr. Antje Wichels[1]; Dr. Luis Giménez[2]; Dr. Margot Deschamps[3]; Prof. Dr. Claudia Piccini[4]

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[2] Bangor University
[3] Ifremer, HMMN, Unité Halieutique Manche Mer du Nord
[4] Instituto deInvestigaciones Biológicas Clemente Estable (IIBCE)

Interactions between microbial communities and their hosts can drive fitness of hosts (by e.g. parasitism or facilitating food digestion) but also the community structure of microbes. For example, marine invertebrate larvae, while dispersing in the water column (usually over scales of 10-100's of km), have the potential to operate as vectors of microbial organisms connecting benthic and pelagic habitats. We quantified ontogenetic patterns in the prokaryotic microbiome community along larval development in two crabs (*Hemigrapsus sanguineus* and *Carcinus maenas*) distributed along North European coasts. Ovigerous females (four individuals per species) were collected in the intertidal of Helgoland and larvae were reared in the laboratory (filtered seawater at 18 °C, ad libitum food conditions). The prokaryotic microbial community of the maternal habitat water, female pleopods, freshly hatched larvae, and megalopa (last larval stage), was analysed by 16S rRNA gene metabarcoding. In both species, bacterial richness and Shannon diversity decreased from the mother-related microbiome to the freshly hatched larvae and megalopa. Beta diversity assessment highlighted large differences between the maternal pleopods and freshly hatched zoea larvae. DESeq2 analysis revealed those bacterial taxa that are significantly enriched: free-living bacteria in the maternal water and symbiotic species in the pleopods, zoea, and megalopa stages. Our findings suggest a filtering or selection process during larval development, supporting the idea that the host exerts selective pressures shaping its microbiome, favouring certain taxa over others as development proceeds. The differences between maternal and larval microbiome suggest limited (ontogenetic-mediated) transport of microbial taxa across benthic and pelagic habitats.

Animal development in the age of heatwaves: from symmetries to developmental robustness

DEV
106

Dr. Luis Gimenez PhD

Bangor University

Heatwaves are discrete events characterised by unusually high temperature. Here, I highlight the importance of ecological developmental biology in the context of recent increases in the magnitude and frequencies of marine heatwaves worldwide. In ectothermic species, increased temperatures experienced during heatwaves accelerates developmental rates, alter phenotype and fitness. Hence, we need better understanding of how such temperature would alter developmental processes to predict responses at the level of populations; mathematical models of developmental processes can help us to achieve such goal. As example, consider the concept of symmetry, applied to the differential equations modelling development (EoDs). Symmetry transformations will leave invariant the solutions of the EoD: a trivial case is the unit conversion of rate parameters (e.g. from hours to minutes), which does not modify the solutions. On the other hand, a scenario of constant temperature, where all biochemical reaction rates are equally sensitive to temperature would be represented as a symmetry transformation where all rate parameters of the EoDs are multiplied by the same scaling constant. For example, in models of embryo segmentation, scale invariance implies that the limit cycle solution remains unchanged by such scaling (except for the period). While symmetry implies developmental robustness, different degrees of sensitivity among individuals (associated to symmetry breaking) represent a form of intraspecific trait variation that might influence population persistence and community structure. Overall, models and laboratory experiments simulating heatwaves can help us to better predict organismal development in an age where heatwaves have become more frequent.

Novel genes specify the neuron cell type identity: Insights from the freshwater polyp *Hydra*

DEV
107

Dr. Alexander Klimovich PhD

Christian-Albrecht University of Kiel

The specialisation of cells into distinct types is fundamental to multicellular complexity. However, the mechanisms that drive cell type individualisation and their evolutionary origins remain poorly understood. Lineage-restricted genes (LRGs), which are unique to specific taxa, are ubiquitously present and highly abundant in animal genomes. Using the freshwater polyp *Hydra* as a model, we investigate the developmental and evolutionary functions of LRGs by combining single-cell RNA sequencing, phylogenomic analysis, functional genetics and behavioural assays. We identify numerous LRGs in the Hydra genome and reveal that they are progressively expressed along cell differentiation trajectories. The neuronal lineage, characterised by the highest diversity of mature cell types, exhibits striking enrichment of LRG transcripts, encoding effector proteins and gene regulatory factors. Using the knock-down approach, we provide evidence for the critical role of LRGs that are restricted to the Medusozoa and Hydrozoa lineages in the individuation of neuronal cell types and the emergence of behaviours that are vital for cnidarian locomotion and feeding. Our results emphasize the central role of LRGs in specifying the identity of neuronal cell types and their broader significance in the evolution of the nervous system across metazoan lineages. Our study establishes *Hydra* as a powerful model for exploring how LRGs complement conserved molecular toolkits to drive innovation. Our work emphasizes the importance of novel genes in shaping organismal complexity and provides a developmental framework for understanding their contribution to evolutionary innovation.

Spider Genomics: Duplication, Diversification & Distinctive Traits

DEV
108
🎓

Chetan Munegowda[1]; Matthias Pechmann[2]; Nikola Michael Prpic-Schäper[1]

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[2] University of Cologne

Spiders exhibit extraordinary diversity in morphology, silk production, venom composition, and behaviour. However, limited genomic resources have hindered understanding of the genetic basis underlying this diversity. To bridge this gap, we generated chromosome-level genome assemblies for evolutionarily significant spider groups, including mygalomorphs (*Acanthoscurria geniculata*, *Ischnothele caudata*) and the basal Mesothelae (*Liphistius*). These genomic assemblies provide an invaluable resource to investigate how gene and genome duplications, particularly an ancestral duplication shared with scorpions, have influenced spider evolution. This new genomic foundation will facilitate future research into the developmental and morphological innovations unique to spiders.

Using genome editing to study development and function of the beetle neuropeptidergic system

DEV 109

Lisha Zheng; **Dr. Vera Terblanche Hunnekuhl**

Georg-August-Universität Göttingen

The neuroendocrine system of insects controls many processes including physiology, growth and development. Despite its adaptive nature some aspects of neuroendocrine function are conserved widely across animals. These include the role of two conserved prohormone convertases PC1/3 and PC2 in neuropeptide processing. To elucidate their expression and function across developmental stages of the beetle *Tribolium* we have used CRISPR-Cas9 induced homology directed repair to create bicistronic lines that precisely reflect gene expression. We found that PC2 is widely expressed in neuropeptidergic cells of the central nervous system, the corpora cardiaca and the gut, making our reporter line an excellent tool to study the developmental specification of these different cell populations. By contrast, PC1/3 is expressed in individual cell of the suboesophageal ganglion and the midgut. Disruption of PC1/3 gene function at the larval stage caused a severe impairment of larval lipid metabolism inhibiting larval growth and developmental progression. Using our gene-reporter fusion line we analysed co-expression with potential neuropeptide targets and found that the prominent expression of PC1/3 in the suboesophageal ganglion coincides with the expression of pyrokinin (hugin). We are further testing how impaired neuropeptide processing in PC1/3 knockdown animals causes the disruption of larval growth and what the specific cellular function of the characterised suboesophageal ganglion neurons might be.

Multiple signaling pathways segregate endoderm and mesoderm germ layer identities in the diploblast *Nematostella vectensis*

DEV 110

Ulrich Technau

University of Vienna

A few years ago, we postulated on the basis of molecular profiling that the morphologically diploblastic sea anemones (Cnidaria) have three segregated germ layer identities corresponding to the bilaterian germ layers. Here, we investigated how these germ layer identities are specified during early development of the sea anemone *Nematostella vectensis*. Our gene expression analysis shows that the mesodermal territory is specified at the animal pole at 6 hours postfertilization, followed by the specification of the definitive endoderm between mesoderm and ectoderm. We then assessed the role of β-catenin, MAPK and Notch signaling during mesoderm and endoderm formation. We show that the mesodermal marker genes are activated by MAPK signaling while being repressed elsewhere by β-catenin signaling. Delta-expressing mesoderm then signals to Notch-expressing ectoderm inducing the definitive endoderm domain at the mesoderm/ectoderm interface. Gain- and loss-of-function experiments showed that Notch signaling is sufficient for endoderm induction. Based on our results, we propose a model of germ layer specification in *Nematostella* defined by a crosstalk of MAPK, β-catenin and Notch signaling. Given the similarity of the germ layer specification between the sea anemone and echinoderms, we propose that triploblastic identities may have predated the split of cnidarians and bilaterians.

Contributed Talks

Can neural crest cells help us to understand the evolution of natural syndromes?

DEV 111

Nathalie Feiner

Max Planck Institute for Evolutionary Biology

Neural crest cells are a fascinating group of stem cells that give rise to a wide variety of cell types, contributing to numerous ecologically relevant traits. They detach from the neural tube in the early vertebrate embryo, migrate throughout the body, and differentiate into pigment cells that give animals their coloration, craniofacial bone and cartilage that shape the morphology of the head, and chromaffin cells of the adrenal gland that influence behaviour. Could the fact that neural-crest-derived traits share a common developmental origin link these traits together and thus facilitate the evolution of natural syndromes?

My team is testing this idea by studying a syndrome in wall lizards. Lizards with this syndrome show exaggerated skull morphology, extensive coloration (overall melanisation, bright green dorsal colouration, and enlarged UV-blue lateral spots), and more aggressive, dominant behaviour relative to ancestral phenotypes. Using a variety of approaches – from staining individual gene expression to single-cell transcriptomics – we compare embryos from populations with the syndrome to those with the ancestral phenotype and identify differences in neural crest cell biology.

We find that the overall migration routes and differentiation patterns of neural crest cells in wall lizards are conserved and highly similar to those described in mammals, birds, and other reptiles. In contrast, embryos from parents with the syndrome show higher neural crest cell abundance, greater migratory capacity, and elevated gene expression levels. This hyperfunction of neural crest cells in syndrome embryos is consistent with the idea that neural crest cells are wiring traits together, thereby facilitating the evolution of natural syndromes.

Sex determination candidate loci in two anuran species groups

EVO
201

Dr. Matthias Stöck[1]; Dr. Heiner Kuhl[1]; Dr. Wen Hui Tan[2]; Sophie Leinweber[1]; Dr. Martin Knytl[3]; Dr. Dmitrij Dedukh[4]; Prof. Dr. Mark L. Blaxter[5]; Prof. Dr. Dr. Manfred Schartl[6]; Prof. Dr. Jacek M. Szymura[7]; Prof. Dr. Christoph Winkler[2]

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Vertebrate sex is determined by repeatedly evolved environmental or genetic triggers. In amphibians, undifferentiated sex chromosomes and large genomes have caused major knowledge gaps. Only a single master sex-determining gene, dm-w in clawed frogs (*Xenopus*; ZW♀/ZZ♂), is known across over 8770 amphibian species. Combining chromosome-scale female and male genomes (3.8 Gbp) of the European green toad, *Bufo(tes) viridis*, with ddRAD- and pool-sequencing, we identified a candidate master locus, governing a male-heterogametic system (XX♀/XY♂). Targeted sequencing across taxa showed structural X/Y-variation in the bod1l 5′-regulatory region, where a Y-specific non-coding RNA (ncRNA-Y), only expressed in males, suggests that this locus initiates sex-specific differentiation. Developmental transcriptomes and RNA in-situ hybridization show sex-specific ncRNA-Y and bod1l expression in primordial gonads, coinciding with differential H3K4me-methylation in pre-granulosa/pre-Sertoli cells, suggesting a new mechanism of amphibian sex determination (Kuhl, Tan et al., https://doi.org/10.1038/s41467-024-49025-2).

Diminished coverage of single-end-sequenced ddRAD-markers in males of a family of fire-bellied toads (*Bombina bombina*) coincided with hemizygous long-read coverage in a male reference genome (9 Gbp, GCF_027579735.1). Therein, we discovered a Y-specific extra-copy of a steroid hormone receptor, present in XY-males of *B. bombina*, *B. variegata*, and *B. orientalis*. I will present work-in-progress on this model of amphibian hybridization and speciation.

Sex-dependent influence of major histocompatibility complex diversity on fitness in a social mammal

EVO
202

Dr. Jamie Winternitz[1]; Dr. Nadine Schubert[2]; Dr. Hazel Nichols[3]; Francis Mwanguhya[4]; Robert Businge[4]; Solomon Kyambulima[4]; Kenneth Mwesige[4]; Prof. Dr. Joseph Hoffman[2]; Prof. Dr. Michael Cant[5]

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Parasite infections affect males and females differently across a wide range of species, often due to differences in immune responses. Generally, females tend to have stronger immune defenses and lower parasite loads than males. The major histocompatibility complex (MHC) plays a crucial role in the adaptive immune response, and extensive research has explored how variation in this region influences infection and fitness outcomes. However, studies of sex-specific relationships between MHC variation and infection are scarce, perhaps because MHC genes are located on the autosomes, which are shared by both sexes. Here, we provide evidence of sexually antagonistic selection in a wild, group-living mammal—the banded mongoose. Using genetic and life history data collected from over 300 individuals across 25 years, we found that both MHC class I (MHC-I) and MHC class II (MHC-II) diversity influence lifetime reproductive success differently in males and females. Specifically, higher MHC diversity is linked to increased fitness in males but decreased fitness in females. Furthermore, MHC diversity did not differ between the sexes, indicating an unresolved genetic sexual conflict. Our findings demonstrate that sexually antagonistic selection acts on the MHC and may operate across both MHC classes but differently. This study contributes to the growing body of evidence that sex is a significant factor in shaping host immunity and fitness.

How the evolution of spatial foraging shaped centres of cognition in Heliconiini butterflies

EVO
203

Dr. Max Farnworth[1]; Stephen Montgomery

[1] University of Bristol

Central neural circuits integrate sensory and internal information to produce behaviour. Evolution can reshape these circuits to adapt behaviour to ecological demands, but how such changes occur within existing developmental and functional constraints remains poorly understood. We address this question by investigating the evolutionary dynamics of two insect brain regions: the mushroom bodies and the central complex.

While the central complex appears highly conserved in size and shape, the mushroom bodies show remarkable diversity across species. To explore the mechanisms underlying such variation, we leveraged neotropical Heliconiini butterflies (Nymphalidae), a large radiation that exhibits striking differences in mushroom body size associated with shifts in the acquisition of a spatial foraging strategy.

Using immunostaining for structural markers and neurotransmitters, neural tracing, and comparative quantitative analyses, we examined how mushroom body expansion is accommodated across various neural circuits. In Heliconiini species with spatially demanding foraging strategies, we found disproportionate growth in specific Kenyon cell populations and an increase in GABAergic feedback neurons, suggesting substantial circuit-level change inside the mushroom bodies. In contrast, the central complex, and other brain areas, remained largely unchanged in volume and architecture. Interestingly, subtle differences did occur, obscured by volumetric conservation, particularly in neurons of the anterior visual pathway and in Allatostatin expression in the noduli.

Our findings highlight a pattern of evolutionary adaptability of only specific parts of circuits, which suggests that cognitive adaptation may proceed through selective modification of more evolutionarily malleable brain regions, while maintaining stability in essential integrative circuits.

Metazoan Transcriptional Responses to Microbiome Dynamics Reveal Species-Specific Adaptations

EVO
204

Dr. Jan Taubenheim[1]; Dr. Lucas Moitinho-Silva[2]; Dr. Felix Sommer[2]; Prof. Andre Franke[2]; Prof. Christoph Kaleta[1]

[1] University Hospital Schleswig-Holstein
[2] Kiel University

Virtually all metazoan organisms harbor microbial communities. The interplay between hosts and their associated microbiomes orchestrates a variety of functions for physiology, development, and immunity. Animals emerged within microbial environments, we thus hypothesized that they have evolved mechanisms to sense microbes and modulate their own physiology accordingly with these regulations likely arising early in the metazoan evolution. To detect and describe these putative mechanisms, we performed RNA sequencing after removing and reintroducing the associated microbiome in eight phylogenetically diverse metazoan species: *Aurelia aurita*, *Caenorhabditis elegans*, *Drosophila melanogaster*, *Halichondria panicea*, *Hydra vulgaris*, *Mnemiopsis leidyi*, *Mus musculus* and *Nematostella vectensis*. We scrutinized the data for common patterns of transcriptional regulation associated with response to microbial colonization. Species specific adaptation to microbial signals appeared to be predominant with even closely related animals showing divergent patterns of evolutionarily conserved transcriptional regulation. Further, some organisms reacted more strongly to the microbiome absence, while others are more prone to responding to microbiome reintroduction, indicating diverse roles of the microbiome in the host physiology. Nevertheless, we detected signals suggesting microbial control processes associated with epithelial cell differentiation, amino acid metabolism and cell motility. Further, we describe patterns of microbiome induced cell proportion changes in tissues which are in contact with the microbiome, giving insights in the role of microbes to tissue homeostasis.

Selection on life-course diversity

EVO
205

Dr. Ulrich Steiner

Freie Universität Berlin

Selection acts on diversity in fitness components among individuals. Evolutionary theories predict that selection in constant environments acts against such heterogeneity. But observations reveal substantial non-genetic and also non-environmental variability in phenotypes. Here, we examine whether there is a relationship between selection pressure and phenotypic variability by analysing structured population models based on data from a large and diverse set of species. Our findings suggest that non-genetic, non-environmental variation is in general neither truly neutral, selected for, nor selected against. We find much variations among species and populations within species, with mean patterns suggesting nearly neutral evolution of life-course variability. Populations that show greater diversity of life courses do not show, in general, increased or decreased population growth rates. Our analysis suggests we are only at the beginning of understanding the evolution and maintenance of non-genetic non-environmental variation.

Evolution of the *C. elegans* metaorganism

EVO
206

Prof. Hinrich Schulenburg
Kiel University

The biology of any organism is profoundly influenced by its associated microbial community — its microbiome. As a result, the microbiome can be a key determinant of the evolutionary adaptation of the entire host–microbiome association, or metaorganism, to novel environments. One possibility is that changes in microbiome composition or in the evolutionary trajectory of a particular microbiome member enable the host to persist under new conditions, subsequently facilitating the evolutionary adaptation of the host itself. Another possibility is that the host may modify its microbial environment as a form of niche construction, thereby influencing the selective pressures it experiences, even when the environment changes. To date, the precise dynamics, selective constraints, and molecular mechanisms that govern metaorganism adaptation remain largely unexplored. In my lab, we use the nematode *Caenorhabditis elegans* as an experimentally tractable model to investigate the adaptation of a metaorganism to novel environments. By combining mesocosm experiments, experimental evolution, and genomic and functional genetic analyses, we find that both the microbiome and the host contribute to adaptation under new conditions. Furthermore, our results strongly indicate that the nematode modifies its microbial environment, consistent with niche construction theory. Furthermore, selection at the level of the metaorganism shapes the evolution of the microbiome community, thereby promoting beneficial interactions between microbial members and their host. Overall, our findings provide novel insight into the evolution of host–microbiome associations, underscore the role of niche construction, and highlight *C. elegans* as a powerful model for investigating the mechanisms of metaorganism adaptation.

From phenotypic plasticity to evolutionary divergence: first results from an experimental evolution study

EVO
207

Dr. Denis Meuthen, Dominik Periša, Nhamo Mutingwende

Bielefeld University

As outlined in the theory of plasticity-led evolution, phenotypic plasticity, which allows individuals to adjust their phenotype in order to optimally respond to their environment, may precede genetic change. This concept is supported by several studies suggesting that phenotypes of derived populations often match the plasticity of a contemporarily existing ancestral population proxy. One of the most convincing examples of adaptive phenotypic plasticity is the induction of antipredator defenses in prey animals. Here, we conduct a long-term experimental evolution study with the freshwater snail *Physella acuta*, a classic model system for studying antipredator responses. Following a split-clutch design, in the first generation, we determined the extent of alarm cue-induced antipredator plasticity in behavior, morphology and life-history. We also assessed epigenomic and genomic profiles. Subsequently, we raised offspring either in the continuous presence or absence of conspecific alarm cues for multiple generations. Despite the absence of selection in our design, the epigenetic modifications underlying phenotypic change may increase the likelihood of mutations to emerge at the same or neighboring loci. Here, we report first results from this long-term study up to the 6th generation, showing to what extent evolutionary divergence between populations has already emerged on a phenotypic level. We might also be able to report initial results on the corresponding epigenomic and genomic changes to disentangle parental effects from genetic change. Our findings may contribute to a better understanding of plasticity-led evolution.

Fatty acid synthase Nvfas1 is essential for the production of storage fat, sex pheromone and offspring in *Nasonia vitripennis*

EVO 208

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Many parasitic wasps do not accumulate triacylglycerides (TAGs) as adults even if they are supplied with sugar ad libitum. Recent studies demonstrated, however, that they are in principle capable of converting sugars into fatty acids (FA) and TAGs, but the question of whether lipogenesis occurs to a fitness-relevant extent is controversial. In addition, genes involved in the biosynthesis of FA in parasitic wasps have hardly been functionally characterised to date. We used RNAi-mediated gene knock-down and stable isotope labelling experiments in the parasitic wasp *Nasonia vitripennis* to investigate the role of the fatty acid synthase Nvfas1 in the production of storage lipids (TAGs) in females and in the biosynthesis of the male sex pheromone. De novo synthesis of TAGs was almost completely absent in Nvfas1-deficient females. Males, after injection of Nvfas1 dsRNA, produced significantly less sex pheromone than control males injected with green fluorescent protein (gfp) dsRNA or water/dye only. Most importantly, females with Nvfas1 knocked down were no longer able to produce offspring, while their lifespan was not affected by this treatment. Thus, our data demonstrate that the biosynthesis of fatty acids can be essential for the reproductive success even in parasitic wasp species that do not accumulate TAGs when having unlimited access to sugars.

Evolution across space and time: Late Quaternary microevolution of endemic Mediterranean island reptiles in response to environmental and anthropogenic change

EVO 209

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What drives phenotypic variation across time and geography remains an important question for evolutionary biologists. Here, we use the Ibiza wall lizard, *Podarcis pityusensis*, which is found on the Balearic islands of Eivissa and Formentera and surrounding islets, as a system to link micro- and macroevolutionary trajectories. We apply an integrative approach linking ecological studies at the population level with fossil data from the Eivissa cave site Es Pouàs, which contains a detailed fossil record of the same species over the past 30,000 years and covers major environmental changes such as the end of the glacial period and human arrival to the island. More specifically, we performed in-vivo bite force measurements of modern populations and combined them with Finite Element Analysis of fossil shapes. Also, we collected modern diet and life history data and linked them to isotopic data from fossil levels, and we quantified shape using both 3D geometric morphometrics of modern and fossil mandibles and Orientation Patch Count (OPC) of teeth. Our results suggest that in deep time, shifting climate has a more significant effect on lizard shape and biomechanics than the arrival of humans, whereas in the modern populations, we find that diet and population dynamics both have a strong impact on the phenotype, with selective forces acting differently depending on the sex. Overall, the precise drivers of phenotype vary according to the level of evolutionary isolation investigated, suggesting an incongruence between micro- and macroevolutionary levels.

A new gastropod genome annotation allows novel insights into its antipredator plasticity

EVO
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Phenotypic plasticity describes the ability of a genotype to differentially express phenotypes in response to environmental cues. A well-studied instance of plasticity are the phenotypic changes triggered by cues indicating predation risk, also known as inducible defenses. One pivotal model for studying these defenses is the freshwater gastropod *Physella acuta*, where damage-released cues from conspecifics (i.e., alarm cues) are known to induce changes to their behavior, morphology and life-history that are beneficial in a predation context. Despite extensive research on these phenotypic changes, the underlying gene expression profiles remain largely unexplored. In this study, using *P. acuta*, we employed a split-clutch design to investigate risk-induced changes in gene accessibility. One half of full siblings was raised from hatching onwards in a high-risk environment, i.e., under continuous exposure to conspecific alarm cues. The other half was raised in a low-risk water control environment. We sampled snails' behavior and morphology at sexual maturity, shortly before obtaining foot tissue for ATAC-sequencing. Differentially expressed open chromatin sections between risk treatments will then be characterized using our new functional annotation of a recent P. acuta genome assembly. We will not only showcase treatment-dependent up- and downregulation of *P. acuta* genes but also correlate them to individual phenotypic changes. This research aims to elucidate epigenomic changes underlying phenotypic plasticity, thereby contributing to an improved understanding of the molecular mechanisms driving adaptive responses within single generations.

The influence of transposable elements on genome architecture and evolution in ants

EVO
211

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Transposable elements (TEs) are major players in evolution and have substantially shaped the structure and function of all genomes, ranging from bacteria to humans. Additionally, TE-genome interactions can be highly dynamic and lead to large-scale genome rearrangements, even between closely related organisms. However, these dynamics still remain poorly understood. In the ant genus *Cardiocondyla*, genome evolution has led to an extraordinary TE distribution, separating slowly evolving TE-poor from highly distinct fast evolving TE-rich regions. By comparative genomic studies across several closely related species of *Cardiocondyla*, we unravel how such extreme genome architecture can evolve, how it affects genome evolutionary dynamics, and how it contributes to species diversification at the genomic and other levels. Our analyses reveal spectacular degrees of genome rearrangements within the genus, resulting in highly divergent genome structures between species. We conclude that the unusual TE distribution in *Cardiocondyla* likely both contributes to and results from these extraordinarily dynamic genome evolutionary changes.

Hunting ecology predicts specialisation and convergence in the modular visual system of spiders

EVO
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Vision is one of the most important senses used by animals for a wide range of behaviours including foraging, navigation, and mating. Much is known about how eye position and orientation correlate to ecology in two-eyed animals, but those with larger visual systems have received comparatively little attention. Spiders are highly successful predators possessing eight eyes with two distinct evolutionary origins, and occupying a range of ecological niches. We used three-dimensional geometric morphometrics and evolutionary modelling to test whether eye configurations, sizes, and interocular angles correlate with hunting strategies in 75 species across the spider phylogeny. We showed how the eye configurations diversified—from the ancestral medially-clustered configuration in trapdoor spiders, through a halo-like configuration in orb-weavers, to the frontal clustering of eyes in wolf spiders. We showed that visual hunters have the highest visual system disparity and evolutionary rates. Moreover, we quantified the extent to which eye configuration is modular, and showed that the position and orientation of each eye pair evolve semi-independently. Finally, we showed that two families with similar carapace morphology, Thomisidae and Philodromidae, separated by over 100 million years of divergence, show convergent evolution of their eye configurations. Our findings demonstrate that these modular visual systems facilitate functional specialization, enabling species with a wide array of hunting strategies, body plans, and ecological niches to fine-tune their eye configurations, eye sizes, and interocular angles. Our work opens up promising avenues for further research into the genetic and developmental mechanisms that drive specialization in multi-eyed visual systems.

Scent and sociality: the evolution of chemical profiles in carrion beetles

EVO 213

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Chemical communication is widespread in insects and often used to differentiate species and sexes, as well as to regulate mating and social behaviors. Despite its prevalence, the evolution of chemical communication in relation to shifts in social complexity is still not well understood. Previous research has focused on eusocial insects, while largely neglecting the evolution of chemical signals in subsocial insects. Here, we examined if the complexity of cuticular lipid profiles increases with the evolution of complex family life and parental care. Therefore, we investigated 5 *Nicrophorus* species, which provide elaborate biparental care, and a sister species *Ptomascopus morio*, which only guards the brood. We analyzed the cuticular hydrocarbon (CHC) profiles of sexually mature, virgin females and males. We show that species express different CHC profiles, indicating their potential importance in species differentiation among subsocial carrion beetles. *P. morio* clustered separately from the *Nicrophorus* species, suggesting that its less complex social behavior may be reflected in a simpler CHC profile. Interestingly, sex-specific differences in CHC profiles were found only in *N. vespilloides* and *P. morio*. This may suggest that the other *Nicrophorus* species rely on different types of chemical signals to distinguish between the sexes. In future work, we aim to broaden the taxonomic scope to clarify whether greater social complexity consistently correlates with more complex chemical signals and to better understand the role of CHCs in sex recognition and social behavior of carrion beetles.

The genomic timecapsule – Using specimen banks to track genome evolution

EVO
214

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The ability for species to adapt to changing environments and new stressors is fundamentally based on the genetic diversity present within and between populations. As evolution is an ongoing process, continuous sampling of the same populations with a standardized method can provide unprecedented insights into long-term adaptive changes. However, continuous standardized time series samples are thus far missing in the context of genome-wide analyses, leaving an enormous knowledge gap unaddressed. A possible solution is offered by the German Environmental Specimen Bank (ESB), which has dedicated decades to amass timeseries samples from various habitats and species. The viviparous eelpout (*Zoarces viviparus*) is an indicator species for pollution and environmental change on coastal systems. Population samples of the species have been collected yearly in North and Baltic Sea since the early 1990's and stored at ultra-low temperatures. We conducted a genome-wide study on time series samples from 6 different locations and additional samples from the geographic range utilizing the cost-effective PoolSeq approach. The full dataset is comprised of 95 locations and time points and spans 2.352.765.864 single-nucleotide polymorphisms (SNPs). The analyses revealed an elevated genetic diversity in the area between the Skagerrak and the Danish Belts. This is hinting towards the presence of North and Baltic Sea adapted Alleles, for which we subsequently searched through the time series and the geographic datasets. Our study highlights the strength of the PoolSeq approach for very large sample sizes and the high value of the ESB samples data for evolutionary research.

Experimental Removal of Niche Construction Alters the Pace and Mechanisms of Resistance Evolution

EVO
215

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Biotic interactions are often shaped by ecological conditions, which in turn can be modified by the interacting organisms themselves. Niche construction, a key eco-evolutionary process describes how organisms alter their environment, potentially influencing both themselves and their interaction partners. Despite its importance, experimental evidence on how niche construction influences the evolution of biotic interactions remains limited. Red flour beetles (*Tribolium castaneum*) modify their environment by secreting quinone-rich stink gland compounds, serving as a form of external immunity. In an evolution experiment, we investigated how disrupting this niche construction via RNAi targeting a gene essential for secretion production—affects beetle adaptation to the bacterial pathogen Bacillus thuringiensis. Across generations, beetles were reared in conditioned flour containing either normal or drastically reduced levels of stink gland secretions. All beetle lines exposed to the pathogen evolved resistance within six generations. However, those with intact niche construction adapted as early as the third generation, suggesting that niche construction initially accelerated resistance evolution. Transcriptomic analysis of evolved beetles revealed that gene expression patterns diverged significantly across selection regimes, indicating that the underlying resistance mechanisms were shaped by niche construction. After nine additional generations, we further examined changes in larval-associated microbiota and beetle secretions. Lines allowed to maintain niche construction exhibited increased microbial diversification. Overall, our results provide rare experimental evidence that niche construction can shape the trajectory and mechanisms of resistance evolution, with potential implications for its genetic basis.

Loss of vision-related genes in the Malagasy mole-like tenrec (Afrosoricida, Tenrecidae, *Oryzorictes hova*)

EVO
216

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Tenrecs (Afrosoricida, Tenrecidae) are native to Madgascar an encompass a wide array of differently adapted species. Among them, the mole-like rice tenrec (*Oryzorictes hova*) exhibits morphological traits seemingly adapted to a subterranean lifestyle, tough this has rarely been confirmed in the wild. However, putative modifications related to (semi)fossoriality may extend to its genome. In environments with limited light, relaxed selective pressure often leads to the degeneration of genes involved in visual function, as previously shown for true moles or golden moles.

This study investigates the genome of *O. hova*, analyzing 218 genes related to vision in placental mammals. For comparison we include genomes of over 30 other species, including clearly subterranean species as positive controls, as well as non-subterranean species as negative controls.

We use TOGA (Tool to infer Orthologs from Genome Alignments) to assess gene status, categorizing them as intact, partially intact, uncertainly lost, lost, missing, or partially missing.

In O. hova has 30 of 218 genes categorized as “lost” or “uncertainly lost”, which is more than in most other mole-like species. Further inspection reveals that at least 13 of 19 “uncertain loss” genes likely no longer code for functional proteins. By comparing these genes with orthologs in closely related species, we are able to estimate when gene loss occurred evolutionary.

This work aims to contribute to our understanding of how convergent evolution in subterranean mammals is mirrored at the genomic level. Moreover, our genomic approach provides further evidence for subterranean lifestyle in this species.

The Evolutionary Mechanisms Underlying Hybridization in Invasive Chinese Mitten Crab Populations

EVO
217

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Invasive species are one of the main drivers of global change, and a major threat to native ecosystems. The Chinese mitten crab is one of the world's 100 worst invasive species. Recently, mitochondrial DNA of a different species, the Japanese mitten crab, was discovered in over 70% of morphological Chinese mitten crabs in some European populations. Such cryptic introductions could increase invasiveness through adaptive introgression. We set out to study this potential hybridization, its genomic mechanisms and possible fitness consequences. Low coverage whole genome sequencing of native and introduced populations revealed limited nuclear contribution of the likely source population from Russia. To discern the drivers behind this observed cytonuclear disequilibrium, we employed simulations, common garden experiments, and COI time-series data. Results suggest that genetic drift, rather than positive selection, is the primary factor generating cytonuclear disequilibrium in this context. However, our findings do not definitively exclude adaptive processes. These insights contribute to understanding the complex interplay between invasion history, genetic admixture, and fitness, highlighting the importance of drift versus selection in shaping invasion dynamics.

A Spider’s Guide to Packing: The Evolution of Prey Wrapping in Spiders

EVO
218

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Prey wrapping is a key predatory behaviour in spiders, serving functions such as immobilization, storage, and even killing of prey. This behaviour occurs in only a subset of the 136 described spider families and shows remarkable variation in behavioural sequences (e.g., wrap-attack vs. post-bite wrapping), silk types (dry vs. sticky), and the use of body parts (e.g., legs). These variations suggest that prey wrapping and its specific characteristics evolved multiple times in correlation with foraging niches. Despite its importance in spiders’ life, the evolutionary history and convergence have not been tested using a phylogenetic comparative framework. To address this, we conducted a comparative survey of prey wrapping behaviour, identified silk glands involved, and measured the mechanical properties of the silk used. Behavioural observations were performed on 52 species across 37 spider families in lab settings, using high-speed video to capture leg and spinneret movements and silk gland activity. Silk wrap samples were collected either post-wrapping or mid-process using coverslips or cardboard frames, and analysed with scanning electron microscopy to identify silk types and diameters. Further, snap freezing experiments were conducted to determine the silk gland activity during wrapping. From these observations, we compiled a character matrix coding the presence/absence of behavioral characters and analysed them in a phylogenetic comparative framework. Our results reveal that prey wrapping evolved convergently across lineages, progressing from simple to complex forms, and was also repeatedly lost. Moreover, the different morphological and behavioral adaptations played a key role in the evolution of prey wrapping.

Whole genome sequencing and the phylogenetic distribution of viral domestication events in ichneumonid parasitic wasps

EVO
219

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One of the most staggering adaptations associated with parasitism is the use of endogenous viral elements (EVEs) by parasitoid wasps to supress the host's immune response. Such EVEs are integrated into the wasp genome and likely result from multiple independent processes of viral acquisition and "domestication". Understanding how viral sequences are distributed among various wasp lineages is crucial to understand the evolutionary processes that promoted the domestication of viruses by parasitic wasps. To that end, we assembled a dataset of 165 whole genomes of Ichneumonidae, of which 121 were newly sequenced, covering 20 subfamilies in all major clades of the family. Searching for EVE sequences within the genomes and mapping them into a comprehensive phylogeny of Ichneumonidae, allowed us to pinpoint precisely the the events of viral acquistion in the family. We found that one type of EVEs, polydnaviruses, are distributed only within a derived subset of subfamilies Banchinae and Campopleginae. Virus-like particles derived from nudiviruses, previously known from a single species, are widespread into a. subclade of Campopleginae. In addition, we found two new events of viral acquisition within specific genera of Ophioninae and Orthocentrinae. Our findings reveal that EVE acquisition in Ichneumonidae is more frequent than previously recognized, involving a mosaic of recent and ancient events. These results not only expand the known diversity and distribution of EVEs in parasitoid wasps but also establish a foundation for future investigations into the genomic architecture associated with different integration events and the mechanisms that underlie the process of viral domestication.

Caste-dependent genomic stability and protection against transposable elements in the superorganism

EVO
220

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In multicellular organisms, the germline is the only tissue that contributes to the next generation. Consequently, it is essential to safeguard germ cells from mutagenic environmental hazards in order to maintain their genetic integrity. In superorganismal social insect colonies, the queen serves as the primary reproductive unit, analogous to the germline of multicellular organisms, and should thus be much more strongly protected against mutagenic influences than workers, that represent the soma of the insect colony.

Transposable elements (TEs) are a significant source of novel mutations in eukaryotes and their activity can be induced by external and physiological stressors. The germline is particularly protected against the activity of TEs in multicellular organisms, raising the question whether the same applies to the queens of superorganismal insects. To explore caste-specific differences in genomic robustness under the influence of stress, we pharmacologically suppressed Hsp90, a central player of the cellular canalization machinery. We used ONT long read sequencing of pools of full-sib queens and workers to assess rates of novel TE insertions in germline and somatic individuals. Together, the results of this study shed light on the convergent evolution of germline genomic integrity of superorganisms and multicellular organisms.

Rapid wire: The fast pace of endosymbiont evolution in novel hosts

EVO 221

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Endosymbiont, *Spiroplasma* is a genus of mycoplasma infecting large range of arthropods. The occurrence and incidence rate of *Spiroplasma* in arthropods are 5-10% and involved in array of symbiotic relationships- commensalism to pathogenicity. These symbiotic relationships are short-lived in evolutionary time scale and endosymbionts jump to different host species, this known as host shifting. To better understand how host-shifting occurs, we performed experimental evolution of Drosophila-*Spiroplasma*. We transfected isolates of *Spiroplasma* into the novel hosts and evolved for 21 Drosophila host generations. We investigated further if *Spiroplasma* evolve in different host species and what are the molecular factors are responsible for such adaptations. In order to achieve that, we performed fitness assay at the start and at the end of experiment. To compliment the phenotypic changes, we sequence at both- start and the end of experiment. We found that *Spiroplasma* strain adapt different in different hosts. Fecundity of all the replicates differ from the native hosts which signifies the potential adaptation at the start of the experiment. The longevity of flies also has differed from hosts. To complement these phenotypic data, we performed qPCR to examine infection dynamics across the 21 host generations. Additionally, we assessed the localisation patterns of *Spiroplasma* in evolved versus non-evolved hosts and compared these to native host localisation. Together, our study highlights the importance of factors responsible for symbiont to adapt rapidly in novel hosts when they do host shifting.

Ecological divergence and post-eclosion brain development shape visual performance in *Heliconius* butterflies

EVO 222

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Understanding how ecological divergence drives neural and behavioural diversification is central to evolutionary biology. In closely related butterflies *Heliconius cydno* and *H. melpomene*, which inhabit contrasting forest light environments, we investigate how sensory adaptations manifest across development. *H. cydno*, found in darker, closed-canopy forests, exhibits larger eyes and increased investment in vision-associated brain regions compared to *H. melpomene*, which occupies brighter forest edges. However, the developmental and behavioural consequences of these visual adaptations remain poorly understood. Using a quantitative optomotor assay, we assessed visual acuity across four early adult stages and found that acuity increases with age in both species, with *H. cydno* consistently exhibiting higher spatial resolution. These improvements coincide with key life-history transitions such as male courtship and female oviposition, suggesting that neurodevelopment during early adulthood may underpin behavioural maturation.To investigate the neural basis of these patterns, we analysed over 80 brain samples using confocal microscopy and a custom deep-learning segmentation pipeline. Our results reveal species-specific differences in optic lobe growth trajectories that parallel observed behavioural performance. This integrative approach links ecological context, brain development, and behaviour, illustrating how sensory evolution can shape species-specific trajectories early in the speciation process.

Measuring virus-symbiont-interactions in solitary bees

EVO
223

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Wolbachia is the most common symbiont of arthropods, in which it occurs intracellularly and is inherited through the maternal line. The success of *Wolbachia* has been attributed to its ability to selfishly manipulate the reproduction of its hosts, thereby facilitating its own spread. However, *Wolbachia* may also provide fitness benefits, such as protection from viruses. Viral blocking *Wolbachia* are successfully employed in programmes controlling Dengue by artificial symbiont transfer into the viral vector *Aedes aegypti*. By enhancing host fitness, viral blocking may thus contribute to *Wolbachia*'s spread in host populations. However, evidence for *Wolbachia* blocking viruses in natural populations of arthropods is lacking. We here tested if *Wolbachia* blocks RNA viruses in solitary bees (Hymenoptera: Anthophila).

To this end, we sampled ca 500 individuals of three common bee species (*Colletes cunicularius*, *C. hederae*, *Andrena cineraria*) over multiple seasons and sites. We individually extracted RNA and sequenced one pool of extracts for each species using Illumina. We reconstructed bee viromes using this metatranscriptomic data, finding exclusively novel, species-specific RNA viruses which were often related to honey bee or other insect viruses. For selected common viruses, and for *Wolbachia*, we determined titres using qPCR in all individual extracts. Correlating viral and *Wolbachia* titres we find no conclusive evidence for *Wolbachia* blocking viruses in the three sampled bee species. However, we observe a strong positive effect of *Wolbachia* on a novel Iflavirus in *Colletes cunicularius*, suggesting a positive interaction between virus and symbiont. We discuss potential implications for *Wolbachia* spread and bee health.

Evolutionary morphology of lizard olfaction revisited

EVO
224

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Convergent evolution, a central concept in evolutionary biology, illustrates how distinct lineages independently develop similar morphological adaptations due to shared environmental pressures. Subterranean lizards, facing unique ecological challenges, often evolve morphological adaptations, such as elongated bodies and reduced limbs enhancing their burrowing ability. Substantial research has focused on the visual systems of subterranean vertebrates, frequently demonstrating reduced vision whereas comparatively little attention has been given to their olfactory capabilities although it is likely they rely heavily on olfaction. Olfaction controls critical behaviors such as foraging and mating, potentially driving the evolution of specialized olfactory structures to offset diminished visual input.

Given the independent multiple transitions to subterranean lifestyles across reptile lineages, our project investigates variation in olfactory organ morphology along the squamate phylogeny. We explore how ecology influences these adaptations in a convergent framework, using diceCT data to compare subterranean squamates with their terrestrial relatives. Our dataset includes roughly 20 independently evolved subterranean lineages and related surface-dwelling species. We assessed potential olfactory adaptations by measuring the relative volume of the olfactory bulb and vomeronasal organ. Some lineages showed marked increases in these structures, suggesting enhanced olfactory function; however, convergence was incomplete across the phylogeny. Notably, we observed significant morphological diversity in the olfactory system of lizards. Ongoing histological analyses aim to deepen our understanding of these intriguing evolutionary patterns.

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

EVO
225

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The intracellular endosymbiont *Wolbachia* is found in 40 % of Arthropod species. Often, *Wolbachia* acts as a reproductive parasite and exerts negative fitness effects on its host, while it may be beneficial in other host species. A recent analysis of > 200 *Wolbachia* genomes revealed the presence of a biotin synthesis operon (BOOM) in 14 *Wolbachia* 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 this BOOM to elucidate the potential function of *Wolbachia* in solitary bees. A screen of over 150 bee species revealed BOOM to be present in 23 %. Phylogenetic analysis of newly sequenced *Wolbachia* genomes showed that two distinct clades of the BOOM exist in bee *Wolbachia*. Lastly, phages were identified as likely mechanisms for the lateral transfer of BOOM genes between *Wolbachia* strains. Altogether these findings indicate a dynamic evolution of an intricate association between solitary bees and *Wolbachia* as a nutritional mutualist.

Transmission, toxins and competition: what drives virulence evolution in spore forming parasites?

EVO 226

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Why do some parasites cause a great deal of harm to their hosts, whereas others only cause mild symptoms? Often, we expect the harm parasites cause to their hosts, or their virulence, to optimise at an intermediate level. Too low virulence can result in missed transmission opportunities, whereas too high virulence can mean that the host and with-it parasite die before transmission has occurred. There are, however, exceptions to this general expectation. Spore formers, for example, can sit and wait in the environment for new transmission opportunities, potentially reducing the costs of higher virulence. The exact circumstances under which high virulence in spore formers is likely to evolve, however, is hotly debated, with some mathematical models predicting that it is tightly linked to certain specific aspects of parasite ecology and biology. These include 1) whether the parasite is transmitted via shedding from alive or dead hosts; 2) whether the parasite produces toxins and 3) whether the parasite is in a single strain or multi-strain infection. We carried out an evolution experiment manipulating all three factors in a model system, using *Caenorhabditis elegans* as a host and *Purpureocillium lilacinum* as a parasite. Toxin producers evolved higher virulence regardless of the selection regime, whereas whether parasites were transmitted via shedding from alive hosts or upon death only impacted virulence evolution when the fungus was in multi-strain infections. These results suggest that parasite ecology and trade-offs beyond those between virulence, transmission and recovery rate determine optimal virulence in spore formers.

Comparative population history of European fireflies and biodiversity in the neotropics

EVO
227

Dr. Ana Catalan

LMU Biozentrum

Fireflies are well-known beetles celebrated for their bioluminescent displays. However, their demographic history and patterns of natural selection remain poorly understood. Furthermore, species delimitation in European and Neotropical fireflies has not yet been explored using genetic data, leaving the status of many species unresolved. To address these gaps, we generated whole-genome assemblies and population genomic datasets to investigate, in a comparative framework, the population genetics of three European genera: *Lampyris*, *Lamprohiza*, and *Luciola*. These genera exhibit distinct geographical distributions, providing an opportunity to examine shared and divergent patterns in effective population size, colonization pathways, migration rates, and selective events. Our results reveal that European firefly species show strikingly different evolutionary histories, even where their distributions overlap. In particular, major geographic features such as the Alps exert variable impacts on gene flow across species. For species delimitation, we applied models including BPP, SNAPPER, and mPTP to our genetic data. This integrative approach clarified species boundaries in Europe and highlighted high species discovery rates in biodiversity hotspots such as Nuclear Central America. Overall, our research reveals a group that is not only rich in species diversity but also remarkable in its genomic and population genetic variation.

The evolution of niche construction in social species

EVO 228

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Niche construction is a process where individuals alter their local environment, like nest or burrow building, often with the goal to bring their local environment closer to their optimal environment. In social species, an individual might consequently also alter the environment of others. Using evolutionary individual-based simulations, we studied the effect of this sociality on the evolution of niche construction, e.g. does niche construction evolve to a similar level for non-social and social animals? Is there cooperation or cheating in niche construction between group members (e.g. do some individuals benefit of the niche construction of others while not contributing to niche construction themselves)? And what happens when individuals in a group have a different optimal environment? We found that niche construction (independent of group size) only evolved when the local environment was very different from the environmental optimum, or when fitness increased a lot with a small change in the environment. Surprisingly, we found that in social groups individuals often cooperated, and that cheating behaviour was rare and often disappeared again in evolutionary time. When groups cooperated, each individual had to invest less in niche construction, so that all individuals benefitted. This model can explain why niche construction is not a common behaviour in many species, but why it still has evolved in some species, and why niche construction also can evolve when individuals have to cooperate in niche construction.

Possible Silk Flow Controlling Muscles in the Spinning Apparatus of Spiders

MOR
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Silk production is a defining characteristic of spiders, with silk being extruded through spigots on the spinnerets, which are one- to multi-membered paired appendages at the abdomen's posterior end. Initial findings revealed that spinnerets possess intricate musculature, enabling precise construction of silk-based materials. Among these muscles are those potentially controlling silk flow within the spinning duct of the major ampullate gland, located in the anterior lateral spinnerets. In orb-weaving spiders, three muscles associated with a valve-like structure in this duct have been described. This structure might enable spiders to brace without the help of their legs during abseiling manoeuvres, or to adjust silk stiffness by modifying shear forces during spinning. However, it is unclear if this apparatus is an autapomorphy of the orb-weaving or all spiders. To investigate this, a comparative anatomical study was conducted utilising micro-computed tomography (µCT), which revealed diverse configurations of possible silk-controlling muscles across different spider lineages. While early branching Mesothelae and Mygalomophae lack muscles associated with spinning ducts, at least one such muscle has been identified in most araneomorph (‘modern’) spiders, with the exceptions of some families (e.g. Pholcidae, Oecobiidae, and Hersiliidae). The most complex arrangement, consisting of three muscles and a duct valve, was observed in Deinopidae, some Uloboridae, and all studied representatives of the super-family Araneoidea, except for Linyphiidae. This indicates multiple occurrences of either the acquisition or loss of muscles. Future research will investigate whether the observed differences in the configurations of the silk flow controlling apparatus impact its function and efficiency.

MOR
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Catch it if you can: Aerial egg transfer in combination with Velcro®-like catching mechanism in stick insects oviposition

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Stick and leaf insects (Phasmatodea) produce hard-shelled eggs exhibiting remarkable phenotypic diversity. The oviposition technique of phasmids is considered the main influencing factor on egg shape and its surface structures. Evolutionary divergence from the ancestral egg-dropping technique to various derived modes of oviposition has resulted in a wide range of adaptations. Depending on the type of oviposition, various structures evolved on the surface of phasmid eggs, ranging from nanoscopic surface patterns up to macroscopic anchors or hooks. Within the southeastern Asian Dataminae (Heteropterygidae), eggs display different types of “hairs” on their surface, whose functions have prompted a range of hypotheses. We discovered that the egg “hairs” of *Orestes draegeri* function as interlocking structures involved in an acrobatic oviposition technique. We provide evidence for their specialisation in the oviposition process and the first high-speed recording of this oviposition technique. To deposit the egg in a previously dug hole, the female throws the egg in an acrobatic launch-and-catch movement from the abdomen to the antennae. The egg “hairs” end in a grappling hook-like structure that interlocks with specific mushroom-shaped cuticular protuberances on the female antennae. Furthermore, we characterized the attachment forces of the mechanism and revealed the first example of a hook and mushroom probabilistic fastener in phasmids. Our study underscores the heterogeneity of oviposition techniques in insects, especially in Phasmatodea, and demonstrates strong potential of their egg surface structures as a source of bioinspiration.

Regeneration research beyond the model organism axolotl: Evolution and diversity of regenerative abilities of salamanders

MOR
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Regeneration research has advanced significantly in biomedicine and molecular biology, deepening our understanding of its molecular regulation, medical potential, and evolution of vertebrate regenerative capacities, including organ, limb, and tail regeneration. The Mexican axolotl (*Ambystoma mexicanum*) has been the primary model organism in this field. Although the axolotl will undoubtedly remain an essential subject for regeneration studies, incorporating data from non-model organisms is increasingly crucial for revealing shared and divergent regenerative mechanisms and broadening evolutionary perspectives. Moving beyond the axolotl, our research highlights the value of alternative research organisms and studying regeneration in natural conditions. This approach provides initial insights into shared and divergent regenerative traits across salamander taxa, expanding the taxonomic and evolutionary scope of regeneration research and identifying future directions. Here we present the tiger salamander as a promising alternative model organism to the axolotl for fracture healing and regenerative biology research of body appendages, especially due to its metamorphic life history pattern, and we demonstrate regenerative capacities in plethodontid salamanders to investigate the effects of life history strategies and habitats on limb regeneration.

Comparative anatomy of endostyles in Appendicularia: cladistic interpretation and functional implications

MOR 304

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The endostyle is a mucus-secreting organ located in the pharynx, primarily used for food particle capture. It is an apomorphy of chordates and considered homologous to the vertebrate thyroid gland. In its ancestral form, as seen in ascidians and amphioxus, the endostyle appears as a longitudinal groove composed of multiple rows of functionally distinct cells. In appendicularians, however, the endostyle is reduced to a shorter structure containing fewer cells and current understanding is largely based on studies of the model species *Oikopleura dioica*. To date, no comparative analysis using modern microscopic techniques or cladistic reasoning has been conducted. In this study, we present a comparative analysis of ten appendicularian species representing all three major families: five oikopleurids (*Oikopleura vanhoeffeni*, *O. dioica*, *Bathochordaeus stygius*, *Megalocercus huxleyi*, *Folia mediterranea*), two fritillariids (*Fritillaria pellucida*, *F. borealis*), and two kowalevskiids (*Kowalevskia tenuis*, *K. oceanica*). We combined serial light microscopy and 3D reconstruction with transmission electron microscopy to characterize and compare endostyle morphology. Our results reveal a higher degree of endostyle diversity within Appendicularia than previously assumed. Morphologies range from a relatively long groove with two rows of glandular cells separated by ciliated zones in *M. huxleyi*, to more compact organs with a single glandular row in other oikopleurids and fritillariids, and a complete loss of the endostyle in kowalevskiids; partially functionally replaced by ciliated pharyngeal projections. Based on these observations, we propose hypotheses of homology for individual cell types and discuss their phylogenetic implications.

Similarities and Differences in the Olfactory Lobe between Isogenic and Non-Isogenic Crayfish

MOR
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The olfactory lobes of aquatic crustaceans are the primary centers for olfactory processing. They are subdivided into complex subunits called olfactory glomeruli, which are areas of high synaptic density. Their morphology and number can vary both within and between species and is thought to reflect differences in their ability to discriminate olfactory stimuli. We want to know to what extent such inter- and intraspecific differences in the number of glomeruli are driven by the genetic background, and ask whether isogenic crayfish exhibit less phenotypic variation in their olfactory system than non-isogenic crayfish, possibly linked to their lack of genetic diversity. We compared the olfactory system of the parthenogenetic marbled crayfish (*Procambarus virginalis*; Lyko, 2017) with its close relative, the sexually reproducing *Procambarus alleni* (Faxon, 1884).

A workflow was established using X-ray micro-computed tomography (µCT) to quantify glomeruli directly. The µCT data were imported into the segmentation program `3D-Slicer´, where each glomerulus was manually tagged and subsequently exported as a 3D-Object. These were then counted in the 3D graphic software `Blender`. Based on the cephalothorax lengths of the animals, we also investigated whether glomerular numbers correlate with body size. The shape of the olfactory lobe, which is formed by the arrangement of the glomeruli, is similar in both species. Our initial results indicate that the number of glomeruli varies slightly more in *P. virginalis* than in *P. alleni*. However, this does not appear to be related to body size in either species. This study was supported by DFG Project Ha 2540/19-1.

Gene expression surveys support the presence of a neural stem cell type during nervous system development of sea spiders

MOR 306

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Sea spiders (Pycnogonida) are understudied marine chelicerates that form sister group of all remaining extant taxa (Euchelicerata). Notably, nervous system development in pycnogonids has been reported to rely on large neural stem cells (NSCs) with high mitotic activity and a morphologically asymmetric division mode. The latter results in their self-renewal and the formation of a second, intermediate neural precursor cell (INP), which in turn divides symmetrically. While this mode of neurogenesis differs from euchelicerates and myriapods, it shows several similarities with neuroblasts and ganglion mother cells, the well-characterized NSC and INP types driving neurogenesis in Pancrustacea (crustacea + hexapods). Until now, however, the gene regulatory networks governing sea spider neurogenesis and neural differentiation have not been studied, impeding validation of the morphology-based distinction of pycnogonid cell types and further comparisons with pancrustacean neuroblasts and ganglion mother cells on the molecular level. To redress this knowledge gap, we employed HCR-FISH to study the expression patterns of a suite of key genes with conserved roles in neural cell specification, maintenance and differentiation during the development of the sea spider *Pycnogonum litorale*. Our study yields first insight into the transcriptional profiles of the cell types involved in sea spider neurogenesis, revealing a general congruence between previous morphological cell type classifications and gene expression characteristics. Beyond this, we show that the first NSCs are specified in segmentally stereotypic positions in the neuroectoderm, similar to the pancrustacean NBs.

Form suggests function in heavily modified ocelli of Apoid Wasps (Hymenoptera, Apoidea)

MOR
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Most insects have not only two large compound eyes, but also three single-lens eyes called ocelli. While the adaptation of compound eyes has been extensively explored, relatively little is known about ocellar modifications.

Although modified ocelli have attracted great taxonomic interest, the internal morphology, and possible functions of modified ocelli in apoid wasps remain enigmatic. Apoid wasps exhibit dramatic changes to the shape and size of their ocelli. Modifications range from slight elliptic deformations to 'C'- or comma-shaped lenses which are often reduced to small slits. Comparable modifications are otherwise unknown in insects, but have evolved five times independently within apoid wasps.

We examined the internal ocellar morphology in four of the five affected lineages. This revealed an organised retina and optic nerve, implying that the ocelli are potentially functional. Moreover, we found some common features of modified ocelli to occur in distantly related taxa with different external lens shapes. A unique rhabdom organisation, producing distinct lines of seemingly interconnected rhabdoms, was found across separate instances of modification and is especially intriguing.

We propose two hypotheses on their function: (I) slit-shaped ocelli might be an adaptation to high-light intensity desert habitats; (II) rhabdom organisation and ocellar shape may improve the detection of light polarisation, potentially improving flight control and navigation.

Functional morphology and sexual selection of the copulatory structures in the millipede *Acanthopetalum carinatum* (Callipodida, Diplopoda)

MOR
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Sexual selection greatly influences the evolution of animals and their genitalia. This phenomenon is particularly well studied in many groups of Hexapoda. Comparable in-depth studies of other arthropod groups will help to test general hypotheses on selection mechanisms underlying genital diversity. In males of the diplopod group Helminthomorpha, one or more pairs of anterior walking legs transform into secondary copulatory organs (gonopods) that interact species-specifically with the female copulatory organs (vulvae). The complex interaction of the morphologically extremely diverse genitalia is thought to be key factor for the radiation of this species-rich group involving various sexual selection mechanisms—including sperm competition, lock-and-key mechanism, female choice, and cryptic female choice.

To reconstruct the sexual selection mechanisms involved in the evolution of helminthomorph gonopods, we investigated the functional morphology of the copulatory organs in *Acanthopetalum carinatum*. This species belongs to the Callipodida, a helminthomorph group that has not been previously examined in this context. The copulatory interface of frozen mating pairs was reconstructed using 3D µCT scans in combination with confocal laser scanning microscopy (cLSM). This approach provides insights into their material properties and allows functional interpretations of various subcomponents of these complex organs. The findings are discussed in an evolutionary context by comparison with other species, enabling inferences about the sexual selection mechanisms acting upon these structures.

Spineless Hunters: Adaptive Insights from Mantis Leg Simplification

MOR
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Grasping structures have evolved repeatedly across animals as key adaptations for capturing and handling food. Among insects, the raptorial forelegs of praying mantises are iconic examples, typically armed with robust spines presumed essential for seizing and immobilising prey. Yet, in a clade defined by these specialised appendages, multiple lineages have independently reduced or even lost their spines. This paradox raises fundamental questions about function, cost, and ecological trade-offs in predatory systems. This project investigates the adaptive significance of raptorial leg simplification in *Perlamantis* Guérin-Méneville, *Paraoxypilus* Saussure, and *Amorphoscelis* Stål. These three mantis genera exhibit convergent and extreme reductions in foreleg armature. Using scanning electron microscopy (SEM) and confocal laser scanning microscopy (CLSM), we characterise morphological structure and cuticle material composition to explore how simplified raptorial forelegs may still support effective prey capture. Complementary gut content analysis and DNA barcoding of wild-caught specimens allow us to assess dietary breadth and prey preferences. We test two competing hypotheses: (1) the 'Diet Specialisation Hypothesis', in which simplification reflects adaptation to a narrow prey niche; and (2) the 'Generalist Hypothesis', where spine loss is functionally neutral or associated with unrelated selective pressures. Preliminary findings suggest that these mantises are generalist predators, though some species have distinct prey preferences. Some species, for instance, seem to feed primarily on ants or butterflies. These patterns indicate that spine reduction may not constrain hunting ability. Instead, they point to functional flexibility and alternative strategies in insect predation, contributing to broader discussions on structural reduction and evolutionary innovation.

Characterizing of Immune organs in Placental and Non-Placental Live-bearing Fishes (Cyprinodontiformes: Poeciliidae)

MOR
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The Poeciliidae fish family contains both placental and non-placental live-bearing species. In this family, placentas have independently evolved multiple times, with a remarkable diversity in placental complexity among closely related species. These features make Poeciliidae an interesting animal model to investigate how immune and reproductive systems have evolved to make placental pregnancies possible. However, detailed fundamental knowledge on these species' biology is missing, for example on the morphology and physiology of their reproductive and immune system. In this project we investigate the morphology of two placental species, *P. turneri* and *P. prolifica*, and compare each with their evolutionary closely related non-placental sister species, *P. gracilis and P. infans*. We hypothesized a similar morphology of the immune system of placental and non-placental species. We first optimized tissue processing and histological staining protocols for these fishes. We then characterized the morphology of the female reproductive system and of a number of important immune organs, such as the thymus, head kidney, spleen, and Nemausean lymphoid organ, a tonsil-like organ. So far, our data confirm earlier-described differences in placental structures but reveal no obvious differences in the presence and location of (immune) organs between the species. Our study provides a foundation to understanding the immunology of placental fish species, working toward a better understanding of the evolution of pregnancies.

Blood-feeders in detail – Morphological investigations of louse flies (Hippoboscidae)

MOR
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Viktor Deines

Ectoparasites have, over the course of evolution, repeatedly adapted in various ways to their lifestyle and close association with hosts. This also applies to species within Hippoboscidae (Diptera), a group of ectoparasitic flies that parasitize a wide range of hosts while typically showing a high degree of host specificity. Through this close host association, numerous morphological adaptations have evolved that reflect their highly specialized way of life, including flight behavior and dispersal strategies.

In the present study, three species of this group - *Lipoptena cervi*, *Lipoptena fortisetosa*, and *Melophagus ovinus* - are examined to investigate how morphological structures differ between species. These species are all parasitizing mammals, but show certain differences in dispersal strategies, host finding and specializations to the specific host species. Macro- and microscopic photography as well as scanning electron microscopy (SEM) are used to analyze these structures, with the aim of drawing conclusions about their function and connection to each species' dispersal strategy.

Furthermore, three-dimensional reconstructions of the proboscis and suction pump based on micro-computed tomography (µCT) are presented, offering new insights into the form and function of these structures. These anatomical data contribute not only to a better understanding of the biomechanics of the blood-feeding apparatus, but also provide insights into the convergent evolution of suction mechanisms within Diptera.

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The evolution of novel mouthpart interlocking mechanisms in ants (Hymenoptera: Formicidae)

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Ant lifestyles center around the unique combination of eusociality, flightless workers, and often predatory habits. No morphological innovations in ants are known to relate to predation. Here, we explore an understudied ant novelty: the ability to close off their mouth. Ants lock their labrum in front of the maxillolabial complex through part of the maxilla pressing against labral hooks. Grooves on the maxillolabial complex additionally allow tighter labral fit in some groups. Variations in both mechanisms lead to different levels of mouthpart closure, with an evolutionary trend to switch from looser to tighter conditions across ants. We find predation to predict tight closure, but models of character evolution indicate that evolutionary dependence between these traits is not the only possible explanation for this pattern. Although tight interlocking is lost in some ants, we find no clear evidence for tradeoffs with other functions such as sensing with the palps. We discuss the origin of interlocking in ants and suggest it may related to a combination of predation, prognathous mouthparts, and multi-purpose mandibles. We discuss the role of mouthpart closure in ant evolution but also highlight limitations of our comparative approach and emphasize the need for focused biomechanical investigations and enhanced natural history data to refine future inferences of adaptation.

Born to run: development of locomotory pattern in fast running centipede, *Scutigera coleoptrata*

MOR
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Centipedes are fierce terrestrial predators that live in or on the soil, under rocks or litter. Generally, centipede locomotion is characterized by strong undulations of the body, by metachronal waves maintained even at higher speeds and by the lack of functional grouping of legs. However, most kinematic and biomechanical locomotory studies are based on relatively short legged scolopendromorphs. Apart from functional interpretations of morphological features – which set them apart from other centipedes – not much is known about the locomotory pattern of the early branching Scutigeromorpha. Adults have 15 pairs of legs and, as no exception from other Chilopods, their ultimate legs exhibit a functional transformation and are not involved in locomotion. Scutigeromorphs are characterized by particularly long and slender appendages and by outstanding speed. Using high speed cameras and tracking software, we analyze the kinematics of their locomotion. Compared to other centipedes, the body undulations of these animals are considerably weaker, and they employ functional units of individual legs at all speeds. Moreover, scutigeromoprhs have an anamorphic development: they hatch with four pairs of legs and add leg bearing segments throughout six subsequent molting cycles. This offers a unique opportunity to study the development of the locomotory pattern throughout ontogeny, from four to fourteen pairs of locomotory legs. Understanding how the locomotory system adapts to such rapid addition of legs in one of the fastest terrestrial arthropods will considerably expand our knowledge of polypedal fast running mechanisms, and could shed light on the evolution of terrestrial locomotion.

Development of the skull of a living fossil- a micro-CT study of the rope eel *Erpetoichthys*

MOR 314

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The Polypteriformes, comprising the genera *Polypterus* (Bichirs) and *Erpetoichthys* (reedfish or rope eels) are morphologically primitive African freshwater fishes that represent the basal-most lineage of the Actinopterygii. Because of a combination of retained ancestral and derived characters, polypterids have been of special interest to comparative anatomists ever since their scientific description in the early 19th century. Despite this wealth of research, questions remain regarding the homology of certain elements (e.g., pre-opercle, rostrals) as well as the developmental association of the lateral line canals with underlying bones. Because of the phylogenetic position of Polypteriformes, answering these questions has important implications for our understanding of early actinopterygian evolution. Studies of ontogeny can be useful to address such questions, however, to date most of these have concerned the more species-rich genus in the order, *Polypterus*, primarily due to the rarity of developmental material for the monotypic genus *Erpetoichthys*. To further our understanding of the cranial osteology in polypterids and early actinopterygians in general, we generated high-resolution computed tomographic scans of a subset of a unique developmental series of *Erpetoichthys* comprising 15 stages ranging from 7.2 mm NL to 39.4 mm TL. We document the development of the cranium of *Erpetoichthys* with an emphasis on those elements for which homology remains uncertain.

The evolution of eyes in Spiralia: a glance at the less explored taxa

MOR
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The complexity and structural diversity of eyes has fascinated natural scientists throughout the ages. Next to shading pigment cells, eyes comprise one of two types of photoreceptor cells. In ciliary photoreceptor cells, the ciliary membrane houses the visual pigment, whereas rhabdomeric photoreceptor cells aggregate the visual pigment in microvillous surface extensions independent of cilia. Additionally, each photoreceptor cell-type functions with its own opsin as part of the visual pigment and its own signal transduction cascade. Since the times of Darwin, people have tried to trace the evolution of eyes in animals. By the turn of the millennium, the question of eye evolution in bilaterian animals seemed to have come to an answer. The eye of the last common ancestor of Bilateria consisted of at least one shading pigment cell and one rhabdomeric photoreceptor cell. The rhabdomeric photoreceptor cell-type prevailed in the eyes of the protostome lineages of Ecdysozoa and Spiralia. More recently, new morphological and molecular data accumulated that warrant a re- evaluation of the current hypothesis on the evolution of eyes. In Spiralia, the discovery of xenopsin, a new type of opsin that is associated with ciliary photoreceptor cells has added a new aspect to the discussion on the evolution of photoreceptors and eyes. The fact that ciliary photoreceptor cells in eyes of spiralian species are more common than originally assumed and the finding that xenopsin is expressed in many of them challenge the current hypothesis of eyes with only rhabdomeric photoreceptor cells in the stem lineage of Spiralia.

The forward kinematics and workspace generation of insect legs

MOR
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The legs of insects represent a fascinating inspiration for biological and biomimetic research, since they combine multifunctionality with efficient design. To understand the form-function relationship of the legs and use them as design concepts for bio-inspired robotic systems, it is essential to comprehend and emulate their kinematic structure. In the present study, a workflow for reconstructing the 3D-workspace of insect legs (all the positions, which the leg tip can reach in 3D space) is proposed on the example of the desert locust *Schistocerca gregaria*. The standard Denavit-Hartenberg-convention was used to describe the natural alignment of consecutive joint axes, and thereby the kinematic chain of one fore-, middle- and hindleg each. Coordinates of the joint articulations were obtained from µCT-scans of the specimen – this coordinate data was used to calculate the Denavit-Hartenberg-parameters using a custom R script. The script is capable to consider both mono- and multiaxial joints, making it applicable to multiple different kinematic architectures of insect legs. The opening angles of individual leg segments were measured manually and served as the joint variables for the kinematic model, providing enough data to calculate the 3D-workspace. This standardized approach can be applied to any variation of arthropod appendages and complements the comprehensive research on inverse kinematics of insect legs that is already established. This combination forms a basis for broad-scale quantitative and comparative analyses to better understand the evolution of arthropod extremities and to potentially apply this knowledge in the design of bio-inspired robots.

Drivers for the extreme head transformations in ant-like litter beetles (Pselaphinae, Staphylinidae): specialized predation or defense?

MOR
317

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The reasons for the enormous morphological disparity of Pselaphinae, second largest (> 10,000 species) sub-group of rove beetles (Staphylinidae, Coleoptera), remain largely underinvestigated. The ecomorphological radiation in these beetles has produced an enormous variety of structural adaptations, linked to predation habits and to a close association with ants. The cephalic modifications in Pselaphinae include not only bizarre enlarged palps and modified antennae, but also various deformations of cephalic skeletal structures. Cuticular invaginations and furrows functionally cause cuticular thickening and are likely linked with structural reinforcement for mechanical defense. A complex cephalic glandular system occurs in several representatives of Pselaphinae, and is presumably linked to predaceous habits. However, the knowledge about the lifestyles and behavior of most of the pselaphine species is very limited, allowing only speculations about the driving forces for the structural modifications. Detailed studies on cephalic structures have already helped to gain insights into hitherto unknown functions of mouthparts and feeding habits in various insect groups. Additionally, cephalic muscles and endoskeletal elements help to understand the evolutionary processes within the group of interest.

Using µCT, 3D reconstructions, scanning electron microscopy and histological sections, we documented in detail cuticular cephalic structures, muscles and glands of pselaphine species from different lineages and analyzed the discovered modifications with respect to the evolution of predation and ant association. The obtained knowledge is a contribution to an ongoing multifaceted project on the evolutionary morphology of the megadiverse Pselaphinae.

Leg mechanosensilla in Drosophila may not feedback to forward walking

MOR
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Campaniform sensilla (CS) are mechanosensors embedded in the cuticle of insects. They are often found at locations near the joints between leg segments. On legs, CS are generally considered to sense cuticle bending arising from forces acting on the cuticle during legged locomotion. It is currently unclear how CS locations influence strain levels at the CS, but this information is crucial for understanding how CS respond to stimuli. Due to the small size of the CS it is not feasible to directly measure cuticle deformation and simultaneously CS activity during typical leg movement scenarios, e.g. during leg stepping. Here we present an accurate simulation approach based on a parametric finite element model of the femoral CS field for *Drosophila* hind legs with 12 general and seven CS-specific parameters each. This model allows testing how changes in CS location, orientation and material property affect strain levels at each CS. We used experimentally acquired kinematic data and computed ground reaction forces to simulate in vivo-like forward stepping. The displacements found in this study at the physiological CS field location near the trochanteric-femoral joint were found to be smaller than those necessary for conformation changes of ion channels involved in signal elicitation. Also, variation of material properties of the CS had little influence on displacement magnitudes at the CS cap where the sensory neuron attaches. Our results indicate that ground reaction forces alone are unlikely to serve CS activation of the studied CS field during forward stepping in *Drosophila*.

Comparative analysis of epiphyseal fusion in rodent limb bones

MOR 319

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Epiphyseal fusion, the process where the growth plates of bones close, is widely used as a marker of skeletal maturity in mammals. However, the timing and pattern of fusion can differ greatly across species. A 1925 study on laboratory rats revealed a discontinuous sequence of epiphyseal fusion in limb long bones, with some fusing more than two years apart. Subsequent studies in various rodent species confirmed that fusion may be significantly delayed or may never occur at certain sites throughout the animal's life. To explore these patterns more broadly, we conducted a clade-wide statistical analysis of epiphyseal fusion in rodent limb bones. Utilizing CT scan data from hundreds of individuals across numerous species, we evaluated the fusion status of 15 different epiphyseal sites. Focusing only on specimens showing at least one fused site, we found consistent trends: for instance, the humeral trochlea invariably fused, while the distal epiphyses of the radius and ulna rarely did. We used the frequency of fusion across species as a proxy for fusion sequence—assuming that more frequently fused sites typically fuse earlier. This approach revealed significant differences in fusion patterns among major rodent clades, suggesting a strong phylogenetic signal. Interestingly, no clear relationship emerged between fusion patterns and either body size or ecological lifestyle. These initial findings prompt further questions about how evolutionary changes in epiphyseal fusion might influence the biomechanical function and adaptability of trabecular bone structures in rodent limbs.

Combining tissue clearing with classic histological techniques for fast and simple investigations of Microplastics in tissues of *Lumbriculus variegatus*

MOR 320

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Due to the omnipresent occurrence of microplastics (MPs) in all environmental compartments, their ingestion and associated toxic effects have been shown for all kinds of organisms. In freshwater especially benthic invertebrates might be predominantly exposed to these particles due to the accumulation of MP in sediments. Nonetheless, histological evaluation of potential effects still remains difficult due to the lack of MP-compatible protocols. Particularly protocols, allowing a fast and simple detection of unlabeled MP inside whole organisms and subsequent histopathological analyses on the same specimen are missing. Therefore, we established three workflows that allow a simple and fast identification of previously unlabeled PS-MP particles in the benthic freshwater invertebrate *Lumbriculus variegatus* via tissue clearing and subsequent histological sample preparations like paraffin sections, cryo sections as well as scanning electron microscopic examinations on cleared specimens. Our protocols do not only allow identification of MPs in the specimens after the optical clearing but also allow identification of the particles after application of the subsequent histological approaches. Further, tissues of the cleared worms still showed integrity comparable to uncleared specimens. The established workflows could be used for detailed investigations of histopathological effects caused by MPs, opening up the path to even examine specimens collected from the natural environment.

RHODOPSIN 7: a non-canonical opsin with ancestral features links light perception to behavior in *Drosophila*

NEU
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Light perception is crucial for various aspects of animal behavior and physiology. It enables organisms to respond to environmental signals and maintain internal balance. In *Drosophila melanogaster*, seven distinct rhodopsins primarily mediate this function. RHODOPSIN 7 (RH7) is an evolutionarily ancient opsin that differs structurally and functionally from the canonical rhodopsins RH1-RH6. While the latter primarily mediate imaging vision in the retina, RH7 has unique features and is expressed in neurons outside the retina, including cells in the optic nerve head and the circadian clock network. These findings suggest that RH7 plays specialized roles beyond traditional phototransduction. Phylogenetic and structural analyses have revealed that RH7 is the oldest fly rhodopsin, with homologs found in panarthropods. Its elongated N- and C-termini resemble classical G-protein-coupled receptors rather than typical rhodopsins. Behavioral assays demonstrate that RH7 is crucial for activity in the dark, including the subjective night and transient light interruptions. Interestingly, the Darkfly strain, which has been adapted to live in complete darkness for generations, has a C-terminal deletion in RH7. Structural modeling indicates that this region plays a crucial role in regulating the activity state of the receptor. Behavioral data indicate that the deletion enables the Darkfly strain to bypass standard receptor control mechanisms and be more active in the dark. Our results establish RH7 as a non-canonical opsin with ancient evolutionary roots and adaptive potential. Beyond imaging vision, RH7 mediates basic light-dependent functions by linking ambient light to behavioral states and fine-tuning responsiveness to darkness.

Exploring the Feasibility of EEG in Elephants

NEU
402

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Elephants possess the largest terrestrial brains, yet we know remarkably little about their neurophysiology. This project aims to explore the feasibility of recording somatosensory evoked potentials (SEPs) in an Asian elephant (*Elephas maximus*) using non-invasive electroencephalography (EEG). To our knowledge, this is the first attempt at any neurophysiological recording in an elephant. In collaboration with mobile EEG specialist Klaus Gramann (TU Berlin) and Easycap, we developed a custom 8-electrode EEG cap adapted to elephant morphology. Our subject, Anchali—a 15-year-old female elephant at the Berlin Zoo—has been successfully trained to participate in a vibrotactile stimulation set up while wearing the EEG equipment. Despite the significant challenges posed by thick cranial bones and skin, preliminary results indicate we are able to record biological signals. Ongoing efforts are focused on improving electrode adhesion and identifying optimal scalp locations, with promising results using a high-conductance paste and electrode placements on the back side of her head. While data quality and consistency are still under evaluation, our initial findings suggest that elephant EEG is likely feasible. Establishing non-invasive neurophysiological methods in elephants opens up unprecedented opportunities to investigate the neural basis of sensorimotor control in these unique large-brained mammals. Ultimately, this work may contribute to a deeper understanding of brain scaling and the neural representation of the elephant’s uniquely versatile trunk.

The magnetic compass of *Cataglyphis* ants

NEU
403

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The geomagnetic field provides important cues for navigation. Both the polarity and the inclination can be used as a magnetic compass. A crucial question for a mechanistic understanding of magnetoreception is whether animals rely on inclination- or polarity-based magnetic information. *Cataglyphis* ants are ideal experimental models for insect navigation and magnetoreception. Their magnetic compass is a unique example of an essential magnetic compass used for close-range navigation. During initial learning walks, ants use magnetic information to align the gaze directions towards the nest entrance, i.e. directional information of the magnetic field is used for path integration at the beginning of the ants' outdoor careers. The ants' compass is polarity-sensitive and the ants do not rely on magnetic inclination. This finding has important implications for the mechanism underlying the ants' magnetic sense. Furthermore, geomagnetic information is also crucial for learning-dependent neuronal plasticity in higher order brain centers such as the mushroom bodies (centers for learning and memory) and the central complex (center for navigation).

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Appetite for Aggregation: How starvation fuels locust social life

NEU 404

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Desert locusts (*Schistocerca gregaria*) undergo a dramatic phase change between cryptic (solitarious) and swarming (gregarious) forms, culminating in locust outbreaks that threaten global agriculture. With rising temperatures, recurring extreme weather events, and droughts, climate change is expected to intensify the frequency and severity of outbreaks. Drought conditions reduce food availability, driving locusts to aggregate around scarce resources, which can trigger a cascade of behavioural and physiological adaptations, leading to crowding and swarming. While much research has focused on gregarious locusts, less is known about the solitarious phase and the mechanisms that drive gregarisation, particularly in relation to hunger.

In this study, we explore how starvation affects locust behaviour, especially focusing on aggregation tendencies. Through a combination of behavioural experiments and functional calcium imaging, we investigate how the locust's internal states influence social preferences and neural responses to conspecifics and food-related odours. Our behavioural assays reveal that hungry solitarious locusts exhibit a heightened tendency to aggregate, highlighting the role of hunger in triggering locust aggregations, and potentially swarming. Calcium imaging of the antennal lobe allows mapping the neural processing of social and food odours in both fed and starved locusts. Our findings suggest differential odour responses based on feeding state, offering insights into the neural mechanisms driving behavioural changes during gregarization.

The study highlights the importance of internal states and environmental factors in regulating locust phase change and contributes to the global effort to manage the increasing risks of future locust outbreaks.

Fine-scale navigation: searching ants use multiple guidance mechanisms

NEU
405

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Navigation is of crucial importance for the survival of many species. To guarantee the successful completion of a journey, insects engage in very efficient systematic searches to pinpoint their target. The resulting search patterns are highly structured – systematic – while retaining strong levels of adaptive flexibility. It remains unclear how this sophisticated behaviour is generated by the insect central nervous system. I examine the involvement of several candidate guidance mechanisms in the expression of searching behaviour in the desert ant *Cataglyphis nodus*. Restricting the ability of ants to form visual memories around the nest entrance results in nest searches that retained their systematic structure but suffered from reduced precision. Interestingly, asymmetrical restriction led to asymmetrical searches. This indicates that searching ants employ visually guided steering mechanisms, in which the perceived environment is matched to visual memories. Where such memories are lacking, the steering mechanism is impeded. Further experiments in an entirely featureless visual environment reveal that ants can still perform systematic, area-restricted searches in the absence of meaningful visual input. These results suggest the involvement of innate movement routines. A further mechanism, guidance by path integration, has previously been identified in the literature. In the natural context, all three mechanisms are most likely active and integrated in the animal to give rise to sophisticated systematic searching behaviour. More broadly, the outcomes allow us to ask questions of fundamental importance about how brains work to produce adaptive behaviour.

Signal in Time: Neuropeptidergic coupling of *Drosophila* larval rhythms

NEU 406

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The diurnal fruit fly, *Drosophila melanogaster*, exhibits both circadian and ultradian rhythms in rest (sleep) and activity, with activity peaks at dawn and dusk. In addition to circadian patterns of feeding, the fruit fly also displays ultradian bouts of feeding that vary depending on food availability and quality. The interaction between these circadian and ultradian rhythms remains to be elucidated. Starvation and nutrient restriction alter sleep and activity patterns, likely mediated by neuropeptides that coordinate multiscale rhythms. This study explores the hypothesis that neuropeptides released by clock neurons oscillate on multiple time scales, integrating behavioral rhythms into a unified framework. Specifically, the role of the ring gland (RG) in synchronizing neuropeptide release from pars intercerebralis and subesophageal ganglion neurons with circadian timing was examined. Behavioral tracking and mass spectrometry (MS) analyses were conducted on individual larvae (early L3 and wandering stage) under various nutrient conditions (fed, 24 h starved, 48 h starved) and Zeitgebertimes (ZT0–ZT23). Larvae showed daily oscillations in behavior across conditions, with peak activity at dawn, dusk, midday, and midnight. Foraging behaviors such as head turning and reorientation were prominent and modulated by starvation, with specific time points (ZT0, 4, 8, 12, 16, 20) showing significant changes. Semiquantitative MS analysis identified key neuropeptides in the RG, including adipokinetic hormone, pyrokinin-2 (hugin), sNPFs, SIFamide, orcokinins, CAPA-pyrokinin and corazonin, which were found to play a significant role in the observed behavioral pattern. Furthermore, it has been demonstrated that e.g. myosuppressin levels remain constant under starvation conditions.

How heatwaves threaten bumblebee survival and development

ECO 501

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Heatwave are becoming more frequent and intense due to climate change, posing a significant threat to global biodiversity. While the decline of crucial pollinators like bumblebees is well-documented, the specific impact of heatwaves on their developmental stages remains largely unknown. We investigated the effects of varying heatwave lengths (3-7 days) and intensities (36-38°C) on *Bombus terrestris* pupae in vitro. Our findings reveal that pupal emergence can be drastically reduced, and wing deformities increased significantly. Our study highlights the profound consequences of heatwaves on bumblebee pupal development, with potential cascading effects on colony fitness, local populations, and ecosystem services.

The heat is on: effects of heat waves on bumblebees' ability to detect floral scents

ECO 502

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Climate change disrupts vital ecological processes and biotic interactions. Recent increases in the frequency and severity of heatwaves prompt the evaluation of physiological processes that ensure the maintenance of key ecosystem services such as pollination. Experimental heatwaves are used to investigate how high temperatures affect the bumblebees' ability to detect floral scents. Heatwaves induced strong reductions in antennal responses to floral scents, and these reductions were generally stronger in workers than in males. There was no consistent pattern of recovery 24 h after heat events. The results suggest that the projected increased frequency and severity of heatwaves may compromise bumblebee-mediated pollination services by disrupting the chemical communication between plants and pollinators. The reduced chemosensitivity can decrease the bumblebees' abilities to locate food sources and lead to declines in colonies and populations.

Microbial booze: The evolutionary ecology and endogenous origins of ethanol in honeybees

ECO
503

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Ethanol, a microbial fermentation product common in floral nectar, plays a potentially important but understudied role in pollinator ecology. We examined how honeybees (*Apis mellifera*) respond to low, ecologically realistic ethanol concentrations. First, bees were exposed to acute and chronic low doses of ethanol to assess effects on cognitive performance, mortality, flight endurance, and lipid stores. Second, we analyzed crop contents of caged and foraging bees to quantify ethanol levels and characterize microbial composition. Third, we tested whether infection with the gut parasite *Nosema ceranae* alters ethanol preference. Bees showed high tolerance to ethanol exposure: acute doses did not affect odor discrimination or cognitive judgment bias, while long-term exposure only modestly increased mortality in older individuals. Hemolymph trehalose levels rose under ethanol diets, indicating metabolic adjustments rather than toxicity. Ethanol was detected in the crop contents of naturally foraging bees, confirming environmental exposure, but also in caged bees, suggesting endogenous accumulation. Microbial profiling of caged bees revealed crop communities enriched in fermentation-capable taxa such as *Gilliamella* and *Lactobacillus*. Additionally, *Nosema*-infected bees exhibited a significantly stronger preference for ethanol-spiked sucrose than uninfected controls. Although ethanol did not reduce parasite load, it slightly buffered survival costs in infected individuals exposed to higher concentrations. These findings indicate that honeybees not only tolerate ethanol but may also modulate their intake under physiological stress. Ethanol, whether encountered through nectar or microbial processes, likely plays a more significant role in pollinator behavior and health than previously recognized, shaping adaptive responses in complex plant–pollinator–microbe systems.

ECO
504

Submersed Electroantennography for Decoding Kairomone Perception in *Daphnia*: Linking Neural Responses to Ecologically Relevant Chemical Cues

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Daphnia, a keystone genus in lentic ecosystems, can detect predator-released kairomones and respond with morphological, behavioural, or life cycle adaptations to reduce predation risk. Chemoreception in *Daphnia* is hypothesized to occur in the first antennae, however the chemosensory mechanisms underlying *Daphnia*'s responses to kairomones and the molecular identity of most kairomones remain poorly understood. Until recently a method for directly assessing their chemical perception was still lacking. A promising tool for measuring chemoperception in *Daphnia* is underwater electroantennography (EAG) of the first antennae. This submersed EAG allows for direct measurement of electrical responses from chemosensory neurons upon exposure to chemical stimuli, providing a fast and sensitive method to screen potential kairomones and other ecologically relevant compounds. We established a submersed EAG for *Daphnia magna* and *Daphnia longicephala*. We established a positive control through an algal volatile that reliably elicits nerve impulses in several cladoceran species. Significant electrophysiological responses to natural roach (*Rutilus rutilus*) kairomones were then demonstrated in *D. magna*. Testing the HPLC fractions of the roach extract enables us to identify the physiologically active components of the roach kairomone. This allows us to develop new biotests with the identified active compounds linking the submersed EAG measurements to behavioural responses, similar to experiments in terrestrial chemical communication research. The submersed EAG with *Daphnia* enables the identification of various substances perceived by these aquatic invertebrates, thereby speeding up the process of unravelling the molecular structure of kairomones and enabling us to measure semiochemicals directly in the aquatic realm.

Wear patterns reveal substrate interaction and material strategies in radular teeth

ECO
505

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In vertebrate ecology, tooth wear is a well-established proxy for dietary reconstruction, masticatory function and habitat use. In invertebrates its proxy potential is heavily underresearched. Here, we investigate the wear patterns of radular teeth in the gastropod *Vittina turrita*. Tooth structure, composition and properties were characterized using nanoindentation (ND), energy dispersive X-ray spectroscopy (EDX), scanning electron (SEM) and confocal microscopy (CLSM, 3DST). In feeding experiments, snails were fed on substrates mimicking selected natural conditions in biofilm feeding (rough algal-coated rock [coarse sandpaper], coarse sand [abrasive particles], smoother rocks [medium sandpaper] and fine silted biofilms [fine sandpaper]). ND, EDX and SEM indicated that the teeth consist of a hard, calcium-enriched coating and a softer, fibrous chitinous interior, with targeted reinforcement. 3DST revealed a wear regime that can be linked in fine and medium substrates to consistent material loss, indicated by reduced Sa (mean height) and increased Spd (peak density) indicating uniform abrasion but high surface fragmentation. In coarse substrates, fewer but more extreme mastication leads to catastrophic fracture events characterized by spalling and crack formation reflected in large Sa, low Spd, and large voids (Vvv). Wear severity was the highest in ontogenetically older teeth, where the outer coating had been worn. Here, the vulnerable fibrous core surfaces showed large Sa values, which are likely the result of failure or removal of entire chitin fibers during substrates impacts. Our study highlights that analyzed wear reflects tooth-substrate interaction and structural adaptation of gastropod teeth, offering a new proxy tool for tracing molluscan diet.

Moisture matters more than heat for evolution of reproductive genes in *Drosophila*

ECO 506

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Environmental variation shapes reproductive strategies and sexual selection/conflict, yet the role of specific ecological drivers in the molecular evolution of reproductive genes remains underexplored. Using whole-genome population data from 144 *Drosophila* melanogaster populations worldwide, we investigated how climatic factors influence the evolution of seminal fluid proteins (SFPs), key mediators of postcopulatory sexual selection. Crucially, our Bayesian modelling revealed that humidity and precipitation, rather than temperature, are dominant ecological factors that correlate with molecular variation in SFPs. Notably, the Sex Peptide gene - a central player in sexual selection - exhibited πN/πS ratios suggestive of balancing selection, with allele frequencies strongly linked to precipitation and expression-modulating SNPs showing environmental sensitivity. These findings highlight the overlooked role of moisture-related climate factors in shaping sexual selection, conflicts and reproductive gene evolution in an era of accelerating climatic change.

ECO
507

InsectMow - A story about insect- and spider-friendly mowing

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Intensive agriculture threatens species-rich grasslands, with frequent mowing contributing to the reduction of arthropods. The interdisciplinary project “InsectMow” investigates the negative effects of mowing on grassland ecosystems, as well as how these effects can be mitigated through technical modifications. We aimed to develop (1) a modified disc mower that causes fewer arthropod losses, and (2) an effective insect chasing device that enables insects to escape. In a three-year experiment, we investigated the direct- and medium-term effects of mowing with various mowing techniques and chasing devices on eight abundant arthropod groups in grasslands, covering two seasonal mowing events each year.

Our results show that bar mowers affect the arthropod fauna in a similar way to disc mowers. Immediately after mowing, the average number of arthropods was approximately 35% lower for both mowing techniques than in the unmown control. However, chasing devices showed great potential in deterring arthropods before mowing with the effectiveness depending on the type of chasing device and driving speed. Additionally, we observed medium-term effects of mowing (two to four weeks after mowing), regardless of the mowing technique or cutting height, with 27 to 90% fewer individuals on mown plots than on, depending on the taxonomic group. Our findings suggest that mowing generally has a negative impact on abundant arthropod groups in grassland independent of the mowing technique. Therefore, to protect spiders and insects from the negative effects of mowing, other factors such as the maintenance of uncut refugial areas, and mowing regimes should be seriously considered.

Scaling up from moss to mountains: how micro- and macroenvironmental factors shape diversity patterns in tardigrades

ECO 508

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Mountains offer a natural laboratory to study how environmental gradients shape biodiversity. Yet, microscopic animals remain underrepresented in such research. We examined how taxonomic, functional, and phylogenetic diversity in tardigrade communities varies along an altitudinal gradient in the Italian Alps. Using COI DNA metabarcoding, we identified 169 tardigrade OTUs from 546 bryophyte samples and compiled trait data including body size, buccal tube width, pigmentation, and egg-laying strategy. We grouped predictors into macroenvironmental factors (e.g., altitude, vegetation type) and microenvironmental factors (e.g., bryophyte biological and ecological traits). We found that species richness declined with elevation, but standardized functional and phylogenetic diversity increased. Therefore, though species-poor, high-elevation communities were composed of distantly related and ecologically distinct taxa. In contrast, communities at lower elevations were richer but had more overlap in their functional diversity and were more closely related. Microhabitat features, particularly bryophyte structure and moisture, were better predictors for community composition than bryophyte species identity. Pigmented taxa were associated with exposed, dry conditions, while oviposition strategy and body size varied across altitude. Both traits were also related to the overall availability of suitable habitat, defined here as the presence of large, long-shoot pleurocarpous mosses. Our findings reveal that local microhabitat characteristics filter traits at small scales, while macroenvironmental gradients drive species turnover. Together, these processes generate structured diversity patterns even in microscopic, highly dispersive animals. In our study, tardigrades emerge as a powerful meiofaunal model to link microhabitat filtering to macroevolutionary patterns.

Impacts of human footprint on *Bombus* genetic diversity: a macrogenetic look

ECO
509

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Genetic diversity contributes to the capacity of populations to cope with environmental change, including those brought about by human impacts like urbanization and agriculture. Understanding the extent to which population genetic processes are 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.

This presentation showcases a macrogenetic analysis of *Bombus*. We compiled a dataset consisting of 4620 individuals across 243 populations and 14 *Bombus* species. The dataset is built using microsatellites, which are highly polymorphic and neutrally evolving, from population genetics studies. First, we estimated two measures of genetic diversity (allelic richness and gene diversity). We then used mixed effects linear regression models to test the effects of human-driven land use change, such as urbanization and agriculture, on the genetics of *Bombus* populations. In areas with a higher human footprint, some species, such as *B. hypnorum* and *B. ruderatus* tended to have lower levels of genetic diversity. On the contrary, other species such as *B. occidentalis* and *B. terrestris* had higher levels of genetic diversity in areas with a higher human footprint. This pattern may be influenced by their role as commercial pollinators in fields and greenhouses. 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.

The intricate relationship between *Drosophila* and *Caenorhabditis* in their natural habitat

ECO
510

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Model organisms are central to biological research, yet their ecology is often overlooked. To address this gap, we studied two of the main model species of the life sciences in their natural habitat and surprisingly discovered a direct and very intimate interaction between the nematode *Caenorhabditis* and the larvae of *Drosophila* fruit flies.

By sampling decomposing apples, we found that *Caenorhabditis* and *Drosophila* larvae coexist in small substrate patches and share most of their microbiome. Compost mesocosms simulating natural conditions confirmed this interaction and showed that *Drosophila* presence reduces worm population size. Subsequent laboratory experiments demonstrate that fly larvae feed on nematodes and can even utilize these worms as the sole food source. *C. elegans* occasionally survives the fly gut and can be released back into the environment, thereby potentially promoting worm dispersal.

Moreover, the presence of *C. elegans* increases mortality in developing fly larvae, and unexpectedly, the worms establish proliferating populations within dead pupae—using them as both shelter and food source—indicating necromenic or mildly parasitic behavior. The interaction between both model organisms induces a defined transcriptomic response, including the upregulation of two neuropeptide-like proteins in the worm, that we show to underly worm survival.

In summary, studying two model organisms in their natural habitat uncovered a completely unknown relationship between *C. elegans* and *D. melanogaster* that is likely to shape ecological dynamics of the two taxa in nature: These two species engage in apparently unfavorable interactions, where each benefits from harming the other.

Body condition and alarm cues: effects on anti-predator responses in a freshwater gastropod

ECO 511

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Predation is one of the most pervasive selection pressures faced by prey individuals throughout their lives. Thus, the ability to assess and respond to predation threats is critical to individuals' lifetime fitness. *Physella acuta*, a freshwater gastropod, utilises chemical alarm cues from injured conspecifics as a source of information regarding local predation risk. Recent studies show that chemical alarm cue production is condition-dependent, with high-condition donors producing cues that differ in composition and effectiveness at inducing antipredator behaviour compared to those from low-condition donors. This variability may influence prey's ability to assess predation risk and initiate defensive behaviours. Our study focuses on the condition-dependence of alarm cues in *P. acuta* to address this issue and employ a combination of analytical and behavioural trials. First, we extract alarm cues from high and low-condition donor snails and profile the specific chemical compounds present using gas chromatography-mass spectrometry (GC-MS). Second, we tested the efficacy of these cues by studying crawl-out behaviour in *P. acuta* before and after exposure to high-condition alarm cues, low-condition alarm cues, or a water control treatment. Here, we report our first results showing to what extent alarm cue production in *P. acuta* is condition-dependent. Additionally, we report our first insights into potential key compounds within *P. acuta* alarm cues. We may also provide insights into the biological concentration levels of these compounds in *P. acuta*. Altogether, our study may provide valuable insights into the chemical communication system of gastropods and the mechanisms underlying their estimation of predation risk.

Parental Microbiome Engineering: Adaptive Pre-Hatch Care in Carrion Beetles

ECO
512

Eric Grubmüller; Prof. Dr. Sandra Steiger
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Ephemeral diets such as carrion are nutrient-rich resources but prone to rapid microbial degradation. Some carrion feeding insects have evolved several behavioral and physiological adaptations to reduce the microbial competition to protect these resources. Burying beetles (*Nicrophorus* sp.) use small vertebrate carcasses as brood resource for their larvae. Before hatching, parents engage in extensive pre-hatch care by burying the carcass, forming a ball, and consistently coating it with antimicrobial secretions. Previous studies have shown that pre-hatch care aids in preserving and concealing the carrion resource. However, the literature shows conflicting results regarding the consequences of pre-hatch care for the larvae, potentially due to the use of experimental substrates with unnaturally low microbial challenge. By comparing carrion that was either prepared by parents or incubated on forest soil presenting a sufficient microbial challenge, we show that *N. vespilloides* parents manipulate cadaveric VOC emissions to deter dipteran and congeneric competitors. Using prepared and aged carcasses across different soil types, we demonstrate that soil influences the carcass microbiome. Despite this, *N. vespilloides* parents can override these effects, shaping the microbial community in their favor. Additionally, we found that the necessity of pre-hatch care is context-dependent: essential in microbe-rich environments, but potentially detrimental under microbe-poor conditions. In summary, our findings reveal that pre-hatch care in *N. vespilloides* serves multiple adaptive functions, particularly under high microbial pressure.

Surviving the City: Population genetics and survival of red squirrels across an urban-rural gradient in Berlin

ECO
513

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Urbanization alters animal habitats, creating selective pressures on wildlife and underscoring the growing relevance of cities for biodiversity conservation. This study investigates how urbanization affects the genetic structure and survival of Eurasian red squirrels (*Sciurus vulgaris*) across three contrasting habitats in Berlin, Germany: a woodland area, a walled urban cemetery, and a highly frequented urban park used for dog walking, recreational stays and public events such as festivals. Since 2021, red squirrels have been live-trapped biannually in spring and autumn across three study sites representing different levels of urbanization, resulting in a sample of over 140 marked individuals. We genotyped all individuals at 16 microsatellite loci and analysed genetic structure using Bayesian clustering with STRUCTURE. Additionally we calculated standard population genetic metrics to assess genetic diversity and differentiation among sites. Capture–recapture data were analysed using Cormack–Jolly–Seber models to estimate survival and detection probabilities in open populations. Our results reveal detectable genetic structuring between sites, potentially shaped by urban fragmentation. The woodland area and the cemetery show similar genetic structure while the urban park not. The urban park showed also a higher inbreeding rate than the other study sites. Survival varied with season, sex, and degree of urbanization, with lower survival for females in urban parksSurvival probabilities differed between males and females depending on site-specific urbanization levels. This study shows how urbanization shapes genetic structure and survival in red squirrels, offering insights into their persistence in cities and highlighting factors that support long-term population viability in urban environments.

Supercolony formation in invasive *Tapinoma magnum* ants

ECO 514

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Invasive social insects can rapidly colonise new environments and outcompete local species. A key factor in their dominance is their ability to form vast supercolonies, with individuals collaborating over distances of several kilometres. From a social evolution standpoint, this lack of boundaries between local nests is puzzling because, in theory, local cheaters should be able to exploit global cooperation. The current spread of the ant species *Tapinoma magnum* in Germany enables us to observe the expansion of an invasive ant species in real time, helping us to better understand how local invasions turn into large supercolonies. We collected ants from locations in the Upper Rhine Valley where *Tapinoma* has become established within the last five years, and we investigated the genetic structure of the population. At the same time, we conducted behavioural experiments and analysed nestmate recognition cues to determine whether a supercolony had formed. Our findings suggest that the Upper Rhine Valley has been invaded by ants of different origins, some of which are part of the same supercolony, but not all. Using these data, we have reconstructed the possible invasion history and proposed different scenarios for how supercolonies can form from initially separate local invasions.

Maiden Flights of Common Swifts: New Tracking Devices Collect First Migration Data of Young Swifts

ECO
515

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While animal migration has become a topic of large interest, data sampling comes with a variety of challenges. For researchers studying small animals tracking individuals remotely comes with limitations to sampling sensor data and accuracy of location data. More accurate and complex tracking devices can only store but not send data and therefore animals have to be recaptured after the migration event to retrieve the device.

In this study the autumn migration of Common Swifts (*Apus apus*) was tracked. For tracking the migration of adult Swifts GPS tags are widely used, however these need to be retrieved to receive data. Compared to adult Swifts, which return to their breeding colony yearly, young swifts return to their hatching place at a much lower rate. Therefore, these GPS tags are not suitable for tracking young Swifts' first migration.

With a new generation of the ICARUS-TinyFox tags we received first real-time data on the maiden flights of Common Swift fledglings on their way to Africa. These tags use the Internet of Things (IoT) and collect various types of sensor data while including positional estimates of the birds in Europe.

Here we present new migration data of adult and young Common Swifts of two breeding colonies in Germany. While giving an overall idea of what is possible when using novel technologies, this study is the first one to track the autumn migration of young Swifts. Here we would like to share our experiences and present first information on the migration performance of Swift fledglings.

Variability and heritability of cuticular hydrocarbons in a parasitoid wasp

ECO
516

Christopher Winkler; Martin-Stribor Vukusic-Jerman; Daniel de Luca; Dr. Tamara Pokorny

University Regensburg

The insect cuticle is covered by a lipid layer, primarily cuticular hydrocarbons (CHCs). They protect the insect from desiccation, while the species-specific CHC profiles are often additionally used for communication. On the one hand, successful communication requires stable signals, while on the other hand, CHC profile plasticity in response to environmental conditions may be essential to prevent desiccation. Enzymes involved in the biosynthesis of CHCs are genetically determined, but internal and external factors may influence pathway regulation. To understand the differential effects of genetics and temperature on CHC profiles, we studied *Tachinaephagus zealandicus*. This parasitoid wasp uses CHCs for mate recognition, and females additionally exhibit a CHC polymorphism with three distinct chemotypes. We investigated CHC heritability, and variability in response to differing temperatures during development and also during adulthood. Chemotypes remained distinct, indicating that chemotypes are genetically determined. Within-chemotype variability was influenced by wasp lineage, showing that genetic factors influence the composition of CHC profiles also on a finer scale. In addition, temperature affected CHC profiles in all chemotypes. Changes in CHC composition related to temperature may be an adaptation to climatic conditions, which could affect CHC-based communication.

Opening museum collections for ecological and evolutionary research

ECO 517

Prof. Dr. Marie (Mariella) Herberstein

Leibnitz-Institut zur Analyse des Biodiversitätswandels

Research museums hold millions of specimens in their collections. The collection of the Leibniz Institute for the Analysis of Biodiversity change alone contains over 16 million zoological, mineralogical and paleontological specimens. Each object holds a wealth of data, including spatial and temporal signatures, molecular data and traits data. We want to unlock these data and thus the value of museum collections in answering questions about the past and future of biodiversity. The key to opening up these collection and mobilising the data within is digitisation and collaboration with ecologists and evolutionary biologists. Here I present examples of digitised collections from the LIB to illustrate how, at a broad temporal and spatial scale, the data held by museum specimen can be used to answer questions in community ecology, trait evolution or functional morphology.

“Seq and the city” – linking biodiversity, genomic and earth observation data to investigate the ecology and genetics of urban *Drosophila*

ECO
518

Dr. Martin Kapun; MSc Sonja Steindl; Dr. Elisabeth Haring

Natural History Museum of Vienna

Several fruit fly species of the genus *Drosophila* are common human commensals, yet their ecology in urban environments remains understudied. We launched a Citizen Science project all across Austria to sample *Drosophila* specimens in- and outdoors – particularly focusing on the capital city of Vienna and neighboring suburban areas, engaging 168 participants. From May to December 2024, 91 participants returned 278 traps, yielding 19,100 flies from 13 species. Notably, *D. virilis* and *D. mercatorum* were recorded in Austria for the first time, with *D. mercatorum* dominating in urban environments. By combining species abundance data with comprehensive climatic, demographic, economic and other earth observation data available for the sampled geographic region, we performed species distribution modeling, which revealed that *D. melanogaster* preferred semi-natural areas, while *D. mercatorum* was dominant in highly disturbed urban sites. Moreover, by investigating genome-wide data from more than 40 pooled *D. melanogaster* samples in the context of quantitative genomic data from hundreds of European *Drosophila* samples collected in rural areas, we find that urban flies from Vienna are closely related to fly populations collected in close-by regions, which indicates that their genetic composition is predominantly influenced by local populations. However, a few outlier samples show signals of migration from distant populations – most like as a result of human economic traffic. A final survey indicated strong participant engagement and increased interest in biodiversity. Our project demonstrates the power of Citizen Science in studying urban insect ecology while fostering public interest in science.

Multiscale niches of predators in a human-dominated landscape

ECO
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🎓

Katharina Kasper; Stephanie Kramer-Schadt; Elise Say-Sallaz; Marcin Churski; Paulina A. Szafrańska; Dries P. J. Kuijper; Aimara Planillo

Human-dominated ecosystems reshape wildlife communities, particularly predator-prey relationships. Humans often function as super-predators and suppress or extirpate conflict-prone carnivores. As such, the gray wolf (*Canis lupus*) is only recently returning to former ranges across Europe after centuries of absence, negotiating its place alongside other carnivores, wild prey, and a diverse patchwork of human disturbance. We investigated spatiotemporal habitat use and species interactions using a systematic camera-trapping survey in Poland's Tuchola Forest – a landscape recolonized by wolves approximately a decade ago. Our models reveal distinct temporal patterns and scale-dependent associations, highlighting a tense push-and-pull dynamic in which wolves are drawn towards prey while avoiding human activity. Despite a legal hunting ban, wolves continue to exhibit fear of humans. They co-occur with mesopredators and show limited direct association. While much ecological research remains focused on protected or low-impact areas, our study offers insight into adaptive strategies and niche partitioning under layered pressures in a densely human-modified landscape.

Automated invertebrate measurements: a case study on *Daphnia*

ECO
520

Philipp Kropf[1]; Dr. Magdalena Mair[2]; Prof. Dr. Christian Laforsch[2]; **Dr. Matthias Schott[2]**

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Accurate measurements of the body structures of invertebrates are essential for researching life history and phenotypic plasticity, as well as for studying sublethal ecotoxicological effects. To enable faster, more reliable measurements, we have developed an open workflow that uses You Only Look Once convolutional neural network (YOLO-CNN) algorithms to automatically recognise body parts and measure body dimensions. We tested the precision and accuracy of this method using members of the zooplankton genus *Daphnia*, which is an ecological keystone. *Daphnia* body part measurements are carried out in laboratories all over the world as time-consuming and expensive experiments. Reliable detection of *Daphnia* body parts in our test datasets, including low-quality images, enabled us to make automated measurements of body regions with human precision, but without observer bias. Additionally, we were able to utilise a standard convolutional neural network (CNN) to classify species. Our current model can classify images of *D. magna*, *D. pulex*, *D. longicephala*, *D. longispina* and *D. cucullata* with 99% accuracy. Automated recognition of the heart region, combined with frequency amplification, enables automated measurement of *Daphnia* heart rates. Our model and algorithms are open source and adaptable to other research questions.

Inbreeding and demography interact to impact population recovery from bottlenecks

ECO 521

Dr. Jia Zheng[1]; Ella Rees-Baylis[1]; Dr. Thijs Janzen[2]; Prof. Zhengwang Zhang[3]; Prof. Xiangjiang Zhan[4]; Prof. Daiping Wang; Prof. Xiang-Yi Richter[1]

[1] University of Bern
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[3] Beijing Normal University
[4] Chinese Academy of Sciences

Biodiversity loss driven by climate change and human activities poses a critical global challenge. Population restoration and reintroduction programs are essential for mitigating this threat to endangered species, yet their outcomes often remain unpredictable due to poorly understood success factors, such as the inevitable inbreeding during bottleneck events. The conservation program of the crested ibis (*Nipponia nippon*) marks a successful example where the population rose from just seven individuals to over 9,000 in the past four decades. By developing an individual-based model that simulates the restoration process and incorporates species-specific demography and inbreeding data, we conclude that this successful restoration is mostly repeatable, as our results closely mirror empirical recovery time and population-level inbreeding coefficients. To establish general guidelines for reintroduction programs, we compared how inbreeding depression influences the recovery success of two reintroduction strategies involving small founder populations. Our simulations reveal that the ‘firework’ approach (one-source translocations) outperforms the ‘stepping-stone’ (serial translocations) approach in restoration effectiveness. Furthermore, by expanding analyses over a broad demographic space, we demonstrate that the net effect of inbreeding varies with species-specific demography and highlight the importance of considering their interaction when interpreting conservation outcomes and designing future reintroduction programs.

Mate assessment in an insect with a pheromone polymorphism

ECO
522

PD Dr. Tamara Pokorny; Simon Franke; Maximilian Steurer; Oliver Maier

University Regensburg

Mate assessment and preference for mates of higher quality can enhance an individual's fitness. Cues that correlate with, e.g. fecundity, often elicit preferential choice/higher courtship investment, and intraspecific mate preference can thus indicate the presence of such cues. In the parasitoid wasp *Tachinaephagus zealandicus*, males show differential preferences for females exhibiting different chemical phenotypes (chemotypes). However, female chemotype does not influence the number of offspring. We investigated whether male preference relates to beneficial fitness returns in another way. In many insects, female body size is an indicator of fecundity, as larger females usually can produce more eggs than smaller ones. Thus, males were confronted with two females of the same chemotype, but of different body sizes. Relative fitness, i.e., the relative number of daughters, was indeed higher for the paring with the larger female. However, males invested more time courting the larger females only in two of the three chemotypes - those that were preferred in previous bioassays. This suggests that in this species, mate assessment is not based on visual or tactile cues, but rather on chemical ones.

The impact of *Microcystis aeruginosa* on *Daphnia magna* is shaped by ambient temperatures

PHY
601

Prof. Dr. Bettina Zeis[1]; Nadine Hoffschröer

[1] Universität Münster

Along with increasing temperatures and eutrophication of lakes by nutrients, harmful algal blooms frequently challenge aquatic zooplankton organisms. Their poor food quality is due to lacking cholesterol and poly-unsaturated fatty acids. As ectothermic planktonic crustaceans show high metabolic rates, high growth rates and fast reproduction in warm conditions, their elevated demand for food must be met by high food ingestion rates at elevated temperatures. Accordingly, the detrimental impact of low-quality-food was assumed to increase corresponding to rising ambient temperatures. *Daphnia magna* were fed with the green algae *Desmodesmus subspicatus*, the cyanobacteria *Microcystis aeruginosa* or a mixture of both. Strains of *M. aeruginosa* free of microcystin but containing inhibitors of the digestive proteases chymotrypsin or trypsin (NIVA Cya 43 or PCC 7806) were used. Animals were acclimated at 10°C, 20°C and 30°C. Life table experiments documented impacts of the food regime and temperature conditions on growth and reproduction. The concentration of stored carbohydrates, lipids and proteins determined after 48 hours at various feeding conditions was affected by the ambient temperature as well as by the quality of the offered food. When only cyanobacteria were available, the energy status was comparable to starvation conditions. The energy reserves were depleted most strongly at warm temperatures. However, growth and reproduction were negatively affected by cyanobacteria also under cold conditions. The role of inhibition of the respective proteases will be discussed.

The effect of salinity and shore height on the energy stores of the beadlet sea anemone *Actinia equina*

PHY
602

Dr. Amanda Wiesenthal[1]; Pascal Lüder[1]; Dr. Jack Thomson[2]

[1] University of Rostock
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The intertidal zone is a challenging habitat because it is highly dynamic and organisms must cope with several abiotic factors such as extreme temperatures, UV radiation, periodic air exposure or the mechanical force of waves. Extreme heat and sun radiation can lead to evaporation from rock pools and consequently increase the salinity, while heavy rain introduces freshwater to the habitat and decreases salinity in rock pools. The beadlet sea anemone, *Actinia equina*, is found on coasts of the northeast Atlantic and Mediterranean Sea. During low tide, individuals at high shore heights either become emerged or sit in rock pools (intertidal zone), while individuals at low shore heights remain submerged (sublittoral zone) in sea water. Thus, intertidal individuals periodically experience extreme conditions. We hypothesised that intertidal individuals are more tolerant to extreme salinities and therefore deplete their energy stores less than sublittoral individuals under hypo- or hyperosmotic conditions. To test this hypothesis, *Actinia equina* were collected from the intertidal and sublittoral zones on the coast of Heligoland in the North Sea and exposed to one of seven different salinities (17, 22, 27, 32, 37, 42, 47) for at least 5 days. Subsequently, protein, lipid, carbohydrate and glycogen content were determined in tentacle and oral disc, column and pedal disc tissue. While salinity affected the protein and lipid content, carbohydrate and glycogen content were determined by shore height with intertidal individuals having consistently higher concentrations. There was, however, no conclusive evidence that intertidal individuals depleted their energy stores less than sublittoral individuals.

The role of fatty acid binding protein (FABP) in the formation of the elytral cuticle of *T. castaneum*

PHY
603

Marius Beck; Prof. Dr. Hans Merzendorfer

University Siegen

Fatty acid binding proteins (FABPs) have central functions in lipid-associated biological processes. In both vertebrates and invertebrates, they contribute to fatty acid transport, lipid homeostasis, membrane dynamics, and stress responses. In insects, they have additionally been implicated in detoxification, development, and behavior. Recent evidence from Drosophila melanogaster suggests a role for FABPs in chitin formation based on the interaction between FABP and chitin synthase 1 (CHS1).

We investigated the function of FABP in chitin biosynthesis and cuticle maturation using the elytra of *Tribolium castaneum* as a model. Injection of dsRNA into early pupae resulted in a loss of CHS1 immunosignal in the elytral epidermis and impaired chitin deposition. The pupae continued to develop into adults, but the adult elytra were crinkled and transparent. The latter finding suggests some defects in melanization.

Our results indicate that FABP is not a core factor of chitin biosynthesis but acts as a modulatory or accessory protein, possibly stabilizing CHS1, promoting its membrane association, or enabling lipid-based trafficking.

To further explore the role of FABP in melanization, we investigated the impact of dopamine on cuticle maturation through RNAi and immunohistochemistry. Our results suggest that FABP may serve as a regulatory link between lipid metabolism, chitin synthesis and processes essential for post-molting cuticle maturation.

Life on hold: a physiological model of a low-temperature clock in a diapausing insect *Pieris napi*

PHY
604

Anouck Four-Chaboussant; Dr. Philipp Lehmann; Dr. Sabine Ziesemer

Greifswald University, Zoological Institute and Museum

To cope with seasonally occurring stress, such as winter, animals have evolved different survival strategies. Insects use diapause, a type of deep dormancy, characterized by an arrest in ontogenetic development, to survive seasonal stress. Diapause usually consists of three physiologically distinct phases: initiation, maintenance, and termination.

Research has thus far mainly focused diapause initiation, leaving a gap in knowledge on diapause termination. This is surprising, since diapause termination is critical for emergence synchrony in spring. Studies on *Pieris napi*, a pupal diapauser, reveal that accumulation of cold temperatures drive diapause termination. Only after diapause has been terminated can ontogenetic development resume. The molecular mechanisms of this cold accumulation remain unclear.

Since diapause manifests as an arrest in development, it is most likely regulated by the development hormonal pathway. In insects the main developmental hormones are the prothoracicotropic hormone (PTTH) and 20-hydroxyecdysone (20E), with PTTH stimulating 20E production. Here I present patterns of PTTH production and release, the availability of the PTTH receptor Torso, the production of 20E and the availability of the 20E receptor, throughout non-diapause and diapause development.

Preliminary results demonstrate that PTTH, Torso, and the 20E receptor show different patterns in non-diapausing and diapausing pupae, with high dynamics in the former, and almost none in the latter. Still, all members of the PTTH-ecdysone axis are detectable also in diapausing pupae, with conspicuous patterns when diapause presumably is terminating. After pupae have terminated, they display similar dynamics in these hormonal factors as do directly developing pupae.

Structural Organization and Chitin Composition of the Peritrophic Matrix in *Tribolium castaneum*

PHY
605

Mario Wegmann; Prof. Dr. Hans Merzendorfer

Universität Siegen

The gut of most insects is lined by the peritrophic matrix (PM), a semi-permeable membrane essential for digestion and protection against mechanical stress, chemicals, and pathogens. While recent research has elucidated many functional aspects of the PM, the molecular mechanisms underlying its structure and physicochemical properties remain poorly understood. In particular, the roles of peritrophic matrix proteins (PMPs) and chitin modifications by chitin deacetylases (CDAs) and chitinases (CHTs) in shaping the 3D organization of the PM are largely unexplored.

To assess the impact of the degrees of deacetylation and polymerization on PM structure, we systematically silenced TcCDA genes via RNAi in the model beetle *Tribolium castaneum*. We analyzed phenotypic consequences on growth and viability and examined physicochemical properties of the PM. Mass spectrometric determination of the degree of acetylation (DA) revealed a strikingly high DA of 0.979 ± 0.008 (± SD, n=3). Knockdown of TcCDA8 and TcCDA9 increased DA by ~1.4% to 0.993 ± 0.01 (± SD, n=3). Additional CDAs and group IV CHTs (e.g., TcCDA6, and TcCDA7) were investigated for their roles in organizing the chitin network. To directly probe chitin structure, we performed X-ray diffraction (XRD) analyses on PM samples at BESSY II. The resulting data confirmed that the PM primarily consists of β-chitin, with no significant differences in chitin allomorphs across anterior, median, or posterior midgut regions. These structural insights complement our biochemical data and support a model in which PM integrity depends on both chitin modifications and the supramolecular organization throughout the gut.

Why age matter: effects of bumblebee age on flight performance

PHY
606

Milena Gilgenreiner; **Dr. Christoph Kurze**

Universität Regensburg

Flight is essential for insect pollinators, such as bumblebees. Despite their relatively large body size, bumblebees exhibit impressive flight capabilities, enabling them to navigate challenging conditions. While their body size has been linked to foraging range and flight ability, the influence of age remains less explored. Our research revealed that age was the mainly affected flight distance and duration, while body size had a minor effect. However, we found that flight speed is predominantly affected by body size. Our findings challenge the prevailing notion that body size is the primary determinant of flight performance in bumblebees, suggesting that age plays a more significant role in shaping their foraging behavior and task allocation within the colony.

Love your Data! -- Kickstarting Data Organization with a Dedicated Folder Template

SYS
701

Dr. Jeanne Wilbrandt

Leibniz Institut für Alternsforschung - Fritz-Lipmann-Institut (FLI)

It is essential for researchers to create findable, accessible, interoperable, and reusable (FAIR) data and metadata. To achieve this, effective research data management (RDM) is crucial -- as increasingly acknowledged by policies and funders. FAIRness and good management of research (meta)data hinge upon being organised and documented in an understandable manner, which includes consciously storing files in a clear folder structure.

It is a good idea to establish a sensible folder structure early in a project, however little knowledge about upcoming needs and potential struggles often thwart especially junior researchers from deliberate planning. Here, ready-made templates can provide a standardized starting structure, saving time and resources that would usually be required to lay out and expand or restructure a folder structure as a (thesis) project unfolds.

We recently developed* a folder structure template that comprehensively covers the storage needs of early career researchers in the life sciences beyond data production for a single work package; i.e., comprising space for administrative documents, presentations, etc. Additionally, the template is enriched with RDM best practice guidance and metadata recording prototypes to promote informed, sustainable RDM habits.

This talk will cover the basics of RDM -- repetition never hurts -- and present our folder structure template and its features. It aims to encourage researchers, students, and PIs to talk about RDM, review their habits, and collectively shift academic culture towards more love for data.

Descriptron: Testing Artificial Intelligence for Automating Taxonomic Species Descriptions with a User-friendly Software Package

SYS 702

Alex Van Dam PhD; Dr. Liliya Štarhová Serbina PhD

Museum für Naturkunde Berlin

Descriptron is a platform that automates morphological feature extraction using CNN-based computer vision and seamlessly integrates vision–language models (VLMs) like GPT-4o to generate taxonomic species descriptions from labeled biological images. Our evaluation shows that GPT-4o integrated via Descriptron dramatically accelerates the production of morphological descriptions and taxonomic keys, though its outputs still require expert taxonomist oversight to correct residual errors and prevent hallucinations. Freely available under an Apache 2 License, Descriptron represents a substantial advance toward automating species description workflows while preserving the indispensable role of human expertise. Descriptron is available from: https://github.com/alexrvandam/Descriptron.

Latitudinal genetic diversity gradients steepen toward the poles

SYS
703

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The latitudinal gradient in biodiversity is a well-known biogeographic pattern. Multiple components of global biodiversity, including species richness, phylogenetic diversity, and functional diversity, decrease from the equator to the poles. Though genome-wide genetic diversity is an important component of biodiversity that underlies species' adaptive potential, whether it also varies latitudinally like other forms of biodiversity is unclear. Additionally, unlike other biodiversity patterns that are typically measured at the species level, genetic diversity has both within- and between-species components that may each be predicted to covary with latitude. Within-species genetic diversity patterns emerge in part from population-level microevolutionary processes, while spatial patterns of genetic diversity between species are products of species-level variation and species turnover. Together, within- and between-species patterns of genetic diversity can contribute to a more comprehensive understanding of the evolutionary and ecological processes maintaining global biodiversity patterns. The increasing availability of publicly accessible, neutral nuclear genetic data allows us to investigate whether a latitudinal gradient also exists in genome-wide genetic diversity. Here, we use a unique dataset of nearly 60,000 individual microsatellite genotypes sampled from 100 mammal species and 1426 local populations to investigate latitudinal patterns of genome-wide genetic diversity. We found no evidence for an overall latitudinal gradient in genetic diversity within or across species, however we detected a marked pattern of increasingly positive latitudinal gradients within species distributed at higher latitudes. We will discuss our results in light of hypothesized processes underlying the species richness gradient and their predictions regarding population-level processes.

Genomic basis for the mito-nuclear discordance in *Elephas maximus*

SYS
704

Kristín Erla Tiedemann; Dr. Patrick Arnold

University Potsdam

The Asian elephant *Elephas maximus* possesses two deeply diverged mitochondrial haplogroups termed α and β, which co-occur almost in the entirety of the species' geographic range. Such coexistence of two divergent clades within the same region is rather unusual, as stochastic extinctions of mitochondrial lineages through random genetic drift are generally the norm. On the nuclear level, there is no distinction between α and β individuals among mainland elephants, but there is a distinction between elephants inhabiting the Sunda Islands Borneo and Sumatra to the remaining mainland elephants. The aim of this study was to unravel the underlying cause of this mito-nuclear discordance by performing several genomic and phylogenetic analyses on the nuclear genomes of 22 Asian elephants. We specifically investigated whether this pattern originated due to incomplete lineage sorting, introgression of an extinct lineage, secondary contact after allopatry or sex-biased dispersal. Our results argue against introgression of an extinct lineage as well as secondary contact after allopatry as potential causes for the mito-nuclear discordance. Incomplete lineage sorting among populations or retention of ancestral polymorphism in a single large population appear to be the most plausible explanations for the mito-nuclear discordance in the Asian elephant. This research highlights that relatively simple stochastic processes can result in confounding patterns in phylogenetic markers like the mitochondrial genome. The inferred population structure and demographic history could have further implications for elephant conservation and management.

Museomics as a tool to study the phylogeography of rare African small mammals

SYS
705

Dr. Patrick Arnold

University Potsdam

The African continent harbors a rich diversity of small mammals, especially in tropical forests and savannas. Many species tough face significant threats from habitat loss due to agriculture, deforestation, urbanization, and climate change, and thus might be lost before even formally described. Nevertheless, African small mammals remain poorly understood and are notoriously understudied due to limited infrastructure in remote areas, habitat inaccessibility and political instability. As a result, genetic samples for phylogeographic analyses are often hard to collect. Here, I show that this obstacle can be overcome with the use of museomics, especially for rare mammal species with little economic impact such as sengis, otter shrews and golden moles. Museomics is an emerging field that aims to extract and analyze archival DNA from the uncounted specimens housed in historical museum collections. Advances in laboratory and bioinformatic methods now allow to deal with the problems of low DNA quantity but high fragmentation. Applying this approach to skin samples of sengis, otter shrews and golden moles proves its suitability across different taxonomic groups and museum collections. Deeply divergent but morphologically cryptic intraspecific lineages are uncovered in all three test cases. These lineages do not fit traditional taxonomy of the clades but are often related to comparatively old biogeographic events such Mio-Pliocene fragmentation of ancient pan-African forests. Minimally-invasive sampling of historical study skins thus offers a valuable resource for these rare animals.

SYS
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Genomic diversity in otter shrews (Mammalia, Afrosoricida, Potamogalidae)

Lara Dreide; Dr. Patrick Arnold

Universitaet Potsdam

Little is known about the semiaquatic, afrotherian family of otter shrews (Potamogalidae). The most prominent member is the Nimba otter shrew (*Micropotamogale lamottei*), which is native to the Mount Nimba area in West Africa and classified as “Vulnerable” by the IUCN Red List. The Potamogalidae includes two additional species: the giant otter shrew (*Potamogale velox*) and the Ruwenzori otter shrew (*Micropotamogale ruwenzorii*), found in Central Africa. Both species are classified as “Least Concern”. The Nimba and Ruwenzori otter shrews in particular suffer from habitat loss and fragmentation due to deforestation and mining, as well as from fish traps.

In this study, we aimed to gain a better understanding of their genomic variation and population structure, focusing on *M. lamottei* and *M. ruwenzorii*, to estimate and compare their conservation status. We assembled genomes for all three potamogalid species and assessed heterozygosity and population structure of *M. lamottei* and *M. ruwenzorii*. All world-wide available tissue samples were included in the analysis, resulting in a sample size of seven for *M. lamottei* and twelve for *M. ruwenzorii*.

The results indicated low heterozygosity, with theta values ranging from 0.0004 to 0.0009 for both species. Principal component analysis revealed clustering by geographic location, indicating smaller habitat ranges and limited gene flow. Genetic variation can significantly contribute to a population's vulnerability and may be enhanced by isolated populations. Studies concerning population size and ecological requirements would be beneficial, and a reassessment of the IUCN Red List status may be justified.

A novel genus of freshwater isopods (Phreatoicidea) from Tasmanian caves

SYS
707

Christopher Schreier[1]; Dr. George D.F. Wilson[2]; Prof. Dr. Stefan Richter[1]

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Cave and groundwater crustaceans, along with their adaptations to extreme habitats, have always been a source of great fascination. Due to their long isolation, reconstructing the pathways into subterranean environments is almost unfeasible for taxa such as Spelaeogriphacea, Stygiomysida, and Thermosbaenacea. Taxa with both surface and cave species, such as the genus *Anaspides* within Anaspidacea, offer a more tractable approach to this problem. Research on cave colonization among freshwater isopods has concentrated exclusively on the genus *Asellus*.

The isopod suborder Phreatoicidea offers an ancient group with a Gondwana distribution and the highest generic diversity on the Australian island of Tasmania. In addition to surface-dwelling species, cave-dwelling representatives from three families (Amphisopidae, Hypsimetopidae, Phreatoicidae) are also known. Here, we report a new cave-dwelling genus of the Phreatoicidae from the island of Tasmania. So far, potential new species have been collected from four caves within the Mole Creek karst system, including Marakoopa Cave II, Diamond Cave, Mersey Hill Cave, and Den Cave. These cave-dwelling phreatoicids exhibit classic troglomorphic traits such as depigmentation, reduced eyes, and elongated appendage. Light microscope and confocal laser scanning microscope (cLSM) images were applied to generate detailed images of these species. The morphological features of these presumptive new species were added to a DELTA dataset of nearly 900 characters for characterizing new species and identifying the closest relatives of the new genus. Additionally, the genetic differentiation within the genus has been studied using COI as well as SNPs using the double-digestion restriction site-associated DNA (ddRAD) approach.

SYS
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Disentangling cryptic diversity in the honeypot ant species complex of *Myrmecocystus mendax*

Nils Rensing; Dr. Magnus Wolf; Prof. Dr. Jürgen Rudolf Gadau

Universität Münster

The genus *Myrmecocystus*, colloquially known as “honeypots”, is a unique group of desert-dwelling ants possessing multiple rare life history traits. The taxon is most famous for producing replete workers, a food storage cast providing resistance to nutrient scarcity. Due to multiple revisions and species reassignments, the *Myrmecocystus* taxonomy has remained both turbulent and unresolved. Both morphological measures and molecular taxonomies have indicated the existence of cryptic species, specifically inside the *M. mendax* species complex. We investigated the *M. mendax* complex with a combination of phylogenomic and population genomic approaches to disentangle cryptic clades with high resolution. Our sample set comprised 140 *Myrmecocystus* individuals from the South-Western USA as well as Mexico, with a focus on including multiple specimens per morphospecies. A set of 2519 UCEs (Ultraconserved Elements) was compiled to provide a genome-wide sampling suitable for intraspecific delimitations. Our phylogeny shows multiple distinct clades for both *M. mendax* and *M. placodops*. In *M. mendax*, the separated clades are allopatric and show signs of ancestral gene flow. Contrarily, gene flow is absent between the separated *M. placodops* clades in spite of sympatric samples. Our evidence strongly indicates the existence of at least two undescribed *Myrmecocystus* species, adding confidence to the idea of crypsis as a common phenomenon in ants.

Fine-scale ecological insights into terrestrial mammal and bird communities in two tropical forest ecosystems of the Greater Annamites ecoregion

SYS
709

An Nguyen; Dr. Andrew Tilker; Dr. Rahel Sollmann; Dr. Andreas Wilting

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Understanding biodiversity distribution is fundamental to advancing ecological theory and informing effective conservation. At broad spatial scales, such as global or regional levels, tropical rainforests are widely recognized for their exceptional species richness and have accordingly received high conservation priority. However, these broad-scale patterns often mask ecological variation at finer spatial scales and offer limited insight for ecological understanding of species occurrences and site-level management. We hypothesized that the global paradigm of high diversity in tropical rainforests forests would also apply to terrestrial mammal and bird communities in the Greater Annamites ecoregion. To test this, we analyzed camera-trapping data from two distinct forest ecosystems in southern Viet Nam using multi-species occupancy models. In the Langbian Plateau, a landscape of broadleaf evergreen and coniferous forests, species richness was highest in broadleaf evergreen forest, particularly in remote and less rugged areas. In contrast, in the nearby coastal dry forest ecosystem of Nui Chua National Park—where habitats range from low-elevation dry forest to high-elevation evergreen forest—species richness was lowest in broadleaf evergreen forest and peaked in the transitional semi-dry forest ecotone, forming a hump-shaped diversity pattern along the habitat gradient. These results suggest that global diversity paradigms should not be assumed to apply uniformly at local scales. Across both landscapes, species occurrences and diversity patterns were strongly shaped by habitat structure and anthropogenic influences. Our study highlights the ecological importance of fine-scale biodiversity research, particularly in habitats often overlooked by broader assessments, and underscores its value in informing local conservation planning.

Comparative phylogeography and speciation in correlation with glaciation and cave colonization in Tasmanian mountain shrimps (*Anaspides*, Anaspidacea, Crustacea)

SYS
710

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The Tasmanian Mountain Shrimps (*Anaspides* spp.) are enigmatic freshwater crustaceans and prefer cold and clear waters, which they mostly find high up in the mountain areas and in various cave systems all over the island. Their current distribution is heavily influenced by the Pleistocene glaciations as most habitats such as mountain tarns and pools, creeks, runnels, and rivers in alpine areas are of postglacial origin. This glaciation also led to multiple independent colonization's of caves, with some of these lineages having evolved into obligate cave dwelling species. Moreover, the glaciation also played a crucial role in speciation and separation of population, which is especially obvious in the A. richardsoni species clade. This species clades comprises 6 closely related species, with one being an obligate cave dweller (*A. eberhardi*), some having surface and cave forms (e.g. *A. richardsoni*) and one being only found in a single big post-glacial lake (*A. spinulae*).
Using various genetic methods such as ddRAD and Sanger sequencing, we analyzed the relationships within this species clade, the mode of speciation as well as the number of independent colonization's into the subterranean habitat, their population structure, underground migration patterns and interaction with surface populations. Furthermore, we use molecular clock approaches to date these migration events.

Biogeography and diversity of the land-locked atyid freshwater shrimps of Sulawesi, Indonesia

SYS 711

Dr. Thomas von Rintelen[1]; Muhammad Iqram; Dr. Kristina von Rintelen

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Within the Indoaustralian Archipelago, Sulawesi stands out for its exceptional diversity of atyid species, with 63 species in five genera recorded, mostly in the genus *Caridina*. Most of these species are endemic to the island (n=44) and most of these are found in the island's ancient lakes, which have historically been the primary focus of research on Sulawesi's *Caridina*. The origin of atyids on Sulawesi and their species diversity in the island's rivers has not been well studied to date, though.

Based on sampling across the entire range of Sulawesi's endemic atyids, we have addressed (1) the timing and origin of their colonization of Sulawesi in relation to the island's paleogeography, (2) the relationship between geological and catchment changes and their subsequent diversification, and (3) the species diversity and distribution of endemic *Caridina*, by calculating divergence times using sequences from two mitochondrial gene fragments and deducing the ancestral ranges of species.

Our results show that (I) the endemic atyids of Sulawesi originated from five separate colonization events; (II) the majority of endemic species fall into two major *Caridina* clades; (III) these clades exhibit a different geographic distribution in the west and the east; respectively; (IV) the diversity of riverine species is greatly underestimated; (V) our data do not support the supposed widespread distribution of some described species. In summary, Sulawesi atyids are in clear need of an integrative taxonomic revision, and further exploration of the island, especially in karst regions, is likely to reveal more endemic species.

Integrating the past into modern phylogenetics - a new "total evidence" morpho-molecular analysis of extent and fossil malacostracan crustaceans

SYS 712

Dr. Markus Grams; Prof. Dr. Stefan Richter
Universität Rostock

Combining morphological and molecular datasets is the posterchild of the "total evidence" philosophy. Yet, ever since the beginning of genetic analysis, combining datasets tended to be unbalanced, leaning more or less heavily towards molecular data - a trend increasing drastically with the constant improvement of genetic methods. Although such ever-improving molecular analyses of ever-larger datasets are of course great accomplishments, the problem of outweighed morphology is equally growing with it. Still, the endeavor of finding ways to consider phylogenetic signal from both types of data is worthwhile already in itself – and even more, it is a bare necessity for including fossil taxa into a molecular phylogenetic framework.

The malacostracan crustaceans represent a taxon with decades of phylogenetic dissent between morphological and genetic analyses. Our explorative analysis combines a new and vastly extended transcriptomic dataset with a morphological dataset of about 215 characters, scored for over 60 extant and fossil species across the taxonomic spectrum of Malacostraca (representative of all 19 extant orders). Based on our results we explore the possibilities, challenges and pitfalls of integrating fossils into a combined analysis of molecular and morphological datasets of extant taxa.

The phylogeny of nereididae based on whole genome shotgun data

SYS
713

Thilo Schulze

Georg August Universität Göttingen

Nereididae BLAINVILLE 1818 are a family of cosmopolitan marine polychaetes with over 700 species that shows considerable ecological and reproductive variability. Scientific research on this taxon has increased considerably in recent decades. *Platynereis dumerilii* is emerging as one of the main model systems studied within the clade Lophotrochozoa. Genera such as *Alitta*, *Hediste*, *Neathes*, or *Perinereis* are used in ecological, reproductive and developmental studies. Despite the presence of Nereididae in science, their ingroup phylogenetic relationships are not well resolved. We obtained sequencing and assembly data of over 80 species primarily gathered from museum collections. The phylogenetic relationships of Nereididae were investigated using three datasets: First, we deployed Patchwork, a novel hit-stitching tool designed to retrieve single-copy markers from low-quality fragmented assemblies via genome skimming to mine the BUSCO geneset. Second, we infer the evolution of mitochondrial ribosomal and protein-coding genes. Lastly, WASTER is used to create a species tree from short-reads by utilizing whole genome sequencing data. Further, we map morphological characters historically used to delimit nereidid species, as well as the evolutionary diagnostic order of mitochondrial genes onto the created phylogenies. Through this study, we not only aim to clarify many unresolved questions regarding nereidid relationships, but also highlight powerful tools for processing low-quality assemblies.

Delimiting species boundaries within the Babyloniidae (Mollusca: Gastropoda: Neogastropoda) using multi-locus phylogenetic analysis

SYS
714

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The Babyloniidae is a family of marine snails consisting of 21 species and two genera. Current taxonomic debates on the Babyloniidae are mainly due to their extremely similar shell morphologies, which have led to incorrect locality records and mislabelling in legal or illegal international trade. We have therefore constructed a phylogeny of the Babyloniidae with high species coverage (57% of the family) by using multi-- locus genes (cytochrome c oxidase subunit I [COI], 16S, and H3) with four species delimitation methods (Best Close Match [BCM], Assemble Species by Automatic Partitioning [ASAP], Bayesian Poisson Tree Process [bPTP] and Multi-rate Poisson Tree Processes [mPTP]). Based on our results, 13 clades/operational taxonomic unit were observed, which confirms pre--existing species status for 10 *Babylonia* and one *Zemiropsis* taxa: *B. areolata* (Link, 1807), *B. borneensis* (Sowerby II, 1864), *B. feicheni* Shikama, 1973, *B. formosae* (Sowerby II, 1866), *B. japonica* (Reeve, 1842), *B. lutosa* (Lamarck, 1816), *B. pieroangelai* Cossignani, 2008, *B. spirata* (Linnaeus, 1758), *B. valentiana* (Swainson, 1822), *B. zeylanica* (Bruguière, 1789) and *Z. papillaris* (Sowerby I, 1825). A monophyletic group with four species collected from Indonesia which includes *B. spirata f. balinensis* Cossignani, 2009, *B. spirata f. semipicta* (Sowerby II, 1866) and *B. angusta* Altena & Gittenberger, 1981, implying they should belong to a single species, *B. semipicta*. Additionally, we suggest *B. formosae habei* Altena & Gittenberger, 1981 should be escalated as *B. habei*, and not as a subspecies.

From Physiological Mechanism to Ecology: Using Weakly Electric Fish to Link Laboratory and Field Studies

BEH 801

Dr. Stefan Mucha

Humboldt-Universität zu Berlin

Understanding the function and evolution of behavior and physiological mechanisms requires studying them within the ecological context of the species. However, this poses a dilemma: controlled laboratory experiments are well-suited to uncover mechanisms and characterize behavior, but they rely on artificial conditions. In contrast, observations in natural environments are essential to determine ecological relevance but are often technically challenging—particularly in aquatic systems. Weakly electric fish provide a unique opportunity to bridge this gap. By detecting their self-generated electric fields, they can be monitored non-invasively in their natural habitat. Utilizing autonomous recording devices, I recorded the daily activity and presence of weakly electric fish in a severely hypoxic swamp wetland in Uganda. Combining these field observations with respirometry and morpho-physiological measurements, I found that laboratory-derived indicators of high hypoxia tolerance were consistent with sustained activity during extended periods of severe hypoxia in the field. These findings show (i) that weakly electric fish can be a valuable model for linking laboratory and field approaches, and (ii) how integrating mechanistic and ecological perspectives can provide a more comprehensive understanding of animal behavior and physiology.

Invasive ants evade toxic baits by active abandonment

BEH
802

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Invasive ants, such as the Argentine ant, pose a severe economic and ecological threat. Despite advancements in baiting techniques, effectively managing established ant populations remains a daunting challenge, often ending in failure. Ant colonies employ behavioural immunity against pathogens, raising the question of whether ants can collectively respond to toxic baits. An unexplored possibility is that ants can actively abandon toxic food, thus evading control efforts. We provided two sucrose feeders, each generating a new foraging trail, with one transitioning to offering toxic food. Six hours later, ant activity on that path decreases, while activity on the non-toxic food and the trunk trail remains unaffected, which excludes factors like population decline or satiation as reasons for the activity decline. Laboratory experiments confirmed that ants remained alive six hours after ingesting toxic food. Ant presence remains low on the toxic food path for days, gradually decreasing along the nearest section of the trunk trail. This abandonment is not driven by an aversive pheromone, and is at least in part driven by memory, but how information about food toxicity spreads is a mystery. Abandonment behaviour minimises the entry of harmful food into the nest, acting as a protective social mechanism. The evasion of toxic bait-treated areas likely contributes considerably to control failures. Understanding the behavioural response to toxic baits is essential for developing effective strategies to combat invasive ant species.

Plant- and Fungi-associated Ecological Roles of Fossil Holometabolan Larvae

BEH 803

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LMU Munich

Insects inhabit nearly every corner of the Earth and have adopted an extraordinary range of ecological roles across diverse biotopes. Each lifestyle carries its own trade-offs, and the wide variety of reproductive strategies among insects reflects the multiple evolutionary solutions to ensuring offspring survival. Some species produce large numbers of poorly protected eggs, thereby maximizing quantity over individual survival. Others invest heavily in fewer offspring, providing them with greater protection against predators and environmental stressors.

At some point in their evolutionary history, insects developed a novel strategy: depositing eggs in or near food sources that also offer shelter. This behaviour is seen in insects that lay their eggs in plant tissues or fungal bodies. These environments provide nutritional resources and protection from predation, while also buffering environmental extremes such as temperature fluctuations and desiccation. Other holometabolan insects construct protective cases from available materials.

We explore the ecological roles of holometabolan larvae with a focus on their protective behaviours. For instance, caterpillars of the moth group Psychidae construct cases from plant debris—a strategy that dates back at least 40 million years, as seen from specimens preserved in amber. Similarly, larvae of modern beetle groups such as Endomychidae (handsome fungus beetles) and Mycetophagidae (hairy fungus beetles) feed on fungi within plant or mushroom tissues. Remarkably, fossil counterparts exhibit morphologies consistent with similar ecological roles. Additionally, we report new fossil specimens that significantly extend the known record of such larvae. These findings shed light on the long-term evolutionary continuity of these larval strategies.

What is the effect of a magnetic pulse on navigation of desert ants (*Cataglyphis nodus*)?

BEH
804

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Many animal species use the geomagnetic field for spatial orientation, but the mechanisms underlying magnetoreception are not completely understood. To study how animals sense the magnetic field, we can manipulate the magnetic sense of desert ants *Cataglyphis nodus*, exceptional experimental models for insect navigation. They use their magnetic sense to align their gaze directions during learning walks. *C. nodus*' navigational system is not completely equipped from the start. At the beginning of their foraging lives, they use up to three days to perform learning walks, explorative trips around the nest entrance. During learning walks, the ants learn information about the nest surroundings and perform rotational elements (voltes and pirouettes). A pirouette is a turnabout the ant's body axis, throughout which an ant stops numerous times. During the longest stopping phase, the ant gazes at the nest entrance, an invisible hole in the ground. The geomagnetic field is a necessary and sufficient cue to align the gaze directions during learning walks. Recent work suggests that *Cataglyphis*' magnetic compass is polarity-sensitive indicating a particle-based mechanism for magnetoreception. The ferromagnetic hypothesis states that in animals detecting the geomagnetic field with a particle-based mechanism the magnetic sense should be disturbed by a magnetic pulse, resulting in a change of the behavioral response. In this study, we exposed naïve ants to a magnetic pulse. Will the ants' gazes still be directed at the nest entrance after that the ants have been exposed to a magnetic pulse? What will happen to them when they become foragers?

BEH
805

fru gene specifies cooperative male behaviors in honeybee colonies

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Behavioral interactions among conspecifics bind individuals into groups. In the Western honeybee (*Apis mellifera*) social interactions are largely innate and deeply hardwired into the nervous system, making these cooperative behaviors trackable to genetic and neurobiological investigations. However, which genes and which neural circuits program these sophisticated behaviors in the brain are unknown. Male social food exchange behavior is of special interest for this study: it newly evolved from solitary living male ancestor bees during the evolutionary shift towards eusocial organization. We screened for male-specific expressed transcription factor genes and found that only the fruitless gene was solely expressed in male nervous system. GFP co-expression showed that the fru gene is spatially restricted expressed in the nervous system. Computer-assisted behavioral tracking of male bees with loss-of-function mutations in experimental colonies revealed that fru is specifically required for the rate and/or duration of social approach and feeding behaviors, suggesting that the gene scales the bee's participation in the collective nutrition task. However, general sensorimotor functions remained unaffected, suggesting a specific role in specifying cooperative behaviors. Effects on a sex pheromone response suggest that the fru gene still has a conserved role in hardwiring sexual behaviors as in other insects. These comparison with other insects suggest the fru gene has been evolutionary co-opted in honeybees to specify cooperative behaviors. Together, our study establishes a gene-based specification of behavioral decision processes and provides insight into the connection between cooperation and defined neural populations.

Better Together – How Sibling Presence and Kinship Shape Benefits Across Family Contexts

BEH
806

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University of Bayreuth

Parental care is traditionally considered the primary driver of family life, but family groups entail much more multifaceted interactions between their members. Offspring interactions, for example, range from fierce competition to cooperation. Sibling cooperation is a key feature of eusociality, and recently emerging views hypothesize that it might have been a major driver in the early evolution of social and family life. Nevertheless, while the effects of isolated family interactions have been extensively studied, the intricate dynamics between different family interactions and their reciprocal impacts, especially in subsocial species, have gained little attention. For instance, while examples of sibling cooperation were found in the absence of parental care, in the presence of parents, siblings were seen as rivals for resources, competing for parental attention, thereby aggressively fighting each other, jostling for the best position, or exaggerating begging signals. Using a full-factorial social isolation experiment in the subsocial burying beetle *Nicrophorus vespilloides*, where we isolated offspring from siblings and/or parents, we showed that offspring benefited from the presence of both, parents as well as siblings. Surprisingly, the positive effects of siblings were evident in the absence but also the presence of parents, though they manifested differently. Without parents, growing alongside siblings resulted in higher larval mass at dispersal, while in the presence of parents, having siblings accelerated early growth and increased survival. Our results further show that relatedness amplifies the positive effects on growth but also increases mortality rates in the late development stages.

Assessing the impact of realized relatedness on primate sociality using whole genome sequencing

BEH
807

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Genetic relatedness is a key factor in the evolution of social behaviour through kin selection. While pedigrees have traditionally been used to estimate relatedness, they offer only average expectations for pairs of individuals within a given kin class. However, due to recombination, the actual amount of DNA that is identical-by-descent (IBD), also referred to as realized relatedness, can vary greatly among pairs within the same kin class. This results in overlapping distributions of relatedness between different kin classes. In this study, we examine whether and to what extent realized relatedness shapes kin discrimination and kin-biased behaviour beyond what can be explained by pedigree estimates. To do so, we studied multiple groups of free-ranging rhesus macaques (*Macaca mulatta*) on Cayo Santiago, Puerto Rico, for which extensive long-term behavioural and experimental data on social preferences are available. We will discuss two major parts key components of this ongoing study. First, we recently developed a method to accurately quantify realized relatedness using whole-genome sequencing data, demonstrating that we can infer the number and length of DNA segments that are IBD across the genome with high accuracy even at 0.5× sequencing depth. Second, applying this approach to a dataset of 850 individuals, we found that realized relatedness explains social behaviour and affiliative preferences differently compared to pedigree relatedness. Integrating genomic and behavioural data offers a novel framework for understanding the mechanisms of kin recognition and yields new insights into the strength and variability of kin bias in animal societies.

Importance of native and ornamental plants as a food source for insect pollinators

BEH
808

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"Humans cultivate ornamental plants since thousands of years. Because they are not used for food consumption, they are bred as decorative elements and therefore often show enhanced and altered visual features, like changes in flower colour, patterns and size.

However, for insect pollinators, these visual flower features are important for all stages of foraging, including flower choice, approach flight, landing guidance, and nectary search, thereby reducing the energy spent during a flower visit. Although interactions between insect pollinators and ornamental plants have been studied, no detailed investigation of how visual appearance impacts flower visits compared to native plants exists.

In this project, we aim to understand how the visual differences of native and ornamental plants impact the use of ornamental flowers as food sources by insect pollinators. With different lifestyles, but comparable visual systems, *Bombus terrestris* and *Macroglossum stellatarum* serve as representatives for two important pollinator groups, Hymenoptera and Lepidoptera. We investigate and compare their flower preferences, foraging efficiency and nectar contents of visited flowers to assess the importance of native and ornamental plants as food sources for insect pollinators.

The Function of Wing Fanning in the Courtship of a Parasitoid Wasp

BEH
809

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Sexual signals play an important role in mate attraction and courtship. They can convey a variety of essential information such as species identity, sex, and individual quality. While some courtship signals are highly conspicuous, those in less intuitive modalities, such as chemical or vibrational signals, are often overlooked. Wing fanning, a vibrational courtship signal ubiquitous in insects is one such example. In the parasitoid wasp *Leptopilina heterotoma*, male wing fanning is condition dependent and a higher wing fanning frequency leads to increased mating success. However, in other species, wing fanning courtship behavior has also been shown to communicate male (wing) symmetry and species identity. Here, we investigated if wing fanning in *L. heterotoma* can communicate several different aspects of male quality simultaneously.

While wing symmetry is important in the acoustic courtship of *Drosophila melanogaster*, we found no such effect in *L. heterotoma*. Cutting off one or even both wings did not stop the males from vibrating their flight muscles and did not reduce their mating success.

Because, in *Cotesia* wasps, each species produces a distinct wing fanning pattern, we also investigated species specificity. We compared vibrational patterns in the wing fanning of four *Leptopilina* species and the closely related *Ganaspis xanthopoda*. We demonstrate that *G. xanthopoda* exhibits a distinctly different wing fanning pattern than more closely related *Leptopilina* species. Therefore, it is likely that wing fanning can indicate genus, but not species identity.

Composure and Decomposition: State of carcass, not parental care pattern, shapes investment into personal immunity of *Nicrophorus vespilloides* offspring

BEH
810

Leon Müller[1]; Patrick Limburg; Prof. Dr. Sandra Steiger[1]; Dr. Maximilian Körner[1]

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During the period of post-hatching care parents take over energy consuming tasks, e.g. social immunity and foraging, which benefits the offspring yet is costly for parents. Biparental care reduces the individual costs by dividing the workload between both parents, as each parent often specializes in different care aspects, e.g. males typically providing less food and focusing on brood guarding. The facultative biparental care of *Nicrophorus vespilloides* involves control of the carcass microbiome through application of antimicrobial exudates, shielding their offspring from potential pathogens. To explore how social immunity and its effect on the offspring is shaped by parental care, we presented breeding beetles of *Nicrophorus vespilloides* with old or fresh mouse carcasses and manipulated the mode of parental care during the period of post-hatching care, by removing either the female or male parent. We then investigated how offspring are affected by monitoring performance parameters as well as their investment into personal immunity and found that carcass age and mode of parental care influenced early larval development and survival, while carcass age alone affects the number of haemocytes of larvae, indicating an investment into their personal immunity depending on their surroundings. Simultaneously, our results show that uniparental care is more costly to a single parent than if the work is divided between two parents. Overall, we show that offspring of a facultative subsocial species can adjust their investment into personal immunity based on environmental threats independently of the parental care they receive.

Shaped by the city: unpacking urban syndromes in small mammals

BEH
811

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Urbanization is a rapidly expanding global phenomenon that profoundly alters ecosystems and imposes novel selection pressures on wildlife. Species that persist in urban areas often exhibit characteristic trait changes, termed "urban syndromes", including shifts in morphology, physiology, and behavior. However, the specific traits linked to urban tolerance can vary widely across taxa and regions. We examine morphological and physiological responses to urbanization in three small mammal species, wood mice (*Apodemus sylvaticus*), yellow-necked mice (*Apodemus flavicollis*), and bank voles (*Myodes glareolus*), across an urban–rural gradient in Münster, Germany. We collected data on body mass and head width, and calculated the scaled mass index as a measure of body condition (n = 617 measurements). We also obtained non-invasive measures of stress physiology via fecal corticosterone metabolites (n = 338 fecal samples). We will explore associations between morphology, body condition, and physiological stress along the urbanization gradient in all three species, assess whether consistent trait shifts emerge across species, and whether physiological stress responses are aligned with or decoupled from morphological and body condition changes. These results will help clarify whether shared trait responses constitute a common urban syndrome across species, or whether small mammals exhibit species-specific strategies for coping with urban environments.

The impact of multigenerational inbreeding on cognitive behaviour along the brain-gut axis in cichlids

BEH
812

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Reduced cognitive abilities can have severe consequences for fitness, for example when predators are not detected, food resources are not exploited optimally, or low-quality mates are chosen. Although inbreeding can greatly affect fitness-related traits, its impact on cognitive traits is not well understood. In this study, we examined the impact of multigenerational inbreeding on the cognitive abilities of the biparental cichlid fish *Pelvicachromis taeniatus*. This species exhibits kin mating preferences, which are adaptive due to the benefits of kin selection (e.g. improved brood care by related parents). We investigated the effects of inbreeding on cognition in various contexts, such as foraging, mate selection, and shoaling behaviour. Furthermore, we analysed its impact on brain and eye size and gut microbiome diversity. Our results revealed significant inbreeding effects on cognitive behaviour, eye size, brain size and microbiome diversity. We discuss potential mechanisms underlying inbreeding effects in relation to the brain–gut axis hypothesis.

Jump All Day, Sleep All Night: Establishing Sleep in the Jumping Spider *Portia fimbriata*

BEH
813

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Sleep is a universal yet poorly understood phenomenon, occurring across the animal kingdom with diverse expressions. The discovery of a REM (rapid eye movement) sleep-like state in a jumping spider has opened new paths for understanding the evolution and function of sleep across taxa. Building on this, we present a comprehensive investigation of sleep in a salticid known for its cognitive capabilities (*Portia fimbriata*).

Our work first establishes sleep-like behavior in P. fimbriata through baseline activity tracking under constant and naturalistic light conditions, revealing consolidated rest phases and circadian rhythmicity. To test whether these rest phases qualify as sleep, we measured arousal thresholds and found reduced responsiveness during REM-like states. To further explore regulatory aspects of this state, we conducted controlled sleep disruption and rebound experiments.

To broaden the ecological perspective, we present new fieldwork data from spiders collected at Australian field sites—offering a more naturalistic contrast to lab-reared populations. Investigating spider sleep in the wild will be a central focus of our future work, aiming to explore its ecological relevance and adaptive value.

Together, these findings offer emerging evidence for regulated sleep in spiders and highlight the value of combining lab and field approaches to study non-traditional model organisms—positioning spiders as a powerful system for investigating the evolution and function of sleep.

Social and personal immunity investment of three *Nicrophorus* species with varying offspring dependency

BEH
814

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Many species exhibit parental care, which provides fitness benefits to offspring, including protection against pathogens through social immunity. However, the degree to which offspring depend on parental care varies widely across species, and how this variation influences the expression of social immunity remains poorly understood. Here, we investigate both personal and social immunity in three species of *Nicrophorus* burying beetles—a model system known for elaborate parental care and social immunity. These species differ markedly in their offspring's ability to survive without parental care, ranging from complete dependence to full independence. We measured sex-specific personal and external (social) immunity in adult beetles before, during, and outside of reproductive bouts. Our results show that species with more dependent offspring invest more heavily in social immunity. In contrast, personal immunity was primarily influenced by beetle size, while reproductive state affected immunity differently across species. Parental care is a key evolutionary step toward higher sociality and understanding how offspring dependency shapes social immunity can provide valuable insights into the foundations of complex social systems.

Who to sleep with? Daytime sleeping associations in nocturnal gray mouse lemurs

BEH 815

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Many nocturnal mammals spend the day in nests or other shelters, but this aspect of their social organization remains obscure, despite interesting variation among species, seasons and individuals in whether they also sleep alone or in association with conspecifics. To contribute new comparative data on this neglected aspect of sociality, we monitored the occurrence, structure and stability of sleeping associations of 329 wild nocturnal gray mouse lemurs (*Microcebus murinus*) in artificial nests across four years. We found that most of these small primates slept in association with 1-8 other individuals, but virtually never with members of the opposite sex. A third of the individuals always exhibited the same sleeping tactic (20% always solitary, 13% always in association). Among the more flexible individuals, males, but not females, were more often found in sleeping associations during the birth season than during the annual mating season. Sleeping associations of both sexes were stable, with the same two individuals often being found together on subsequent days. Females, in particular regularly formed stable sleeping associations within seasons. In line with our predictions, the observed variation in sleeping patterns revealed a significant interaction between sex and season, highlighting a need for additional study of the drivers of individual and sex-specific tactics, such as kinship. More generally, our study exemplified implications for the classification of the social organization of species that are solitary during their period of activity and gregarious during their period of inactivity.

Identification and seasonal abundance of web- and air-borne sex pheromone components of western black widow spiders, *Latrodectus hesperus*

BEH
816

Dr. Andreas Fischer[1]; Alexandra Fischer[1]; Regine Gries[2]; Emmanuel Hung[2]; Kelvin Lau[2]; Aryan Monfrared[2]; Prof. Dr. Gerhard Gries[2]

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Widow spider males are attracted to sex pheromones disseminating from female webs. Upon arrival on a web, males court in response to web-borne contact pheromone components. N-3-Methylbutanoyl-O-methylpropanoyl-L-serine methyl ester (1) is the single known, weakly effective, contact pheromone component of female western black widows, Latrodectus hesperus. Moreover, the seasonal periodicity of pheromone signalling by female spiders is unknown. We tested the hypotheses that females of *L. hesperus* (1) deposit multiple contact pheromone components on their web that transition to mate-attractant pheromone components, and (2) increase pheromone signalling during the primary mating season. Analyses of web extract by gas and liquid chromatography-mass spectrometry (GC-MS; LC-MS) revealed N-3-methylbutanoyl-O-methylpropanoyl-L-serine (2), the corresponding acid of 1. Web extract of unmated female *L. hesperus*, and the synthetic blend of 1 and 2, were equally effective in eliciting courtship by males but web extract induced more sustained courtship. Tested singly, 2 prompted longer courtship behaviour by males than 1. Synthetic isobutyric acid (3), the hydrolysis product of 1 and 2, attracted male spiders in a field experiment. The abundance of 1 and 2 on female webs, with expected corresponding dissemination of 3 from webs, peaked during the summer when males are most abundant, indicating strategic sexual signalling by female spiders.

Cooperative breeding and sleeping associations in grey mouse lemurs

BEH
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The ecological constraint hypothesis proposes that ecological conditions, e.g. limited breeding resources, constrain dispersal and solitary breeding and promote cooperative breeding. The impact of climate and weather variables on cooperative plural breeding, where all females in a group can reproduce, are unclear. Female grey mouse lemurs, *Microcebus murinus*, forage solitarily at night, and sleep either solitarily or socially with kin; hence, they participate in solitary or cooperative plural breeding during breeding seasons. We used sleeping nest data to assess the effects of density, the El Niño-Southern Oscillation, temperature and precipitation on cooperative and solitary breeding in a wild, female grey mouse lemur population during the breeding season from 2017 to 2021 in Kirindy, Madagascar. We recorded 2192 social and 2107 solitary sleeping observations of 169 females. As density increased, the likelihood to cooperatively breed and the number of females per nest increased. These results did not support the ecological constraint hypothesis, since most nests were unoccupied. An increase in density may have increased the number of kin in the population, and female grey mouse lemurs cooperatively breed with kin. The likelihood of cooperative breeding and the number of females per nest increased with el Niño and la Niña events compared to normal phases, and there was no significant difference between el Niño and la Niña events. Temperature and precipitation did not significantly influence the likelihood to breed cooperatively and the number of females per nest. These results suggest that female grey mouse lemurs breed cooperatively when environmental uncertainty increases.

Fumigation or Self-fumigation? Protecting Small Landbirds of the Galápagos from the Deadly Impact of the Invasive Avian Vampire Fly

BEH
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Most small landbirds of the Galápagos Islands are threatened by the invasive Avian Vampire Fly (*Philornis downsi*), whose larvae feed on the blood of incubating females and nestlings, leading to high nestling mortality. Consequently, several species—including the iconic Darwin’s finches and the endemic Little Vermilion Flycatcher—have experienced significant population declines. Some island populations of the flycatcher have even gone extinct. To prevent further extinctions, it is critical to implement effective short-term mitigation strategies while long-term solutions are developed. Our study builds on two already existing insecticide-based control methods: (1) Self-fumigation, where birds incorporate insecticide-treated nesting material into their nests, that kills developing larvae, and (2) the Spritz technique, which involves spraying insecticide around the nest entrance to prevent parasite infestation. We aimed to refine both approaches to improve their effectiveness and broaden their applicability across species. We tested various nesting materials treated with a slow-release formulation of permethrin (Permacap CS®) at concentrations of 0.5% and 1%. Permacap-treated materials significantly reduced parasite loads and increased fledging success in Darwin’s finches and the Little Vermilion Flycatcher. A 1% concentration was most effective, requiring only 0.6 cm^3 of treated material to nearly completely prevent infestations in Darwin's fინces. The Spritz technique, enhanced with a lightweight, pole-compatible applicator and using 0.5% Permacap, also improved fledging success while minimizing nest abandonment—an issue previously observed with higher concentrations. Our findings demonstrate the potential of targeted, insecticide-based interventions to mitigate the impact of *P. downsi* on threatened Galápagos landbirds.

Forced into the city – uncomfortable decisions under duress

BEH
819

Dr Nikolaus von Engelhardt

University of Plymouth

Urban spaces present different opportunities and threats than natural environments. Some species seem to thrive in cities but are in fact under threat due to natural habitat loss. One example, the herring gull, is on the UK red list but often considered a nuisance in coastal cities. We investigated how urban environments shape herring gull behaviour which should help understand their decision-making, the consequences for themselves and to manage conservation and human-animal conflicts. Herring gulls visited locations with more or fewer anthropogenic features at different times of the day, and changed their behaviour according to location, time or both. In areas of high anthropogenic food availability juveniles frequently resorted to begging behaviour, whereas in other areas they more often foraged individually. Herring gull vocal communication, which can serve both to attract and to repel others, was shaped by the presence of food, humans and heterospecific gulls in the vicinity. When looking at food preferences, we found that urban herring gulls responded similarly strong to less prevalent natural food (fish) and highly prevalent, but less suitable anthropogenic food (bread), and least to unsuitable food (apples). Overall, our results suggest that herring gulls make highly flexible use of the urban environment, while retaining preferences from their natural habitats. While herring gull aggressive foraging, nest and chick defence causes conflicts with humans, their behavioural flexibility and decision making may also be usefully employed to change when and where they go and how they behave and thereby minimize conflicts.

How a fish thinks and what this tells us about vertebrate cognitive evolution

BEH
820

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Fish have traditionally been considered the least intelligent vertebrates, partly due to their relatively simple nervous systems compared to tetrapods, especially mammals and birds. However, research over the past few decades has shown that fish possess many of the cognitive abilities observed in other vertebrates, enabling meaningful comparative studies. One particularly intriguing feature of fish cognition that has gained increasing attention is the striking individual variation in cognitive performance: in certain tasks, some individuals perform dozens of times worse than others. In this talk, I will present how this variation has revealed fundamental mechanisms of cognitive evolution. By analyzing the expression of key genes in the brain, we have identified candidate proteins that may underlie individual differences in cognition, and thus represent potential targets for selection on cognitive traits. At the same time, our findings show that fish exhibit high levels of phenotypic plasticity in cognition, suggesting that animals with simpler brain architecture may rely more on adaptive plastic responses than on classical genetic evolution to meet environmental demands. Finally, while we found evidence of direct selection on cognitive traits in fish, we also detected complex patterns of covariation with other traits, suggesting potential evolutionary constraints and highlighting the role of indirect selection in shaping cognition.

Assortative mating in a weakly electric fish hybrid is driven by inherited, not learned, mechanisms

BEH
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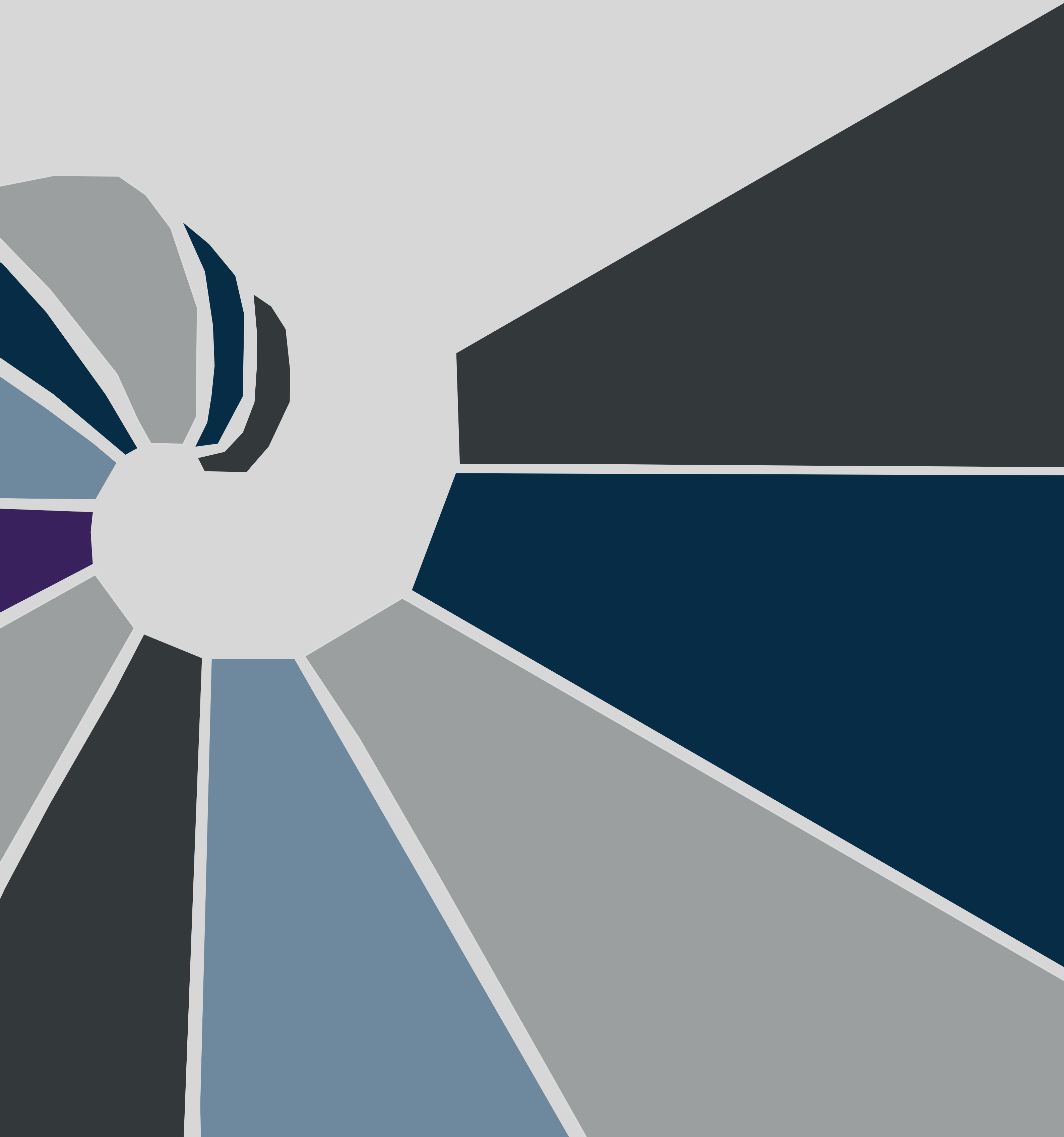
Assortative mating is a behaviour that is thought to increase the likelihood of sympatric or parapatric speciation by ensuring members of a particular cohort preferentially mate with individuals who share a particular trait, ensuring non-random mating in the absence of physical barriers. It can be broadly grouped into two mechanisms – Matching Rules and Preference Trait rules3. While assortative mating has been demonstrated in a genus of weakly electric fish; *Campylomormyrus*, it has yet to be established which of the two mechanisms of assortative mating are responsible for this behaviour. Here we utilise an artificial interspecific hybrid of *Campylomormyrus* to attempt to resolve this question. Hybrids were presented with three combinations of parental species and hybrid playback signals in dichotomous tests, under both non-breeding and breeding conditions, and their responses assessed. Under non-breeding conditions we detected no assortative behaviour in all but one playback condition, and only in females. Under breeding conditions, preference was detected with each parental playback, but only when the alternative playback was hybrid specific. Since the hybrids were raised only with siblings, and so naïve to the parental signals, we conclude that the assortative behaviour in this genus is a result of an inherited preference and thus is driven by a Preference/Trait mechanism as opposed to a Matching Rules mechanism.

Poster Abstracts



Development and evolution of spider eyes

DEV
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Many animal groups have independently evolved eyes and they show striking diversity in eye types and morphology. Pax6 is thought to be involved in eye development in all animals, being described as a master regulator gene, which regulates a conserved set of retinal determination genes (RDGs). Spiders have highly complex multi-ocular visual systems, usually composed of four eye pairs, the principal eyes, and three pairs of secondary eyes, but can differ in number, arrangement and size. Previous studies have suggested that Pax6 is not involved in the initiation of spider eye development in contrast to other animals. Furthermore, while many of the RDGs are duplicated and expressed in spiders, only sine oculis and eya are consistently found in both eye types among species. My project aims to identify which gene(s) initiates eye development and the cellular/genetic differences in eye size among spider species. To do this I'm using a combination of in situ hybridization and single cell data to identify candidate genes in *Parasteatoda tepidariorum* and *Pardosa amentata* while, also investigating how the gene regulatory network of both eye types differs compared to Drosphila in these species. Additionally, I aim to compare the development of evolution differences in eye size in the jumping spider *Marpissa muscosa* and the wolf spider *Pardosa amentata* which have enlarged anterior and posterior median eyes respectively.

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Developmental repatterning „types“ underlying the evolution of cranial morphological diversity in South American killifishes

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What are the modifications to developmental processes underlying the morphological disparity of the actinopterygian cranial systems we see today? The cranial system of most actinopterygians is highly mobile consisting of over 100 bones, numerous muscles, tendons and joints. This complex system is thought to be highly adaptive, allowing the specialization to a wide array of feeding modes. The genus Austrolebias is one of multiple killifish genera that posses a lifecycle adapted to ephemeral habitats by bridging the dry-season with dessication-resistant diapausing eggs. This allows them to exploit this extreme habitat type mostly inhabited by aquatic invertebrates and other annual killifishes. This lack of competition might have allowed the burst-speciation of the genus that occurred within the last 10 million years resulting to more than 60 species. During this speciation event the species diversified their feeding modes from generalistic invertivory to more specialized modes such as mulloscivory and piscivory. The modifications of developmental processes resulting in, e.g., the elongated heads of piscivorous species, are still unknown. Here we used µCT, synchrotron-CT, cLSM, and Anatomical Network Analysis to quantify and describe the changes of the cranial development of different Austrolebias species to investigate which type(s) of developmental repatterning - heterochrony (changes in timing), heterometry (changes in growth rate), and heterotopy (changes in location) underlie their craniofacial diversification.

The role of juvenile hormone in the regulation of caste determination and differentiation in an ant

DEV 133

Devashree Joglekar; Dr. Eva Schultner

University of Regensburg

Division of reproductive labour between queens and workers is the defining trait of eusocial insects. In ant species with morphological castes, whether an individual develops into a queen or a worker is decided during development, prior to the imaginal moult. Juvenile hormone, which together with ecdysone regulates development across insects, is known to play a key role in caste determination and differentiation across different species of ants. In the ant *Cardiocondyla obscurior*, adult workers completely lack reproductive organs, and the female caste is already determined by late embryogenesis, likely via maternal effects. We investigated how juvenile hormone affects caste determination and differentiation in this ant by feeding egg-laying queens as well as queen- and worker-destined larvae with a juvenile hormone analogue. First results show that neither caste ratios nor body size or morphology are affected when only larvae are fed with juvenile hormone, consistent with the idea that caste is irreversibly determined by maternal effects during early development. Accordingly, when whole colonies containing egg-laying queens were fed with juvenile hormone, they almost exclusively produced new queens. We are currently testing how the production, morphology and physiology of new queens are affected when only egg-laying queens receive juvenile hormone-supplemented food. Together, the results from these experiments will bring new insight into our understanding of the hormonal regulation of maternal caste determination in ants.

Development of cranial topology in anurans with different life cycles supports the adaptive decoupling hypothesis

DEV
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Many animals have complex life cycles that consist of two or more distinct postembryonic life phases, which often differ considerably in their biology. These life phases are subject to different selective pressures that can lead to their independent specialization and the subsequent adaptive decoupling during evolution. Ancestrally, amphibians (caecilians, caudates and anurans) exhibit an indirect life cycle including an aquatic larva that already resembles the adult. In anurans a more specialized larval type called tadpole evolved that differs significantly from adults in regard to feeding modes, locomotion and overall lifestyle exploiting diverse ecological niches unavailable to adults. A drastic metamorphosis has evolved in parallel with specialized larvae and adult and is regarded to underlie their evolutionary success in terms of morphological diversity and species numbers. This has led to the hypothesis that the evolution of larval and adult life phases of anurans is shaped by their adaptive decoupling. Here we use Anatomical Network Analysis (AnNA) to analyze the cranial musculoskeletal topology of anuran tadpoles and their corresponding adults. The dataset includes suspension feeding, predatory, diverse grazing and endotrophic, direct-developing species. Our results indicate that the cranial musculoskeletal topology of tadpoles is substantially different from that of adults based on connectivity, complexity, and modularity, supporting the adaptive decoupling hypothesis.

Comparative Transcriptomics of Uniquely Developmentally Truncated Pectoral Fins in Pipefishes

DEV 135

Tarek Gerhard; Dr Ralf Schneider; Dr. Arseny Dubin; Prof. Dr. Olivia Roth

Christian-Albrecht University of Kiel

Pipefishes, commonly studied for their unique male pregnancy and iconic derived morphology, feature highly diverse morphologies, such as variable numbers of fins. While most pipefishes primarily use pectoral fins for locomotion, in *Nerophis ophidion* (straightnose pipefish) these are developmentally altered: although functional during the larval stage, fin development appears to become truncated early in development and pectoral fins are ultimately lost during maturation. Thus, they are a valuable model to investigate developmental processes facilitating life-stage dependent appendage loss – a rare feature among vertebrates. To explore the molecular basis of this phenomenon, we conducted skeletal analyses of pectoral fins throughout development in two syngnathids: *Syngnathus typhle* (broadnosed pipefish; exhibiting a normal pectoral fin development) and *N. ophidion*. Additionally, we performed transcriptomic analyses characterizing gene expression profiles across crucial fin developmental stages in *S. typhle*, defining core pectoral fin regulatory pathways. We compared these to profiles of *N. ophidion*'s truncated phenotype, and supplemented analyses with genomic screens. Our findings revealed a strong activation of key developmental pathways in *S. typhle*, particularly Hedgehog signaling and its downstream effector genes, a pattern absent in *N. ophidion*. Gene sequence and genomic analyses further suggest regulatory evolution underlying this divergence: insertions of random repetitive elements in non-coding regions of affected genes appear as potentially causal. Thus, we propose that evolutionary downregulation of Hedgehog signalling, mediated by alterations in non-coding regulatory regions, may drive the truncation of pectoral fin development in *N. ophidion*. These results highlight a potential molecular mechanism underlying appendage reduction in syngnathids.

Spider ‘Organizing’ Gene Regulatory Networks

DEV
136

Ruixun Wang; Philipp Schiffer; **PD Dr. Matthias Pechmann**

University of Cologne

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

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

Trade-offs in virulence evolution: a Hierarchy-of-Hypotheses approach

EVO 231

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Freie Universität Berlin

Understanding the evolution of virulence, i.e. the harm a pathogen causes to its host, is of great interest for public health, veterinary medicine, conservation, and pest control. A central concept in the literature on virulence evolution is the so-called 'trade-off hypothesis', describing a seemingly straightforward relationship between virulence and transmission. However, in current terminology related to this hypothesis there is substantial ambiguity, which needs to be resolved to avoid confusion and miscommunication, and in turn facilitate further progress in understanding and predicting virulence evolution. To address this issue, here, we apply a Hierarchy-of-Hypotheses (HoH) approach to provide structured, visual representations of ideas linked to the 'trade-off hypothesis', generating three important outcomes. Firstly, our HoH approach emphasizes that the 'trade-off hypothesis' is a complex set of many different hypotheses and trade-offs. Our illustrations make this diversity apparent and more accessible – especially to newcomers in this research field. Secondly, our framework reveals that the classical trade-off nomenclature, as well as associated descriptions and predictions overemphasise the benefits of virulence while ignoring potential costs. Thirdly, we clarify ambiguities in commonly used terminology in the current literature, which we hope will mitigate against future misunderstanding. In this light, when referring to the trade-off hypothesis, we recommend that the specific trade-off ideas being tested are explicitly defined. Taken together, we anticipate that our HoH approach will stimulate further thinking on trade-offs in virulence evolution, in turn helping to advance our understanding of host-pathogen interactions and their evolution.

Cuticular hydrocarbon profile stability among populations of a major agricultural pest, the Coffee Berry Borer, *Hypothenemus hampei*

EVO 232

Dr. Ameka Myrie; PD Dr. Eva Schultner; PD. Dr. Jan Oettler; PD. Dr. Tamara Pokorny

Universität Regensburg

The Coffee Berry Borer (CBB) *Hypothenemus hampei* (Ferrari) (Coleoptera: Curculionidae: Scolytinae) is the most economically damaging pest of coffee worldwide, having invaded all major coffee-producing areas and causing significant losses. Since its discovery 40 years ago on the island of Jamaica, CBB has progressively expanded its range from lowland regions with comparably warm and dry climates to higher altitudes with cooler and wetter conditions in the Blue Mountains. Other pest insects have been shown to react to such environmental variation with changes in their cuticular hydrocarbon (CHC) profiles.

To determine whether this is the case in CBBs, we characterized the CHC profiles of CBBs collected from different areas varying in altitude and climate across Jamaica and from a farm in Panama, using gas chromatography coupled with mass spectrometry (GC/MS). We found that CHC profiles of CBBs did not differ based on farm location or rearing conditions (lab or field). CHC profiles are relatively simple, mainly composed of straight-chain alkanes and methyl-branched alkanes. Furthermore, the coffee berries provide a microclimate that shelters the beetles from conditions outside the coffee berries for the majority of their life cycles, thus potentially buffering CBBs from external environmental selection pressures.

Comparative Single-Cell Analysis of Long Non-Coding RNAs in Primate Brain Organoids

EVO
233

Keyue Fan; Prof. Dr. Katja Nowick

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Human-specific brain functions are thought to result from cortical expansion and increased cellular diversity, while the underlying mechanisms, especially those located in noncoding regions of the genomes, remain poorly understood. Long non-coding RNAs (lncRNAs), which are abundant in the brain, play critical roles in regulating neuronal differentiation, function, and plasticity. In the human genome, approximately 40% of annotated lncRNAs are specifically expressed in the brain, yet their expression and function in non-human primates remain largely unexplored.

To shed light on lncRNA functions in primate developing brains, we performed a comparative analysis of lncRNA expression dynamics during cerebral organoids development using human and chimpanzee stem cell. We first analyzed lncRNA expression patterns across different cell types and developmental stages. Using integrated single-cell transcriptomic data, differential expression analysis revealed species-specificly expressed lncRNAs, suggesting functional divergence during neurodevelopment. Future analyses will investigate how these lncRNAs contribute to regulatory networks and infer molecular mechanisms that may drive human brain evolution. This work will also provide insights into how noncoding elements shape human-specific brain features.

Association between MHC genetic variability and T cell receptor repertoire richness

EVO
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Alexej Sinner; Prof. Dr. Tobias Lenz

Universität Hamburg

Recognition of pathogens by the adaptive immune system requires self/non-self-discrimination, mediated by major histocompatibility complex (MHC) molecules that present peptides on cell surfaces. T cells, through their T cell receptors (TCRs), survey these MHC:peptide complexes to recognize pathogen-derived peptides and initiate immune responses. MHC molecules are genetically encoded by the highly polymorphic MHC locus. In contrast to these diverse but genetically hard-wired MHC proteins, TCRs are generated through somatic V(D)J recombination, a process that splices together variable gene segments to produce hypervariable receptors. However, variability is restricted during T cell development in the thymus: while T cells are positively selected for recognizing MHC:peptide complexes, negative selection eliminates overly self-reactive T cells to reduce the risk of autoreactivity.

The immense variability of TCRs together with the restriction during thymic development has made understanding TCR repertoire dynamics challenging. Sequencing results suggest that the TCR repertoire is influenced by factors such as age, disease history, microbiome, and MHC genotype. Here, we analyze TCR repertoire data from public human datasets to investigate differences in repertoire diversity, richness, and structural composition. Various estimators were evaluated to quantify functional diversity from both the antigen recognition and antigen presentation side. Preliminary findings indicate that TCR repertoire richness is non-linearly associated with the MHC variability, indicating a repertoire maximum at a medium-to-high number of unique MHC alleles within an individual. In future work, we aim to use experimentally generated TCR repertoires from sticklebacks, a fish model used to study natural genetic variation, to further investigate this association.

Male mate choice in relation to genome-wide heterozygosity in *Pelvicachromis taeniatus* (Cichlidae)

EVO 235

Benedikt Kröll[1]; Dr. Timo Thünken[1]; Dr. Julia Schwarzer[2]

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Sexual selection drives the evolution of sex-specific behavioral and morphological traits in many species, shaping mate preferences. Genetic compatibility may be a further important mate choice criterion. Despite the potentially adverse effects of kin mating (i.e., inbreeding) manifesting as inbreeding depression, theory predicts inclusive fitness benefits associated with inbreeding, which may result in kin preference. *Pelvicachromis taeniatus* is a sexually dimorphic, socially monogamous cichlid with biparental brood care that exhibits kin-mating preferences in both wild and lab-reared populations. Previous research has demonstrated benefits of kin mating. However, kin-mate preferences appear to be reversed when inbreeding becomes excessive, indicating high levels of homozygosity can be detrimental. In that study, outbred controls showed similar kin preferences as before. Here, we investigate male mate choice in F1 hybrids, which should show a higher level of heterozygosity because they resulted from crosses of different inbred lines. Individual males were given the choice between kin and non-kin females that were matched in body size and coloration. Concurrently, DNA samples of hybrid, inbred and outbred lines and the wildtype were sequenced to estimate genetic diversity measured as genome-wide runs of homozygosity (ROH) and inbreeding coefficients (F) based on single nucleotide polymorphisms (SNPs). Results from the mate choice trials revealed that hybrid-males tended to prefer kin females over non-kin. The observed proportion of kin choices confirms previous findings that kin-preferences are dependent on the own inbreeding level. Further analyses will correlate genome-wide heterozygosity estimates with female attractiveness in the male mate choice experiment and other fitness-related traits.

Microbiota influence on virulence evolution: a tripartite perspective

EVO 236

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Freie Universität Berlin

Animals harbour diverse microbial communities that impact their ecology, behaviour, and physiology. While some microbial associations protect hosts from infections, others cause diseases. During infection, virulence - the decrease in host fitness due to pathogens - is shaped by both host and pathogen traits, with microbiota playing a potential role. However, the impact of microbiota on the evolution of virulence still remains largely unexplored.

Our *Drosophila melanogaster*-pathogen system provides an opportunity to infect hosts with both unevolved and microbiota-adapted pathogens, with or without the co-injection of host-associated microbiota. Here, we will decompose virulence into distinct host and pathogen traits using a reaction norm framework. This approach illustrates the contribution of each virulence component, and the role microbiota play towards infection outcomes.

Integrating microbiota dynamics into virulence evolution research will improve our understanding of host-pathogen-microbiota interactions. Ultimately this might help to further elucidate processes shaping disease outcomes.

Tiny Signals, Big Impacts? Larval Chemical Communication in Burying Beetles.

EVO 237

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University of Bayreuth

Chemical communication plays a central role in social interactions in insects, but most studies have focused on adult insects. This gap is particularly relevant in insects that exhibit parental care, where chemical signals from larvae can influence parental behavior. Previous studies in other insects have shown that maternal feeding responses can be modulated by larval odor, but the chemical identity of these signals remains unknown. In this study, we investigated the chemical profiles of *Nicrophorus* larvae. Burying beetles are known for their elaborate biparental care, whereby the larvae of different species differ in their dependency of parental care. We collected larvae from the first, second, and third instar and subjected them to hexane extraction for chemical analysis. Gas chromatography-mass spectrometry (GC-MS) revealed that the larvae produce a diverse range of cuticular hydrocarbons and lipids. Differences were detected between larval stages, suggesting ontogenetic changes in chemical profiles. Our results provide fundamental evidence that *Nicrophorus* larvae emit chemical mixtures that change with development, supporting the idea that such signals may mediate interactions between offspring and caregivers. Further research is needed to determine whether these compounds act as solicitation signals and how they affect parental decisions. This work contributes to a broader understanding of the role of larval chemical communication in the evolution of social behavior in insects.

Bat malaria parasites: insights from an understudied and diverse host group

EVO
238

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Bats (Chiroptera) harbor a remarkable diversity of haemosporidian (malaria) parasites yet remain among the least studied vertebrate host groups in this context. In contrast to the intensively researched Plasmodium species of primates and rodents, bat-infecting haemosporidians encompass at least seven distinct genera, including *Plasmodium*, *Hepatocystis*, *Nycteria*, and *Polychromophilus*, each exhibiting unique patterns of host specificity, geographic distribution, vector association, and life cycle strategy. In this presentation, based on recent molecular findings, we highlight the evolutionary, ecological, and biogeographic diversity of bat haemosporidians, now documented across at least 10 of the 21 recognized bat families.

Some genera, such as *Hepatocystis*, are widespread and infect multiple host species across Africa, Asia, and Australia, while others, like bat-specific Plasmodium parasites, are highly host- and region-restricted. Notably, all known bat *Plasmodium* lineages are confined four bat species from west and central Africa and are phylogenetically closely related to rodent malaria parasites. Conversely, *Polychromophilus* parasites occur globally and present the only bat malaria parasites known identity of the invertebrate hosts (bat flies). Several lineages display unexpected phylogenetic relationships, challenging existing taxonomy and underscoring the need for a systematic revision of the order Haemosporida.

Developmental differences, such as the loss of erythrocytic schizogony in multiple lineages, further illuminate parasite adaptation and co-evolution with chiropteran hosts. Bat malaria parasites represent a powerful host system for investigating haemosporidian diversity, host parasite interactions, and evolutionary dynamics, providing new perspectives on the origins and diversification of malaria parasites.

Functional analysis of a horizontal gene transfer in *Cardiocondyla obscurior*

EVO
239

Lukas Franke[1]; Janina Rinke[1]; Esther van den Bos[1]; Weizhao Sun[1]; Phoebe Cunningham[2]; Prof. Dr. Jürgen Gadau[1]; Dr. Lukas Schrader[1]

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Lateral gene transfer (LGT) between hosts and endosymbionts is increasingly recognized as a driver of evolutionary innovation in insects, often facilitating the emergence of novel adaptive traits. While recent genomic studies have uncovered a growing number of putative LGTs the functional relevance and physiological integration commonly remains poorly understood. Here, we investigate an LGT encoding a xanthine-guanine phosphoribosyltransferase (XGPRT) in the ant *Cardiocondyla obscurior*, likely acquired from its endosymbiont *Candidatus Westeberhardia cardiocondylae*.

We aim to functionally characterize this gene and assess its potential integration into the host's metabolic pathways. Our approach combines molecular and gene expression analyses, such as quantitative PCR (RT-qPCR), fluorescence in-situ hybridization (FISH), RNAseq analysis and gene knockdown. RT-qPCRs revealed that the transferred gene is predominantly expressed during larval stages, without clear caste specificity. FISH imaging revealed expression patterns possibly associated with the developing ovaries in queen-destined larvae. These findings suggest a developmental role particularly of reproductive organs, possibly linked to nucleotide turnover or nitrogen conservation in larvae.

Ongoing and future analyses will test whether the expression of the transferred XGPRT is correlated with genes involved in the purine salvage pathway, and whether functional disruption affects metabolic or physiological phenotypes. Through this study, we aim not only to elucidate the function of a specific LGT but also to contribute to a broader understanding of how LGTs are functionally assimilated into host biology. Our findings will inform the evolutionary significance of host–symbiont LGTs in ants and more generally the role of LGTs in shaping insect–microbe symbioses.

Taxonomy flying high - showcasing a multilocus DNA barcoding approach using hoverflies

EVO
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Biodiversity loss and its detrimental impact on ecosystem health represent a major threat to the long-term sustainability of human life. Taxonomic knowledge is fundamental to understanding biodiversity and to implementing effective conservation and restoration strategies. The TETTRIs project—an EU-funded international initiative involving 17 European institutions—addresses this challenge by strengthening taxonomic capacity through training, research and innovation.

A key objective of TETTRIs is to enhance species identification and delimitation, particularly in species-rich or cryptic taxa where traditional morphological or single-locus genetic marker approaches are insufficient. Focusing on pollinator communities, we selected hoverflies (Syrphidae) as a model system to develop and validate an integrative molecular workflow. This workflow combines a robust wet-lab protocol including state-of-the-art molecular techniques to generate multilocus DNA barcoding data using Next-Generation Sequencing (NGS) via the MinION sequencing platform (Oxford Nanopore Technologies), with a fully automated and user-friendly software pipeline that carries out all the necessary bioinformatic steps for NGS data analysis (AmpliPiper). The wet-lab workflow presented here is cost-efficient and flexible, allowing researchers to easily adjust the number of individuals and loci investigated. The AmpliPiper pipeline was specifically designed to be easy to use and access, requiring no advanced bioinformatic skills. The integration of these methods into workflows of future taxonomists will be facilitated by publishing best-practice protocols from start to finish in taxonomy journals and make open-source protocols permanently available via open access GitHub repositories.

Understanding the Evolutionary Origin of HLA Diversity in the Americas

EVO
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The interaction between host and pathogens is a dynamic evolutionary process that has led to extensive genetic variation in immune-related genes, particularly within the human Major Histocompatibility Complex (HLA). While pathogen-mediated balancing selection is thought to be a major driver of this diversity, the relative contributions of other evolutionary forces—such as admixture and genetic drift—remain unclear. Moreover, the specific mechanisms of balancing selection and the pathogen-specific versus broad protective effects of HLA alleles are still under debate. To address these questions, we investigate HLA Class I and II diversity in pre- and post-contact Native American populations from Xaltocan, Mexico—providing a temporal perspective on the impact of European-borne pathogens. Using ancient DNA-specific HLA genotyping, we characterize allele frequency changes over time. Analyses are conducted with the TARGT pipeline, complemented by independent validation and OptiType genotyping to ensure consistency. This study provides critical insights into how pathogen exposure and evolutionary forces have shaped HLA diversity in Native American populations. More broadly, our temporal approach offers a valuable model for disentangling the complex drivers of immune gene evolution in human history.

Evolution and Allometric Scaling of Jumping Performance in Orthopterans

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Jumping is a widespread, evolutionarily significant locomotor strategy among animals, enabling rapid escape, dispersal and ecological function. In Orthoptera, remarkable diversity in jumping performance arises from phylogenetic divergence, ecological adaptation and body size-dependent constraints. Here, we test two main hypotheses: (1) that evolutionary transitions in jump actuation – especially the acquisition of latch-mediated spring mechanisms – have driven increases in jumping performance, particularly in open-habitat specialists, and (2) that allometric scaling imposes negative relationships between body mass and performance traits such as velocity, acceleration, and jump distance, resulting in proportionally higher performance in smaller species. To test this, we conducted a comparative kinematic study of jump performance using high-speed videography across diverse Orthopteran taxa. Performance data were mapped onto a phylogenetic tree to explore evolutionary origins and ecological context of jumping traits. We found that enhanced jumping performance is most pronounced in taxa with latch-mediated spring mechanisms, primarily within Caelifera, which are also often associated with open habitats. Allometric analyses across species revealed that maximum velocity, acceleration, and jump height and distance show negative or sub-isometric scaling with body mass, while peak force and kinetic energy scale near-isometrically. These results align with biomechanical theory and earlier findings. Our study illustrates how lineage-specific biomechanical adaptations and general allometric principles together generate the diversity of jumping performance observed in Orthoptera.

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Genomic Insights into the Evolutionary History and Cryptic Diversity of Two-Toed Sloths (*Choloepus*) in Amazonia

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Amazonia's rich biodiversity has been shaped over millions of years. Yet, the impact of environmental events on the diversification of Amazonian species remains poorly understood. Two-toed sloths (*Choloepus spp.*) provide a unique model for studying this connection due to their wide distribution across Amazonia and restricted arboreal lifestyle, which makes them especially sensitive to shifts in the forest landscape. Previous studies have highlighted inconsistencies in phylogeny, karyotype, and morphology between the two *Choloepus* species, questioning the validity of current taxonomy. Here, we present the first genomic dataset representing different populations of Amazonian *Choloepus*, using genome-wide nuclear and mitochondrial data to investigate their phylogenetic relationships in relation to Amazonian biogeography. Our results indicate that *C. hoffmanni* is paraphyletic, with its southern Amazonian population clustering within *C. didactylus*, emphasizing the need for taxonomic revision of *Choloepus*. Nuclear DNA suggests a more recent divergence (~3.57 Mya) between the two species than mitochondrial data previously indicated (~8 Mya). We also find population splits and population size fluctuations coinciding with environmental changes during the Pleistocene. Divergence driven by environmental changes indicate strong dependence on environmental stability and suggests that the distinct evolutionary lineages may require independent conservation assessments amidst the increasing threat of habitat loss.

Female honest signals and male pregnancy

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Christian-Albrechts-Universität zu Kiel

Sexually reproducing species can evolve sexual dimorphism of parental care. Pregnancy in female mammals is an example of a large energy investment into offspring. In turn, males may invest into secondary sexual traits which can work as honest signals to broadcast fitness or immune status and compete for females.

This distribution of “sex roles” is often viewed as fixed across all vertebrates. In the Syngnathidae family, however, seahorses and pipefish males receive unfertilised eggs from the females and brood them in specialised pouches, a tissue type that varies along a phylogenetic gradient of “male pregnancy”. Females of some pipefish species also display dynamic ornaments to compete for access to males.

This reversal of the commonly assumed dynamic allows us to test hypotheses about parental investment and honest signalling outside of the constraints of mammalian models. My research focuses on sexual signalling of pipefish females and male parental investment during pregnancy with special emphasis on trade-offs with immune function.

A phylogeny-aware nomenclature for a large multigene family in Daphnia

EVO
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🎓

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Chemoreception is fundamental to organismal survival, enabling animals to detect food, mates, and predators through complex chemical cues. Ionotropic receptors (IRs), which evolved from ancient ligand-gated ion channels, constitute a diverse and ecologically significant gene family involved in chemical sensing. In freshwater crustaceans of the genus *Daphnia*, IRs play essential roles in predator detection. However, previously identified IR genes have typically been annotated using sequential locus numbers from automated gene predictions, which, however, convey no information about evolutionary relationships. Although a fully phylogeny-aware nomenclature is desirable, creating one remains challenging, particularly given future additions to a gene family repertoire that varies so much within the *Daphnia* genus.

Here, we present a reconciled gene-tree/species-tree framework and a pragmatic, evolution-informed nomenclature that incorporates phylogeny to an informative degree, yet remains stable as new *Daphnia* genomes are sequenced. Our naming system adheres to the established convention ("GspecIR1234"), but the numeric identifier ("1234") represents phylogenetic relatedness within defined parent groups, supplemented by optional suffixes to account for lineage-specific duplication events that cannot be meaningfully captured by a purely phylogeny-based numbering scheme.

We analysed over 700 manually curated IR genes from six *Daphnia* species. Gene-tree/species-tree reconciliation identified distinct parent groups arising from speciation and duplication events. Our nomenclature captures essential phylogenetic structure without requiring renumbering when new paralogues or species are added. By balancing evolutionary precision with long-term practicality, this new system provides a robust foundation for comparative and functional studies of chemoreception across *Daphnia* and beyond.

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Decoding Sexual Attractiveness: Genetic, Chemical and Behavioral Investigation of Sexual Signaling Evolution in Parasitic Wasps

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University of Muenster

Divergence in chemically encoded sexual signals is a major driver of reproductive isolation in insects. Cuticular hydrocarbons (CHCs) serve as essential cues for mate recognition and species-specific mate preference. However, the specific CHC components responsible for these behaviors – and the genetic and biosynthetic mechanisms underlying CHC variation – remain poorly understood. This study uses the parasitoid wasp *Nasonia* as a model and integrates behavioral, chemical, and genetic approaches to address these knowledge gaps. First, we functionally characterized the key gene families in the CHC biosynthetic pathway, including fatty acid synthases (fas), elongases (elo) and fatty acyl-CoA reductases (far), in regulating CHC structural diversity and quantity, thereby shaping sexual signaling in *N. vitripennis*. Second, we investigated the genetic and chemical basis of species-specific CHC variation involved in prezygotic isolation between *N. giraulti* and *N. longicornis*. Exploiting their haplodiploid sex determination and cross-fertility, we generated female recombinant inbred lines (RILs) and conducted quantitative trait loci (QTL) analyses of CHC compounds separately for the diploid female recombinant lines and their haploid male fathers. By correlating quantities of individual CHCs with mate preferences, we identified three key compounds significantly correlated with male mating frequencies. Further zooming into QTL for the species-specific variation of our three key pheromonal compounds, we were able to localize several CHC biosynthesis candidate genes. In summary, this study advances our understanding of the genetic and chemical basis of species-specific sexual signaling, offering broader insights into the mechanisms driving reproductive isolation and speciation in insects.

To see or be seen: morphological mimicry compromises the visual system of ant-mimicking jumping spiders

EVO
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Mimicry is widespread amongst living organisms, but mimics are rarely perfect. This phenomenon has been described as an evolutionary paradox because we expect natural selection to favour more accurate mimicry. One possible explanation is the selection trade-offs hypothesis, which posits that imperfect mimicry results from other, unrelated, selection pressures interacting with mimetic traits, resulting in adaptive peaks away from perfect mimicry. If there are selection trade-offs between mimetic accuracy and other traits, we expect these traits to be functionally hindered in mimics in comparison to their non-mimetic relatives, and that mimetic accuracy is also compromised. One previously unexplored possibility is the interaction between mimicry and sensory system function. Here, we test this in two species of jumping spider, the ant mimic *Myrmarachne smaragdina*, and a closely related non-mimic, *Astia maculata*. We used micro-computed tomography and geometric morphometric methods, comparing the size, shape, arrangement, and orientation of the eyes. We find that due to mimetic constriction of the cephalothorax, the lenses of the ant mimic are significantly smaller, generally less spherical, and arranged in a more compressed and reorientated configuration, compared to their non-mimic relative. Given their predicted functional impacts on vision, these findings suggest a selection trade-off could exist between mimicry and sensory function.

Phenotypic variation in a novel ant male morph

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Sexual selection can lead to the evolution of novel male phenotypes, which differ from ancestral phenotypes in discrete morphological traits. The tramp ant *Cardiocondyla obscurior* produces two distinct male morphs – wingless, long-lived males with sickle-shaped mandibles used for fighting and winged, short-lived, docile males. How these alternate phenotypes originated, and how they are proximately determined, is unclear. I show that the two morphs differ in size in eight morphological traits. Wingless males exhibit higher levels of variation in all traits except mandible length, suggesting that weapon size is under stabilizing selection. Overall male size is influenced by population- and colony-level genetic effects, and different populations also differ in their propensity to produce winged males. Some genetic lines appear to have lost the ability to produce winged males altogether, showing that expression of the dimorphism is unstable. Ultimately, this may lead to the loss of male dimorphism in *C. obscurior*, as has occurred in other species in the genus.

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Rapid evolutionary change of hypoxia physiology and related gene expression patterns in an asexual Daphnia population

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Freshwater ecosystems in the Arctic facing rapid environmental change can serve as important model systems for studying the rapid adaptation potential of their inhabitants. Key members of these Arctic ecosystems often reproduce asexually, raising questions about their capacity to adapt over short time scales, and what the possible mechanisms are. Here, we studied an asexual *Daphnia* population from a meromictic lake in South-West Greenland using resurrected animals dated to ca. 2012 CE and modern descendants from 2022 forming two temporal subpopulations. The anoxic layer of the lake was previously inhabited by anoxygenic photoautotroph purple sulfur bacteria, a possible food resource for *Daphnia*. This microbial population, however, seems now to be destabilized, which could be reducing the presence of *Daphnia* in hypoxic or anoxic waters. In previous work, we found that the two *Daphnia* temporal subpopulations differ in their genetic structure and physiological traits linked to hypoxia and thermal tolerance. To investigate their physiological and transcriptomic responses to hypoxia in more detail, we exposed three clones from each subpopulation to medium and severe hypoxia. We quantified hemoglobin production, one of the main mechanisms of hypoxia response in Daphnia, and measured two oxidative stress markers: glutathione-S-transferase activity and TBARS, a proxy for lipid peroxidation. Diverging physiological responses and associated gene expression patterns between temporal subpopulations will be discussed in the light of rapid evolutionary change in response to ecosystem changes in an asexual population.

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

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The phytophagous lifestyle is a key innovation in insects and has evolved in one third of all insect orders. The evolution of phytophagy involves fundamental behavioural and morphological changes accompanied by chemosensory and metabolic adaptations. To date, the genomic basis and genetic innovations related to evolutionary dietary shifts are poorly understood. Here we focus on two monophyletic groups within the Hymenoptera, Aculeata and Chalcidoidea, that secondarily developed larval phytophagy independently several times. This phytophagy can be characterized by the feeding of pollen, nectar, plant oil or in the formation of plant galls. To shed light on evolutionary processes that shaped the diversity of nutritional adaptations in Hymenoptera we address the following main research questions: (1) Is parallel evolution at the phenotypic level reflected by parallel genome evolution? And (2) did similar genomic innovations appear when independent lineages realized convergent dietary transitions? Here I want to introduce the current state of the project and give insights into newly sequenced genomes of representative phytophagous aculeates. Especially, gene family size evolution of potentially important gene families involved in chemoperception and detoxification will be compared between different phytophagous species. Additionally the situation in closely related zoophagous species will be shown. This information will be helpful to asses the role of gene family expansion and gene loss in context of the evolution of secondary larval phytophagy in Hymenoptera.

Adaptive radiation and social evolution of the ants

EVO
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Dr. Lukas Schrader

Institute for Evolution and Biodiversity

Ants are among the world's most successful lineages of animals. Over the last 150 MY of evolution, they became dominant parts of terrestrial ecosystems and diversified into over 15,000 extant species in 340 genera. In 2017, we initiated the Global Ant Genomics Alliance (GAGA) to generate large comparative genomic, transcriptomic, phenotypic and life history data to address fundamental questions about the evolution of the ants. The analyses of more than 130 high-quality genomes that I will present here have allowed unprecedented insights into the genetic underpinning of ant social traits, their adaptive radiation, and their genome evolutionary history.

Investigating archaic introgression in *Elephas maximus*

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Hannah Smith; Dr. Patrick Arnold

Universität Potsdam

It is known that interbreeding between extant and extinct elephant species occurred throughout elephantid evolution. However, in tropical regions, fossilisation is rare and there is limited accessible ancient DNA from extinct elephantid relatives due to the warm, humid climate. The Asian elephant (*Elephas maximus*) has a tropical distribution across South and South-East Asia which is fragmented as a result of dramatic population decline in recent history; thus, it is challenging to reconstruct its evolutionary history using direct molecular data.

Nonetheless, ancient hybridisation events between closely related lineages provide lingering genetic signatures of archaic introgression in present-day genomes. Methods to detect “ghost” introgression from now-extinct or unknown lineages have primarily been developed for and applied to the study of human evolution, (e.g., in identifying Neanderthal, Denisovan, or “superarchaic” admixture in *Homo sapiens*). These methods detect genomic regions bearing signatures of archaic ancestry without the requirement for ancient reference genomes.

This project applies such approaches for detecting “ghost” introgression to whole-genome data from Asian elephants across subspecies (primarily island vs. mainland-dwelling), to look for genomic signatures of archaic introgression in Asian elephants. By adapting existing computational approaches to the demographic and genomic context of elephantids, the aim is to identify candidate regions of archaic origin and assess their distribution among subspecies. This study aims to contribute to the understanding of the complex evolutionary history of *E. maximus*, and to demonstrate the transferability of human-focussed methods to conservation-relevant, non-model organisms.

Chromosome-level genome assembly of the Common tenrec, *Tenrec ecaudatus* (Schreber, 1778), a new model for early placental mammal evolution

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Damian Hernandez-Roco; Dr. Patrick Arnold

Potsdam University

Remarkably little is known about the origins of early mammals. Due to the paucity of the fossil record, attention is often turned to the extant organisms that share plesiomorphic characters in order to gain insights into the evolutionary history of mammals. Afrotheria is one of the four major clades of placental mammals, accounting for around a third of all mammalian orders, and encompassess a wide array of differently adapted species. Within Afrotheria, Tenrecs are a species-rich group of small mammals native to the island of Madagascar that display several special traits resembling those hypothesized on early placentals regarding reproductive strategies, thermoregulation and growth metabolism. Despite this, Tenrecidae remains heavily understudied in many aspects. Genomic information for this group of mammals is scarce and not up to modern quality standards. In order to address this issue, we present here the complete, chromosome-scale reference genome and annotation of the common tenrec, *Tenrec ecaudatus*. This assembly is a significant improvement over the current state of Afrotherian genomics, arising as a new reference genome for Afrosoricida. Using all the available genomic resources for afrotherians we conducted a phylogenetic reconstruction and divergence time estimation for Afrotheria. Added to this, our comparative chromosome-synteny analyses showed significant rearrangements within afrotherians, specially on the clade shared by tenrecs, elephant-shews and the aardvark (Afroinsectiphilia). Furthermore, this resource provides a valuable genomic resource that paves the way for future studies into early mammal evolution and Afrotherian radiation.

Quantitative morphological analysis of tadpole shrimps: evaluating evolutionary changes and their implications on the idea of evolutionary stasis

EVO 254

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Crustaceans, a large and diverse group of arthropods named for the hard exoskeleton of many representatives, comprise almost 67,000 described species. Characteristics are their larval forms, especially the nauplius, for example, in Copepoda or Branchiopoda (including fairy shrimps or tadpole shrimps). Most crustaceans are free-living aquatic species, but some are terrestrial, some are sessile, and some are parasitic. Notostraca, the group of tadpole shrimps and an ingroup of Branchiopoda, has its evolutionary origins in the Devonian period, approximately 365 million years ago. Tadpole shrimps are iconic components of the freshwater fauna, specifically in ephemeral ponds, muddy puddles, or shallow lakes. Due to their relatively large body size of several centimeters, they are pretty prominent in this habitat. The ability of tadpole shrimps to survive in temporary freshwater bodies originates from their production of desiccation-resistant eggs during the dry periods, known as cysts or dormant/resting eggs. To evaluate this suggestion, we analyse both fossil and extant representatives of tadpole shrimps with quantitative morphological methods. The specimens included in the analysis originate from different collections as well as from literature data. The specimens are photographed with high-resolution compound photography using a digital microscope or a macrophotographic setup. Based on these images, measurements of different body parts and digital drawings of the shield outlines are performed, the latter being the basis for a shape analysis. The resulting data are set into an evolutionary context to check whether the suggested evolutionary stasis is measurable or if this idea must be rejected.

De-novo assemblies and comparative genomic analysis between the cave and surface populations of the fish species *Garra longipinnis*.

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Adaptation to the extreme and stable environmental conditions of caves provides a compelling opportunity to examine how the interplay of evolutionary forces shapes phenotypic changes, with notable traits including eye loss and reduced body pigmentation – collectively termed as troglomorphy. These striking phenotypic characters have raised the central question of whether their emergence is credited to relaxed selective pressures and fixation through genetic drift, or if they offer selective advantages in nutrient-poor and light-deprived environments. To address this, comparative genomic analysis between epigean and cave-dwelling populations of the same species can provide a powerful framework for investigating this question. The Omani fish *Garra longipinnis* represents an ideal model system, as it includes both surface and subterranean populations, enabling the direct examination of the genomic and regulatory changes underpinning these evolutionary trajectories. Furthermore, recent advances in sequencing technologies have democratized access to high-quality genome assemblies, even for non-model organisms. By capturing key aspects of genomic traits, like structural variations and conserved gene orders, the genomic blueprint of an organism enhances the understanding of gene regulation and trait evolution. In this study, we constructed the first de-novo chromosomal-level genome assemblies for both morphotypes of *Garra longipinnis*, along with an outgroup contig-level assembly of *Garra sharq*, to investigate the major evolutionary processes that led to the phenotypic divergence between the two populations. These findings lay the groundwork for future investigations into selection dynamics, gene expression variation, and the broader genomic basis of cave adaptation.

Female fitness and immunity in response to reproductive microbial isolates from distinct bedbug populations

EVO
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Copulatory wounding and the sexual transmission of microbial organisms are common, likely contributing to the dynamic and diverse nature of reproductive microbiomes. These microbes can originate from the environment, the genitalia of both partners, and/or the reproductive organs. Variation in reproductive microbiota composition may exert yet unknown selection pressure on the host to optimise resource allocation between survival, immunity, and reproduction. To investigate variation in microbes and their potential links to immune responses and life history traits, I isolated bacteria from males of distinct and reproductively isolated populations of the bedbug *Cimex lectularius*. Bedbugs offer a unique model for studying these processes, as males employ traumatic insemination by piercing the female's abdomen during mating. To mimic microbial transmission during mating, I pricked the paragenital reproductive organ of virgin females from distinct populations with native and non-native bacterial isolates. Currently, I am measuring the effects of these isolates on host reproduction and immunity to assess whether sharing evolutionary history leads to adaptive trade-offs. The quantification of the effects of bacterial isolates on different host populations is the first step in elucidating the role of reproductive microorganisms in shaping host fitness and immunity.

Tracking down evolution of morphological characters along the major lineages of hyperdiverse ant-like litter beetles (Coleoptera: Staphylinidae, Pselaphinae)

EVO
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Eberhard Karls Universität Tübingen

Pselaphinae Latreille, 1802, the second-most species-rich subfamily of rove beetles, comprises over 10,000 extant species with a cosmopolitan distribution, thriving in tropical forests and temperate regions like Europe. These beetles exhibit remarkable ecological adaptations, including myrmecophily, specialized predation, and troglobitic lifestyles – each associated with specialized traits, like the fusion of abdominal sclerites, antennal modifications, and the reduction or loss of compound eyes. All pselaphines display unique and highly variable morphological transformations across all body regions. Many of them are linked to structural reinforcement and increased rigidity, such as thickened cuticles with deep cuticular invaginations (i.e., fovea), or to chemical defense (e.g., cephalic glandular system). Among the group's many bizarre morphological adaptations, extreme variations of head structures stand out, which range from lateral projections, hypertrophically enlarged maxillary palps, and elongated rostra to frontal protrusions. The classification of Pselaphinae presents exceptional challenges, due to both their astonishing morphological diversity and the widespread occurrence of presumably homoplasious character states across lineages. Most higher taxa fail to be supported as monophyletic groups in molecular and morphological analyses, making the classification of the group contentious. This persistent uncertainty underscores the critical need for the application of more comprehensive phylogenetic approaches.

This study presents the first phylogenetic reconstruction of major lineages of Pselaphinae based on both genomic-scale phylogeny using ultraconserved elements (UCEs) and µCT-based comparative morphology. By addressing long-standing systematic inconsistencies and reevaluating key traits, we aim to provide new insights into the evolutionary history and morphological radiation of this hyperdiverse beetle group.

Electrocommunication signal divergence in African weakly electric fish

EVO 258

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The electric fish has been independently evolved at least six times in the world. Comparing to the strong electric fish, the weakly electric fish has very high species diversity, i.e., Mormyroidae. Mormyroidae fish has much higher species diversity comparing to the strong electric fish, with nearly 200 species. The success of adaptive radiation may result from their diverged electric signals (EOD) that mainly used for navigation and communication. We investigated the possible genetic basis of the EOD divergence (particular the EOD duration) in genus *Campylomormyrus* by comparing the gene expression between the electric organ and skeletal muscle using pure-bred species with different EOD duration. The gene expression exhibits clear pattern that relative to their EOD length. By clustering different gene expression patterns, we identified three groups have significant association with EOD duration. Three potassium channel genes (KCNK6, KCNJ2, KCNQ5) and one transcription factor KLF5 are curated that might affect EOD duration.

In addition, we specifically looked at the allele-specific expression on the F1 cross species hybrids. The EOD in F1 hybrids always resemble to elongated EOD when we cross species with short EOD and elongated EOD. However, the genes with allelic expression imbalance always express with dominance at the allele from the short EOD parental species, with only one exception KCNJ2. Therefore, we think this gene can be a strong candidate that affects EOD duration.

Genomic and phenotypic change within one decade in an asexual Daphnia population

EVO 259

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Obligate parthenogenesis is a widespread phenomenon in extreme environments both in higher latitudes and high altitudes. This has also been observed in the keystone zooplankton grazer *Daphnia*, particularly of species belonging to the pulex/pulicaria species complex which have a circumpolar distribution. Arctic lakes are generally nutrient-poor and have low productivity, but in some meromictic lakes, dense photoautotroph bacterial populations in the anoxic zone of the lake can be an important food source for *Daphnia*. Associated with the recent shift in climatic conditions in the Arctic, this food source may now have diminished considerably, thus relaxing selection pressure on hypoxia tolerance that would have allowed *Daphnia* to feed in hypoxic or anoxic conditions. For a deeper understanding of their capacity for rapid adaptation to such changes, we studied members of an obligately parthenogenetic *Daphnia* population resident in a lake in Southwest Greenland at two time points separated by a decade. We compared genotypic and phenotypic properties of the historical population represented by resurrected lineages dating to 2012 CE, to a those of a modern lake population sampled in 2022 CE. We applied whole genome sequencing to study genomic differences at the temporal subpopulation level and combined this data with physiological trait measurements including respiration rate, critical oxygen limit and thermal tolerance. We will discuss differences in functional traits and their potential genomic underpinnings, providing evidence for rapid phenotypic change with potential adaptive value.

Multiomics Reveal Associations Between CpG Methylation, Histone Modifications and Transcription in a Species That has Lost DNMT3, the Colorado Potato Beetle

EVO
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Insects display exceptional phenotypic plasticity, which can be mediated by epigenetic modifications, including CpG methylation and histone modifications. In vertebrates, both are interlinked and CpG methylation is associated with gene repression. However, little is known about these regulatory systems in invertebrates, where CpG methylation is mainly restricted to gene bodies of transcriptionally active genes. A widely conserved mechanism involves the co-transcriptional deposition of H3K36 trimethylation and the targeted methylation of unmethylated CpGs by the de novo DNA methyltransferase DNMT3. However, DNMT3 has been lost multiple times in invertebrate lineages raising the question of how the links between CpG methylation, histone modifications and gene expression are affected by its loss. Here, we report the epigenetic landscape of *Leptinotarsa decemlineata*, a beetle species that has lost DNMT3 but retained CpG methylation. We combine RNA-seq, enzymatic methyl-seq and CUT&Tag to study gene expression, CpG methylation and patterns of H3K36me3 and H3K27ac histone modifications on a genome-wide scale. Despite the loss of DNMT3, H3K36me3 mirrors CpG methylation patterns. Together, they give rise to signature profiles for expressed and not expressed genes. H3K27ac patterns show a prominent peak at the transcription start site that is predictive of expressed genes irrespective of their methylation status. Our study provides new insights into the evolutionary flexibility of epigenetic modification systems that urge caution when generalizing across species.

Morphology and function of female genital damage in the orb-weaving spider *Larinioides cornutus*

EVO
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Sexual selection and conflict shape the evolution of mating strategies and genital morphology in many species. In polygamous species, adaptations have evolved that mitigate sperm competition, affecting both behaviour and functional morphology of the males, including interactions with the female reproductive anatomy. In the orb-weaving spider *Larinoides cornutus*, females were observed with or without scapus in the field, suggesting that males may remove the scapus during mating, as documented in other orb-weavers. We investigated the causes, mechanisms, and consequences of female genital damage in *Larinioides cornutus* using field surveys, staged mating experiments, and high-resolution imaging (SEM and µCT). Field observations revealed that most females encountered lacked a scapus. Controlled mating observations demonstrated that males are responsible for inflicting damage on the female external genitalia (epigyne). Remating trials revealed that the functioning of female genitalia was impaired and receptivity of the female reduced. SEM imaging was used to compare the intact genital structure of virgin females with those of mated females who exhibited loss, fractures, or partial loss of the scapus and the collar-shaped part of the epigynum from which the scapus protrudes. We elucidated the mechanical complexity of genital interlocking and the structural basis for male-induced damage in female genital structures through micro CT reconstruction of pairs fixed in copula. This study contributes to the understanding of harmful mating in arthropods, highlighting the frequent occurrence and independent evolution of harmful mating strategies in spiders.

Effects of autumn temperature on development and overwintering performance in *Argiope bruennichi* spiderlings

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S.C. Einem; C. Ortiz Movliav; P. Lehmann; E: Frenzel; K.T. Roberts; M. Wurster; M. Lalk; **G.B. Uhl**

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A consequence of climate change is the increased fluctuation in temperatures. Understanding the extent that species are affected by temperature during early development, and subsequent impacts on survival and physiology, will help assess vulnerability to climate change. The wasp spider *Argiope bruennichi* has rapidly expanded its range in Europe northward, suggesting resilience to varying temperatures. Spiderlings hatch from the eggs in autumn and remain in the egg sac until spring. This study investigated the effects of post-oviposition temperature on *A. bruennichi*. Over five weeks post-oviposition, we monitored early development under three temperature regimes: control: regional autumn temperature; warm: 4 °C above control; cold: 4 °C below control. Subsequently, egg sacs that had experienced the three autumn temperature regimes were transferred to a common regime simulating the regional winter climate. Survival proportions of spiderlings and their supercooling point (SCP), an indicator of cold tolerance, were assessed in late autumn, winter, and spring. Survival proportions did not differ between autumn and winter; however, in spring, the warm treatment showed higher mortality (25 %) compared to the control (8 %) and cold (5 %) treatments. The SCP of spiderlings averaged -28 °C across groups, suggesting that their cold tolerance was unaffected by early temperature exposure. Our study indicates that warmer autumn temperatures reduce the probability of spiderlings surviving the winter, and that diminished energy reserves in survivors might further compromise performance in spring. Consequently, even brief periods of warmer temperatures can impact seemingly resilient species such as the wasp spider.

The evolution of eye loss in spiders (Arachnopulmonata, Araneae)

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Spiders have some of the most diverse and successful multi-ocular systems among living arthropods. Although most species have four pairs of eyes in two distinct systems (two primary and three secondary eyes), spiders exhibit a huge variety of configurations in eye size, number, and arrangement. Many taxa have lost one or more pairs in independent phylogenetic events, where reductions to six, four, two, and no eyes are known. However, most reports of these losses are scattered throughout taxonomic literature, making them inaccessible and obscuring analyses about the plasticity of visual organs at a macro-evolutionary scale. Here, we present a review and meta-analysis of eye loss for the order. We found that eye loss occurs in ca. 12% of known spider species, predominantly in the Synspermiata clade. From these, the reduction to six eyes is the most common, with more than 5,000 species having lost at least one pair of eyes. Complete loss of the secondary eye pairs was identified in Caponiidae and Palpimanidae, with the former having 80% of its species retaining only the principal eyes. Different models of character evolution and ancestral states reconstructions inferred that the three secondary eye pairs configuration has evolved at least seven times independently across the order, with reversals to an eight-eyed condition in Synspermiata. Other eye configurations have independently evolved in different lineages. Retention of principal eyes with loss of secondary pairs has evolved in five families. Overall, transition rates between eye configurations are low (<0.01), with their maximum peak ~170 Mya ago.

Evolutionary Genomics of Micronesian Corals

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Staghorn Acropora corals are ecological keystone species in shallow lagoons and back reef habitats throughout the tropics. Their widespread decline coupled with their amenability for asexual propagation propelled them to the forefront of global coral restoration efforts. To guide these efforts and as a blueprint for similar projects, we conducted a comprehensive population genomic study of Acropora pulchra, a major restoration target species in the Indo-West Pacific. Our results revealed that populations in the Mariana Islands are characterized by large clonal clusters and extremely low levels of genetic diversity. Differentiation among populations followed a significant isolation-by-distance pattern and delineated two distinct metapopulations on Guam. Our investigation identified critical population genetic parameters, necessitating targeted management strategies, and provides actionable guidelines for effective conservation efforts. For management and conservation, two sites emerged as pivotal connectivity hubs with elevated genetic diversity. For restoration, we show that A. pulchra populations demonstrated a suitability for extensive asexual propagation and provide guidelines on how to best apply that. To preserve and augment genetic diversity, strategies to mitigate inbreeding are crucial until sexual reproduction can be fully integrated into restoration protocols. Critical sites for restoration include local connectivity hubs, fringing lagoons that connect metapopulations, and back reefs around a particularly isolated population. These findings offer crucial insights into the genetic landscape of a keystone coral species and provide actionable recommendations for coral conservation and restoration.

The Organization of Grooming in Felidae – A Comparative Study of Movement Patterns and Sequence Flexibility

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Grooming is crucial for mammalian health and hygiene, serving diverse functions such as parasite defence, removing dirt, and thermoregulation. The mostly solitary Felidae depend entirely on autogrooming and profit from the high mobility of their legs and spine to fulfill the various functions of body care. To prevent an infestation with ectoparasites, grooming is not purely reactive but is integrated into daily routines and regulated endogenously. In rodents, such endogenously controlled grooming has been shown to follow a sequential structure with predictable patterns and rigid rules. Building on our earlier work on domestic cats, which did not reveal such structured autogrooming sequences, we extended our analysis to include seven additional Felidae species and four carnivoran outgroups. Using video recordings obtained at the Zoo Leipzig, we examined how lifestyle, morphology, and phylogeny influence the organization and movement patterns of grooming performance. Several grooming traits specific to Felidae - including a higher proportion of sequential grooming, longer durations of grooming bouts, a significantly higher proportion of face washing, and a broad array of different postures not seen in any of the outgroup species – were revealed by PCA. A first-order Markov-Chain analysis of grooming targets indicated a high degree of flexibility and a lack of fixed patterns or rigid rules across felid species.

Diversity of tarsal attachment structures in Mantodea (Insecta) includes two distinct attachment pad micro-morphologies

MOR
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Praying mantises (Mantodea) are well known for their predatory lifestyle and striking appearance, yet surprisingly little is known about their tarsal attachment systems. While other polyneopteran insect clades have been the subject of comparative studies based on large taxon samplings revealing variable ranges of ecological adaptations in their attachment structures, detailed investigations into the micromorphology of mantodean attachment pads remain scarce. We studied the tarsal morphology of a selection of 33 species of Mantodea across the phylogeny including the early-diverging lineages *Chaeteessa*, *Mantoida*, and *Metallyticus*, as well as representatives for the range of mantodean lifestyles. Scanning electron microscopy investigations revealed that both functional principles of animal attachment pads (smooth and hairy ones) are found within Mantodea: *Chaeteessa*, which is considered the sister group to all other mantises, features split tenent setae with spatula-shaped tips on their tarsal pads (euplantulae), while the remaining mantodean species possess smooth attachment pads. Some ecomorphological adaptations are observed among the studied species, such as pad asymmetry, ridgelike microstructures on the pad surfaces, and variations in the shape of the euplantulae. However, these adaptations are much less pronounced and variable than the microstructural adaptations found in other Polyneoptera. The predatory lifestyle of mantises potentially results in less strict substrate-specific constraints on their attachment organs compared to herbivorous insect groups that evolved to specialize on certain plant surfaces. Furthermore, functional aspects of the morphological adaptations of the attachment systems of Mantodea are discussed.

Evolution of reproductive strategies in cockroaches: Oothecae in the fossil record

MOR
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Today, the insect group Dictyoptera includes cockroaches, termites and praying mantises with an almost worldwide distribution. The evolutionary origin of dictyopteran ingroups is debated, but there is no doubt that cockroach-like representatives of Dictyoptera (sensu lato) or ‘roachoids’ were already abundant in the Carboniferous more than 300 million years ago.

A special feature of extant species within Dictyoptera is their ability to form a special egg case, the so-called ootheca. According to current knowledge, this characteristic was probably not shown by Carboniferous early roachoids due to the morphology of their egg-laying structures. The first direct evidence of oothecae can be found in fossils from the Cretaceous in amber and limestone. Since this time, cockroaches have developed various strategies with regard to oothecae: Some groups simply drop their oothecae after producing them or carrying them for a while (oviparity), other groups keep the oothecae in a brood pouch just before the nymphs hatch (ovoviviparity), or even longer (viviparity). However, the evolution of these strategies is largely unknown, and oothecae are surprisingly rare in the fossil record.

We present different cases of fossil oothecae in amber and limestone from the Cretaceous, Eocene and Miocene. We discuss different types of oothecae and indications for their mode of oviposition. With these new finds we can provide further information for the evolutionary reconstruction of the reproductive strategies of Dictyoptera in the deep time.

Ceriodaphnia changes morphology as a hydromechanical inducible defence against suction-feeding Utricularia

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Ruhr-Universität Bochum

Water fleas of the family Daphniidae are keystone species in many lentic ecosystems. As the most abundant filter feeders in these systems, they form a crucial link between primary production and higher trophic levels. Due to this central role in freshwater food webs and their capacity to develop predator-induced defences, Daphniidae are widely regarded as model organisms in ecological research. The mentioned inducible defences, representing a form of phenotypic plasticity, reduce an organism's vulnerability to specific predators. In the presence of gape-limited predators like fish, daphnids typically increase their body dimensions by forming helmets and spines, thereby outgrowing the predators' limited mouth width. In contrast to these observations, *Ceriodaphnia dubia* dramatically reduces its body dimensions in response to the coexisting Southern Bladderwort (*Utricularia* x *neglecta*). This suction-feeding plant is gape-limited by its trap door entrance. The change in *Ceriodaphnia*'s morphology coincides with a significant reduction in the predation rate. Using computational fluid dynamics (CFD), we simulated the drag forces acting on daphniids in the typical and the *U*. x *neglecta*-exposed morph. Our results indicate a decreased drag on the plant-exposed morph, likely acting in concert with a reduced probability of contact with the suction-eliciting trigger hairs due to proportionally smaller second antennae. We therefore propose a protective inducible defence mechanism based on altered morphology in combination with modified hydromechanical properties. This newly discovered defensive strategy of hydromechanical adjustments may also be present in other prey species facing suction-feeding predators.

Cephalic anatomy of *Euplectus kirbii* (Coleoptera: Staphylinidae: Pselaphinae)

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With more than 10,000 described species, Pselaphinae comprise 1/6 of the hyperdiverse group of rove beetles. Pselaphines exhibit a wide range of anatomical modifications in all body tagmata, even amongst species with similar lifestyles. However, past studies were almost exclusively focused on external morphology. Cephalic anatomy provides valuable insights in the biology and evolution of pselaphines (Jałoszynski 2022).

The focus of this study lies on the microstructure of the feeding apparatus, as well as the internal morphology of *Euplectus kirbii*, contributing to a project that aims to provide such insights for an extensive number of species across different lineages of Pselaphinae. The results have been compared with the cephalic anatomy of representatives of both basal (Faronus sp., Faronitae) and more derived (*Pselaphus heisei*, Pselaphitae (Beutel 2021)) lineages of Pselaphinae, and thus interpreted in a broader phylogenetic context. The study utilized histological sectioning and light microscopy, synchrotron micro-computed tomography (DESY, Hamburg) and 3D reconstructions of skeletal and muscular features, and scanning electron microscopy (SEM) of intact as well as dissected individuals. In respect to the compared species, *Euplectus kirbii* presents both plesiomorphies, like the presence of anterior tentorial arms, as well as derived features, such as the interruption of the tentorial bridge and shifts of origins of maxillary muscles.

Further anatomical studies of other species of Pselaphines will significantly aid our understanding of the evolutionary history of both their morphological features and their lifestyles.

Integrative study of muscle formation and appendage patterning genes sheds light on sea spider leg development

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One of the most striking features of the marine sea spiders (Pycnogonida) are their four pairs of long walking legs, which can dwarf the remaining body and resulted in their alternative name Pantopoda (=all-legs). During the anamorphic development of pycnogonids, leg development occurs consecutively at the posterior body terminus, whereby an almost complete leg abruptly emerges from a tiny cuticularized limb bud after a single molt. This externally explosive mode of leg formation has significantly hindered the study of proximo-distal (P-D) appendage patterning, as the leg tissues are drastically compressed in the limb bud cuticle prior to release. To overcome these challenges, we combined two modern approaches to interrogate leg development in the sea spider *Pycnogonum litorale*. Taking advantage of the strictly segmental array of intrinsic leg musculature in adults, we employed fluorescent F-actin staining and myosin heavy chain immunolabeling to follow muscle differentiation as a proxy for podomere location. Complementing these morphological landmarks, we applied HCR-FISH to visualize the expression of key genes that underlie the P-D patterning of arthropod appendages. Our study resolves the 3D-folded P-D axis of the compressed leg beneath the limb bud cuticle and shows that muscle differentiation in proximal and distal podomeres predates that in medial leg regions. Moreover, we document a previously unknown muscle group stretching over two podomere borders. Embedding these muscle data in the gene expression domains permits to resolve the P-D regionalization at (near) podomere resolution, providing important novel data for comparative studies on leg development in arthropods.

The leg diaphragm in the house centipede *Scutigera coleoptrata*

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Regenerating legs is advantageous for arthropods as their appendages exhibit crucial functional specializations. A feature in some arthropods that can regenerate their legs is the presence of a 'preferred breakage point' – a specific location where the appendage is predisposed to detach and where regeneration typically initiates. In some species, this breakage point is accompanied by an internal diaphragm, which facilitates wound closure and prevents fluid loss after injury. In the house centipede *Scutigera coleoptrata*, which easily can appendotomize legs, we recently investigated leg morphology and timing of leg regeneration. To understand the cellular organization of the diaphragm, we here analyze the diaphragm using transmission electron microscopy. It is located in the trochanter and composed of a thick transverse layer of connective tissue, featuring voluminous fibroblasts with numerous folded cellular processes, which contribute to the diaphragm's high flexibility. Proximally and distally it is bordered by layers of extracellular matrix – the so-called fibrous layers. The proximal fibrous layer is a thick coat of collagen fibers that contributes to the strength and resilience of the diaphragm. In contrast, the distal fibrous layer is much thinner and the extracellular matrix is present in between cellular processes. The diaphragm supports minimal but essential passageways for neuronal and circulatory continuity, as it only leaves passages to a leg nerve, a hemolymph vessel, and a small intrinsic muscle. Our study highlights the structural and functional complexity of the house centipede diaphragm, and sheds light on its evolutionary significance to facilitate leg loss and regeneration.

Dwarfism Reduces Cell Number, but Not Cell Type Diversity: Insights from the Eye ultrastructure of *Philinoglossa helgolandica* (Cephalaspidea, Gastropoda)

MOR 338

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Philinoglossa helgolandica Hertling, 1932, is a diminutive interstitial euopisthobranch gastropod found in shell detritus and coarse sediments of Helgoland, particularly from the "Amphioxus Grund." This species measures between 1 and 1.5 mm in length and is considered to have undergone evolutionary miniaturization. Its phylogenetic position suggests a trend toward reduced body size over time. The species possesses a single pair of small eyes situated near the cerebral ganglia. These eyes are characterized by a lens, partly surrounded by several corneal cells, a few pigment cells, and three types of photoreceptor cells that form the retina. These photoreceptor cells differ in size and structure.

Although *Philinoglossa helgolandica* is much smaller than other Cephalaspidea species such as Haminoea or Bulla, it shares similarities with *Bulla gouldiana* in the composition of its eye, where more than a thousand cells and three photoreceptor types are present. Despite the difference in size, the photoreceptor cells in both species are structurally identical, suggesting that dwarfism in *Philinoglossa helgolandica* leads to a reduction in cell number, but not in cell type diversity. Our results indicate that while evolutionary dwarfism favors smaller body size and fewer cells, it does not compromise the diversity of cell types needed for maintaining the original functional capabilities of the species.

Analysis of Averaged Locomotion Patterns in *Daphnia*

MOR 339

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Daphnia is a genus of small crustaceans inhabiting the pelagic zone of limnic ecosystems worldwide. Their common name ’water fleas’ derives from their type of locomotion consisting of an active antennal downstroke with upwards propulsion (hop) and a passive phase in which the antennae are repositioned and spread out to slow sinking until the next downstroke (sink). *Daphnia* performs between two and five of these locomotion cycles per second. They are characterised by rapidly changing water flow and strong gradients. One way to visualise the water flow around *Daphnia* is Particle Image Velocimetry (PIV). PIV shows the water flow as vector fields and is established for zooplankton, but previous analyses of PIV recordings covered only one individual locomotion cycle. This hampers a statistical comparison. Since *Daphnia* employ morphological changes as a defence mechanism against predators, a statistical comparison of the water flow around different morphs within the same species is of particular ecological interest. To enable this, we developed a MATLAB algorithm based on alignment and interpolation of vector fields resulting from the PIV analysis. It also takes the spatial and temporal varieties of different locomotion cycles into account. This allows to average locomotion cycles of *Daphnia* and reveal typical and reoccurring locomotion patterns as well as statistical differences between undefended and defended *Daphnia*. It furthermore helps to approach ecological research questions and is designed to work for other animals and applications as well.

Do hinge-like joints really aid in more efficient locomotion? Ground reaction forces and bone microstructure in cursorial mammals

MOR
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Mammals with a cursorial lifestyle exhibit elongated distal limb bones and generally hinge-like joints in the limbs. Elongated limbs and other cursorial traits have been shown to reduce locomotion costs, but the role of hinge-like joints has not been examined independently. Hinge-like joints stabilize the limb against sideways excursion and restrict movement to a single (parasagittal) plane. Besides aiding in the prevention of joint dislocation, it could be argued that this enhances locomotor efficiency, due to force transmission in a single plane in direction of locomotion. However, this assumption has not been explicitly tested in relation to hinge-like joints, independent of other cursorial adaptations. Here, we first aim to assess the hinge-like nature of elbows in mammals of various locomotor types. We will quantify the restriction to a single axis of rotation in the humero-radial joint of cursorial species by measuring and comparing the osteological range of pronation and supination. Next, we evaluate locomotor efficiency during steady-state locomotion by comparing in vivo ground reaction forces (GRF) in the same species. We expect cursorial species to exhibit relatively lower medio-lateral forces. This will indicate how efficiently GRF are channeled unidirectionally in the fore-aft direction during steady-state locomotion. Additionally, to determine whether increased hinge-like morphology corresponds to more unidirectional stresses on elbow bones, we will analyze anisotropy in the trabecular structure of the humerus, ulna, and radius. We expect cursorial species to exhibit lower anisotropy. This study contributes to the understanding of the interface of form and function in mammalian cursorial locomotion.

Looking behind — in vivo investigations on structural motions inside the locust ear

MOR
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Being able to hear allows predator avoidance and prey location as well as acoustic communication. For this, determining from where a sound originates can be crucial. This is particularly challenging for animals which are small compared to the wavelength of sound, such as insects. It has been shown that some insects use their antennae as flagellar ears, while others have developed tympanal ears in a variety of positions on their bodies, usually involving repurposed proprioceptors (chordotonal organs). Acridid grasshoppers possess ears located in the first abdominal segment, with the chordotonal Müller's organ attached to the back of the tympanum. These animals can hear frequencies between less than 1 kHz and about 40 kHz (Suga, 1960, Jpn J Physiol 10). Between the ears lie tracheal sacs transparent to sound. This coupling of the ears is relevant for directional hearing at lower sound frequencies (Römer & Schmidt, 2016, Biol Cybern 110) and is not fully understood.

A technique called optical coherence tomography (OCT) allows us to monitor motions of structures in the body by cross-sectional interferometry. With OCT, we investigate the mechanics of the locust ear in vivo, focusing on the tympanal membrane and the wall of the tracheal sac surrounding the ear inside the insect. Across the entire hearing range of the animal, we will measure sound-induced vibrations and create vibrometry maps of amplitude and phase. With our motion data on structures surrounding the hearing organ, we expect to produce significant advances in the research of insect ear mechanics.

A landmark-free approach to comparing 3D surface patches with homologous outlines

MOR 342

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Geometric morphometrics differentiates shapes based on landmark configurations, for which reliability in terms of homology is assumed. Well-defined fixed landmarks can be sparsely distributed depending on the structure under study. Therefore, modern geometric morphometrics heavily relies on curve and surface semi-landmarks to increase the quantifiable morphological information. Nevertheless, fixed landmarks are often used as anchor points of surface semi-landmark patches to ensure correspondence between specimens. Recently, surface semi-landmark placement via the surface registration method has gained popularity due to its (partial) independence from fixed landmarks.

The surface registration method is based on an ICP algorithm that virtually warps a mesh surface model of one reference specimen, typically of the most fragmented specimen, to best match each surface model of a set of target specimens. The mesh vertices of the target and reference surface models can then be analyzed like landmark configurations. Most applications of the surface registration method still rely on fixed landmarks for an initial registration step.

There are, however, structures where the placement of classical fixed landmarks is impossible. The approach presented herein is aimed at surface structures with clearly defined margins (e.g., muscle attachment sites on bones) but lack well-defined landmarks. Our proposed approach includes an initial pre-alignment based on vertices outlining the surface patch of interest, after which the correspondence of these margin vertices is established, through which the reference mesh can be warped onto the targets. This provides a reproducible quantification approach for otherwise problematic surface structures.

Investigation of Transgenerational Defense Strategies in *D. magna* Against Fish Predation

MOR
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The crustacean genus *Daphnia* is well-known for morphological adaptations induced by predators. Such inducible defense mechanisms include changes in morphology, behavior, and life history. However, little is known about the extent to which these adaptations are passed on to the next generation(s). Furthermore, the degree to which changes in behavior and life history occur, for example concerning swimming velocity, depth selection and number of offspring, remains insufficiently understood. To address these gaps, we investigated the predator-prey system comprising *Daphnia magna* and *Gasterosteus aculeatus*. By utilizing two clones of *D. magna* originating from similar habitats, we aimed to obtain generalizable results rather than clone-specific observations. We simulated constant fish presence throughout our experiment. We then examined the offspring of the first to third generations for morphological changes as well as changes in behavior and life history. By this we obtain a comprehensive characterization of the defensive strategy employed by *D. magna* in response to fish predation. In the future this data can also be used to estimate the cost associated. Integrating the defense mechanism with its costs allows a comprehensive description of this inducible defense in *Daphnia* and will improve our understanding of *Daphnia* ecology in freshwater habitats.

The longer, the better? – An unusual fossil praying mantis and the role of cerci length in the evolution of Mantodea

MOR
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The group Mantodea represents a relatively young lineage within Dictyoptera, first appearing during the Jurassic in the fossil record. Compared to other insect lineages of a similar age not many fossil specimens are known for Mantodea. Here we present an unusual new specimen from Cretaceous amber (c. 100 million years old) with prominent and long cerci. Although there are a few examples of extant mantodeans with proportionally longer cerci than the new specimen, most notably representatives of the group *Chaeteessa* (an early branch within Mantodae), this specimen shows the proportionally longest cerci of any known fossil mantodean. To quantitively assess how unusual this specimen is we compared the relative size of the cerci of extant mantodeans and of all available fossil specimens. We discuss the new implications for the early evolution of the group Mantodea. Furthermore, unusually elongated morphological structures in the Cretaceous have also been found in other groups of Euarthropoda, for example in different groups of lacewings (Neuroptera), in leafhoppers (Auchenorrhyncha) or in centipedes (Chilopoda). There appears to have been an evolutionary advantage for such strongly elongated structures in the past and a selection pressure to reduce their length later on.

Walking to the rhythm: Biomechanical modeling of the tail oscillation in the Late Jurassic sauropod *Giraffatitan brancai* to infer optimal locomotor dynamics

MOR
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The exceptionally large body size of sauropod dinosaurs presents intriguing questions about their locomotor mechanics. However, reconstructing the gait kinematics of extinct animals remains a challenge. Living animals tend to select step frequencies that match the natural resonance of their body parts, thereby reducing energy expenditure. Consequently, investigating the natural frequencies of specific sauropod body structures can provide insights into their optimal locomotor dynamics. Sauropods had large, muscular tails that played both active and passive roles in their movement. These tails were passively suspended by ligaments, functioning as mass-spring systems that oscillated with each step during locomotion. This principle has been used as a proxy for determining the energetically optimal step frequency in previous research, referred to as the Natural Frequency Method. In this study, we apply the Natural Frequency Method to estimate the energetically optimal step frequency and walking speed of the Late Jurassic sauropod *Giraffatitan brancai*. We constructed a biomechanical model based on the three-dimensional morphology of its tail, with each vertebra connected by hinge joints and supported by interspinous ligaments. The model includes 18 preserved anterior caudal vertebrae and 19 hinge joints. The missing distal portion was reconstructed as a 4.34 m cone-shaped segment, replacing up to 40 unpreserved vertebrae. The complete tail model is 7.34 m long, with an estimated total mass of 1688.4 kg, including soft tissue. Our broader aim is to expand this approach to other sauropod taxa with differing tail morphologies, to better understand how tail morphology influences locomotor dynamics.

From ambush to pursuit: Mapping elbow joint mobility across feliform predators

MOR 346

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Extant feliform carnivores are highly effective predators that employ various hunting strategies – often categorized as ambush, pursuit, or pounce-pursuit - to capture and manipulate prey. These variations in hunting style are reflected in their elbow morphology, which has been extensively studied through morphometric analyses. Ambush predators are thought to exhibit a greater general flexibility, particularly in supination, likely facilitating prey manipulation during capture. In contrast, both pursuit and pounce-pursuit strategists show specializations for fast running at the expense of elbow flexibility outside the parasagittal plane. The distinction between pursuit and pounce-pursuit strategists, with pursuit species chasing prey over longer distances than pounce-pursuit predators, is less clear. Species employing either are mostly distinguished by body size and some osteological features, suggesting an even stronger restriction of rotatory elbow motion in pursuit species. With these variables known, the hypothesized effect of hunting style and elbow morphology on joint mobility has not been quantified.

In this ongoing research, we employ a 6-degrees-of-freedom range of motion analysis to biomechanically quantify elbow joint mobility across various feliform species. Our dataset includes digital surface models of humeri, ulnae, and radii of 11 species representing the three hunting strategies. We expect a gradient of elbow mobility from highest in ambush predators to lowest in pursuit species, with pounce-pursuit strategists falling in between. This study aims to add a new biomechanical perspective on the relationship between carnivoran forelimb morphology and hunting style to ultimately offer new functional insights in locomotion and predatory strategies of extinct carnivoran taxa.

Reconstructing Predatory Behaviour of the Iconic Thylacine - Trabecular Architecture Reveals a Fox-Like Predator

MOR 347

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The thylacine (*Thylacinus cynocephalus*) is as enigmatic an animal as it is iconic. Ever since the last specimen died at Hobart Zoo, Tasmania, in 1936 numerous unconfirmed sightings and unsuccessful searches have kept public interest in the "marsupial wolf" at a constant high. As the posterchild of convergent evolution in predatory mammals, scientists, too, have long been interested in the biology and behaviour of *T. cynocephalus*. Especially since, despite its recent extinction and the publics ongoing fascination, virtually nothing is known about this iconic predators behaviour or ecology. Primarily its predatory behaviour has in the past inspired studies and debates. Previous studies were largely based on external morphology and yielded ambiguous results.

Here, we present a novel approach using trabecular bone functional adaptation to infer the thylacine's likely hunting type. As trabeculae remodel in response to habitual loading, their architecture can reflect behavioural patterns. We investigate this relationship using µCT-scans of the humero-radial joint in Carnivora and the thylacine. Using linear discriminant analysis, we are able to not only correlate trabecular architecture with known hunting types, but also firmly reconstruct the thylacines hunting type to be most similar to the pounce/pursuit type most often exhibited by fox-like predators.

Bite Force Estimation in Sirenians

MOR
348

Jasper Maack; Prof. Dr. Christine Böhmer; Daniela E. Winkler

Christian-Albrecht University of Kiel

"While substantial research has been conducted on the bite force of carnivorous animals, a similarly extensive body of research on herbivorous animals is lacking. However, a plant-based diet can pose significant challenges regarding mastication and food processing. This is especially true for plants that exhibit high physical toughness, such as grasses. In this study, we use a well-established dry skull method to estimate bite forces for all four extant sirenian species, as well as a terrestrial grazer (common hippopotamus) and a terrestrial browser (moose). The physical properties of the most common forage plants were systematically compiled from the literature, and bite forces were subsequently compared interspecifically and in relation to respective plant toughness, body length, and skull length. A comparative analysis revealed that all four sirenian species exhibited a significantly higher bite force than the moose, with the hippopotamus demonstrating the highest calculated force. The correlation between body and skull length and bite force was not significant; however, a strong correlation was observed between bite force and the physical toughness of forage plants. Despite the limited sample size and the lack of additional data concerning further plant mechanical properties, the present study is the first to estimate bite forces in sirenians and relate them to their dietary habits. Future work should concentrate on the study of herbivore bite force and mastication mechanics in general, as well as on the relationship between sirenian diet and mastication biomechanics in particular."

Ants on trees have a better view!

MOR 349

Peter Rühr

University of Bonn

Compound eyes are the dominant visual system in arthropods, yet their structural diversity remains understudied across lineages. In ants, the number of ommatidia varies from zero to several thousand, each comprising a lens (facet) and a photoreceptive unit. The angles between the ommatidia influence the eye’s visual acuity and sensitivity, and sensitivity is also governed by facet size.

We developed a high-throughput workflow integrating µCT imaging, 3D-scanning, or histological sectioning with an open source software pipeline to extract the 3D geometry of ommatidial arrays: ommatidial positions, inter-facet angles, and field of view reconstructions. Applying this to 75 ant species across their phylogeny, we reconstructed their visual topologies.

Our phylogenetically informed analyses of the results reveal that visual acuity and sensitivity are tightly linked to the ants’ foraging strategy. Arboreal ants see more clearly than ants that forage close to the ground, in leaf litter or underground. We also found that nocturnal ants have larger facets than diurnal ants. In contrast to what is known from other insect groups, larger ants do not increase their facet size in proportion to eye size, but rather focus on achieving higher accuracy than on increased sensitivity. Our results help understand the evolution of ant eyes by identifying several ecological drivers and unexpected allometric relationships.

RHODOPSIN 7 – a non-retinal rhodopsin with distinct function in *Drosophila melanogaster*

NEU
431

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Rhodopsins are specialized G-protein-coupled receptors involved in photoreception. Drosophila melanogaster has seven types of rhodopsins. RHODOPSIN 7 (RH7) differs from RH1–RH6 in structure and function.
Behavioral assays demonstrate that RH7 is involved in light detection as mutants lacking Rh7 show an altered phenotype, they cannot adapt to challenging conditions and fail to shift their activity into the darkness. Furthermore, optomotor response assays demonstrate that Rh7[0] mutants have reduced contrast perception. The mutants also show a decreased response to abrupt light-off stimuli. Both behaviors were restored when Rh7 was reintroduced under the control of the Rh7-promoter. By using tissue-specific qPCR, Rh7-promotor induced GFP expression, and in situ hybridization, we observed broad Rh7-expression in lamina, medulla and in several neurons in the central brain.
So far, we could identify the expression of Rh7 in the lamina neuron L5, the medulla neuron Mi1 and the dorsal clock neurons DN1p, DN1a, DN2. The fact that Rh7 is expressed in regions that are distinct from those of Rh1-6 and the possible absence of phototransduction components in these cells suggests that Rh7 engages a different signaling pathway.
We show that RH7 is involved in contrast perception and important for activity during darkness. Many characteristics of RH7 resemble those of mammalian melanopsin: (1) RH7 is localized in visual processing neurons and not in the retina itself, (2) it is involved in contrast perception, (3) it may use a different signaling pathway, and (4) it plays a role in adapting and shifting activity to darkness.

NEU 432

Trans-synaptic tracing and functional analysis of the connections between central clock neurons and downstream neuroendocrine cells underlying eclosion gating in *Drosophila*

Prof. Dr. Christian Wegener; Emad Amini

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In order to grow, insects have to molt their rigid cuticle during development. At the end of each molt, they propel themselves out of the old cuticle by a stereotyped fixed-action motor pattern known as ecdysis. Ecdysis behaviour is orchestrated by a hierarchical cascade of neuropeptide signalling initiated by the release of ecdysis-triggering hormone (ETH), as well as eclosion hormone (EH) from endocrine cells in the brain. In most insects, adult ecdysis (aka eclosion) is gated to a particular time of the day.

In the vinegar fly *Drosophila melanogaster*, two clocks are required for gating: the central clock in the brain, as well as a peripheral clock in the prothoracic gland (PG) that secretes the steroid hormone ecdysone. It is, however, unclear whether and how these clocks time the initiation of ETH-EH release that is required to start eclosion behaviour.

We used genetic trans-synaptic tracing techniques to find out whether and which central clock neurons make direct synaptic connections to EH neurons as well as PTTH neurons that we earlier on showed to be required for rhythmic eclosion. We further tested the functional significance of the observed connections for eclosion timing by optogenetic activation and genetic silencing.

Our results identify various subsets of central clock neurons that provide input to both EH and PTTH neurons and suggest that the sLNv-PTTH neuron-prothoracic gland axis is the key neuroendocrine pathway underlying eclosion timing.

Funded by the Deutsche Forschungsgemeinschaft (DFG WE 2652/7-1)

NEU 433

Impact of sub-lethal dosages of the insecticide flupyradifurone on the ascending auditory interneurons in the cricket brain

Marcelo Christian; Prof. Manuela Nowotny; Dr. Stefan Schöneich

Friedrich Schiller Universität Jena

Insecticides are an essential part of modern agriculture. However, their extensive use has also been associated with the world-wide decline of the insect fauna over the last decades. Therefore, it is crucial to better understand the impact of modern insecticides on non-target insects with diverse behavioural lifestyles. Here, we analysed the effect of the insecticide flupyradifurone on the auditory pathway of the field cricket *Gryllus bimaculatus*. Flupyradifurone acts as highly selective agonist at achetylcholine receptors in the insect CNS. We recorded the spiking activity of ascending auditory interneurons AN1 and AN2 using a suction electrode at the brain surface. We measured the spiking response to acoustic stimulation (5, 10, 15, 20 and 30 kHz at 70, 75 and 80 dB) while applying different concentrations (10^-7, 10^-6, 10^-5, 10^-4, 10^-3 mol/l) of insecticide. Flupyradifurone caused a dose-dependent increase of spontaneous spiking activity. In contrast it led to a decrease in stimulus correlated spiking activity of ascending auditory interneurons, peaking in a collapse of activity at the highest measured concentrations. Crickets rely heavily on auditory information for phonotactic mate finding and predator avoidance. Therefore, the disruption of auditory processing may substantially reduce their chances for survival and reproduction.

Neuronal activity mapping across phenotypic transitions in the desert locust

NEU
434

Elvira Mamonova; Dr. Daniele Carlesso; Dr. Sercan Sayin; Dr. Einat Couzin-Fuchs

Universität Konstanz

Desert locusts, a grasshopper species, dwell in a cryptic, sedentary “solitary” phase when food is plentiful and population density low. Food scarcity can force dense populations to aggregate around limited resources and result in the notorious insect pest as the locusts transition to a highly active, swarming “gregarious” phase. With up to 80 million individuals per km^2, swarms can span several hundred square kilometers and severely threaten local and global food security. While phase-specific behavioral and physiological differences are well documented, the proximate mechanisms driving the transition remain poorly understood. Accessing the brain as the first instance of phase change initiation constitutes an evident approach, but robust tools for mapping brain activity in non-model insects are still required.

Recent behavioral history in the brain can be characterized via rapid gene expression of immediate early genes (IEGs) and is already widely established in other animal systems. Such tools offer a window to unbiased, hypothesis-free, exploratory whole-brain analyses without focusing on a particular region. By targeting transcripts of a candidate IEG with the optimized staining method HCR-RNA FISH, we aim to develop a reliable neuronal activity readout in desert locusts. Motion capture technology allows us to continuously monitor the behavior of solitary locusts during their first exposure to marching bands of gregarious conspecifics. Here, we will leverage our expertise by combining behavioral and molecular assays to localize pathways activated during the process of gregarization by timely tracking of whole-brain activity and develop protocols to identify cells or brain regions recruited during crowding.

Surviving at the dry limit: Animal diversity in an ecosystem sustained by lichen and fog in the coastal Atacama Desert

ECO
531

Hsin-Ju Cheng; Prof. Dr. Reinhard Predel; Prof. Dr. Alfonso Pablo Jara Flores; Dr. Simon Matthias May; Dr. Alvaro Zúñiga Reinoso

University of Cologne

Fog oases in the Atacama Desert are known for forming Lomas—vegetated zones where cacti, shrubs, and Tillandsia dominate. These areas enable some animals to survive despite the hyper-arid surroundings. However, they are isolated “islands” within the barren Coastal Cordillera. Adjacent areas without vascular plants have often been assumed to be “dead zones,” even though lichens are the most visible and persistent life forms.

The Pisagua region provides a valuable setting to study biodiversity in fog-influenced zones where lichens dominate. We investigated how environmental variability relates to animal species richness across four sites along a transect. At each site, two systems of five fenced pitfall traps were installed. Traps operated for one year and were checked biannually between 2022 and 2023. Weather data were collected using a weather station, while temperature and relative humidity were recorded with dataloggers at ground level.

Species richness responded distinctly to microclimatic conditions. Results highlight the ecological role of fog-driven humidity in shaping animal diversity in extreme arid environments. Coastal fog is the main moisture source, but topographic features trap fog inland, creating stable humid zones. These support lichen growth and harbor the most diverse communities, forming simple food webs unrelated to distance from the coast.

Interestingly, the least diverse site deviated from this pattern: it supported a secondary community that was not lichen-dependent but instead relied on Maindronia (Insecta: Zygentoma) as the main surface-level food source.

Surviving the City: How urbanization shapes red squirrel survival

ECO
532

Alina Theresa Berger; Dr. Conny Landgraf; Prof. Dr. Stephanie Kramer-Schadt; Sinah Drenske

Leibniz Institute for Zoo and Wildlife Research

Urban growth is rapidly transforming landscapes, increasing the relevance of cities for biodiversity conservation. As urban areas expand, animal habitats become increasingly fragmented and altered, exerting selective pressures on wildlife behaviour, physiology, and survival.

This study investigates how urbanization affects the survival of Eurasian red squirrels (*Sciurus vulgaris*) along an urban–rural gradient in Berlin, Germany. Since 2021, red squirrels have been live trapped biannually in spring and autumn across three study sites representing different levels of urbanization, resulting in a sample of more than 140 marked individuals. Capture–recapture data were analysed using Cormack–Jolly–Seber models to estimate survival and detection probabilities in open populations.

Our results show that survival and detectability vary with season, sex, and degree of urbanization. Survival probabilities differed between males and females depending on site-specific urbanization levels, suggesting sex-specific responses to local environmental conditions.

This study demonstrates how urbanization influences demographic processes in a small mammal with pronounced seasonal cycles. The findings improve our understanding of how red squirrels persist in heterogeneous urban environments and offer valuable insights for urban planning – in particular emphasising the importance of green spaces with old-growth tree-cover as vital habitats, promoting seasonally relevant resources, and supporting long-term population viability in cities.

Surviving the City: Population genetics of red squirrels in Berlin

ECO
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Leibniz Institute for Zoo and Wildlife Research

Urban growth is rapidly transforming landscapes, increasing the relevance of cities for biodiversity conservation. As urban areas expand, animal habitats become fragmented and altered, exerting selective pressures on wildlife behaviour, physiology, and survival.

This study investigates how urbanization affects the population genetic structure of Eurasian red squirrels (*Sciurus vulgaris*) in a woodland area and two urban parks in Berlin, Germany. Since 2021, red squirrels have been live-trapped biannually in spring and autumn across three study sites representing different levels of urbanization, resulting in a sample of over 140 marked individuals.

We genotyped all individuals at 16 microsatellite loci and analysed genetic structure using Bayesian clustering with STRUCTURE. Additionally, we calculated standard population genetic metrics (e.g., observed and expected heterozygosity, allelic richness, Wright’s F-statistics) to assess genetic diversity and differentiation among sites. Our results revealed detectable genetic structuring between sites, potentially shaped by urban fragmentation and associated high mortality or founder effects.

This study highlights how urbanization influences genetic processes in a small mammal. Our findings provide valuable insights into how red squirrels persist in heterogeneous urban environments and emphasize the importance of maintaining green space connectivity and permeability for animal movement. Such insights are essential for designing urban landscapes that support genetic exchange and long-term population viability for wildlife.

Molecular Detection of Vector-Borne Pathogens in Ticks collected from Companion Animals in the Republic of Kosovo

ECO 534

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Tick-borne diseases are an increasing concern for both animal and human health, especially in settings with high vector-host interactions. This study investigated the presence of pathogen DNA in ticks collected from companion animals in Prishtina, the capital city of Kosovo. During the summer of 2024, a total of 305 ticks were collected from 120 dogs and 20 cats presented for routine care at a local veterinary clinic. Ticks were morphologically identified and subjected to DNA extraction for barcoding and PCR analysis targeting specific tick-borne pathogens, such as *Anaplasma*, *Borrelia*, *Piroplasmida*, and *Rickettsia*.

This is the first molecular study in Kosovo focusing on ticks collected directly from companion animals during veterinary visits. The approach demonstrates the feasibility of monitoring tick-borne pathogens without the need for invasive blood sampling or labor-intensive field collection. Importantly, companion animals often live in close contact with humans, making them potential vessels for zoonotic disease transmission.

The findings underscore the importance of awareness among veterinarians and pet owners and urge for the application of preventative measures. Further research is essential to evaluate the zoonotic potential and broader public health implications of these pathogens in Kosovo.

ECO
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The development of social behaviour in juveniles in a population of reintroduced Northern Bald Ibis (*Geronticus eremita*)

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[4] Waldrappteam Conservation & Research, University of Vienna

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Understanding the ecological and social dynamics of animal migration is crucial in times of rapid environmental change. Investigating the development of social behaviour in the Northern Bald Ibis (*Geronticus eremita*, hereafter NBI) can provide valuable insights for conservation management. Juveniles have a short interval between fledging and first migration during which they must learn whom to follow within the colony to increase survival chances. We analysed 37 ad libitum observations of 21 reintroduced juvenile NBI between July and August 2019, to investigate how age, sex, number of neighbours, and food distribution affect social interactions, measured as the proportion of time expressing agonistic or affiliative behaviour. We constructed social networks for the beginning and end of the observational period using the Dyadic Composite Sociality Index (DSI), which reflects the relative strength of relationships between dyads compared to the group.

Time of day affected all categories and food distribution affected overall and affiliative behaviour positively, where juveniles expressed longer durations for social behaviours. Age affected overall and affiliative behaviour negatively where juveniles reduced durations altogether. Sex showed a tendency effect on agonistic behaviours where males showed longer durations than females.

The number of relationships in the networks diminished over time, especially for affiliative behaviour. This study shows that agonistic behaviour seems to play a greater role in early social behaviour development in NBI juveniles, where juveniles potentially focus on establishing their position in the colony for their first migration.

Detecting red squirrels across Germany: What Citizen Science reveals about habitat use and reproduction

ECO
536

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Urbanisation confronts wildlife with growing challenges due to habitat fragmentation and human disturbance. This study investigates how Eurasian red squirrels (*Sciurus vulgaris*, hereafter "squirrels") respond to such pressures by analysing their spatial and temporal distribution, habitat selection and the occurrence of juveniles.

We use data from a nationwide structured German Citizen Science project, launched in February 2024 as cooperation between NABU, NABU|naturgucker and the Leibniz Institute for Zoo and Wildlife Research. Citizens report squirrel sightings or non-sightings and provide additional information such as number of squirrels, number of juveniles, activity, photos, date and location.

Citizen Science provides the opportunity to collect extensive data over large spatial and temporal scales, offering a deep insight into species ecology. Citizens submitted over 31 000 squirrel observations, with roughly 4 000 from rural and 27 000 from urban areas. We used MaxEnt to derive critical variables explaining the occurrence of squirrels and estimate the number of offspring depending on the most important habitat variables derived from the MaxEnt model.

Our results shed light on habitat preferences and seasonal patterns in squirrels. Understanding when squirrels are active and reproduce throughout the year provides a basis for identifying how wildlife adapts to urbanisation and climate change.

Rapid proliferation of life after simulation of rainfall in the coastal Atacama Desert

ECO
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Ecaterina Sclifos; Dr. Alvaro Zúñiga-Reinoso; Alfonso Jara-Flores; Dr. Simon Matthias May; Prof. Dr. Michael Bonkowski; Prof. Dr. Reinhard Predel

University of Cologne

Fog along the Coastal Cordillera of the Atacama Desert locally provides sufficient moisture to support a highly adapted perennial vegetation (fog oases). Particularly at the southern border of this desert (south of 27°S), El Niño Southern Oscillation brings episodic rainfall to otherwise hyperarid regions leading to spectacular desert bloomings. Both fog oases and regions with occasional rainfall have not only a different flora (perennial vegetation vs. short-lived plants) but likely also a very different arthropod fauna. The Paposo area (25°S) is a typical fog oasis and at the same time a region with occasional rainfall, i.e. a transition zone to strictly fog-dependent ecosystems further north. To study the organismal response to sporadic rainfall events in this area, we conducted a large-scale irrigation experiment on fossil alluvial soils below the steeply rising Coastal Cordillera, which show a more abundant perennial vegetation due to stronger fog precipitation. For that, we simulated rainfall of varying intensity on fenced plots equipped with pitfall traps. Organismal response was monitored for three months, together with changes in soil humidity, temperature, and vegetation. Small scale blooming of short-lived plants verified the success of the irrigation. The documented arthropod fauna (~150 different species) can be separated into those species that are primarily adapted to the fog oasis and thus tend to occur independently of rain (most species), and others that only appeared after the irrigation (e.g. *Gyriosomus*: Tenebrionidae). A positive relation between the amount of rain and the diversity/ abundance of arthropods was found.

More than only microorganisms: Metazoan life in a Mars-like landscape in the hyperarid core of Atacama Desert

ECO
538

Alfonso Pablo Jara Flores; Dr. Álvaro Zúñiga-Reinoso; Prof. Dr. Reinhard Predel

University of Cologne

Yungay area is located in the hyperarid core of the Atacama Desert, the driest non-polar area in the world and due it's harsh conditions it has been proposed as an adequate model for the Potential Life Search on Mars. This area has been defined as "dead zone" for animals and plants and only few microorganisms have been documented from this area. To confirm this simple hypothesis, we installed a large-scale cross-shaped pitfall trap system (30m x 30m). Traps were connected by fences and, after sampling a year around, a hitherto unknown ecosystem could be documented. An undescribed and abundant *Maindronia* (Zygentoma: Maindroniidae) possibly serves as keystone species in a very simple food chain, and a *Liolaemus* lizard occurs as apex predator. Studies on the diets and water acquisition by the species encountered are still ongoing.

Impact of SSRIs on the Behavioural Activity of *Chaoborus* Larvae and *Notonecta* Under Variable Temperature Conditions

ECO
539

Frida Pallapies; Roman Epping; Annika Hornkamp; Dr. Linda Weiss
Ruhr-Universität Bochum

Global change impacts freshwater ecosystems, contributing to biodiversity loss and ecosystem instability. Among various anthropogenic influences, rising temperatures and micropollutants, such as antidepressants, are major stressors. Selective serotonin reuptake inhibitors (SSRIs) are increasingly found in freshwater due to rising prescription rates and low removal efficiency in wastewater treatment plants.

These neuroactive substances affect serotonergic pathways in invertebrates, often linked to feeding behaviour and activity patterns. Simultaneously, elevated temperatures accelerate metabolic rates, potentially altering behaviour. Behavioural adaptations are critical for survival in the context of predation. Prey often reduce activity to avoid detection, while ambush predators, like the phantom midge *Chaoborus* or the backswimmer *Notonecta*, rely on motionless stealth to capture prey. Stressor-induced behavioural changes could destabilize these ecosystems. In this study, we analysed the effects of SSRIs in different temperature conditions on the activity patterns of *Chaoborus* spec. and *Notonecta* spec. Results show that temperature had no effect on overall activity and predation rates in *Chaoborus*. SSRIs reduced predation rate in *Chaoborus* and *Notonecta*. No impact on overall activity was observed. Reduced predation by *Chaoborus* or *Notonecta* could lead to increased zooplankton populations, such as *Daphnia*, altering community composition and improving water clarity through enhanced phytoplankton grazing. These changes may disrupt trophic dynamics, reducing energy transfer to higher predators and shifting nutrient cycling processes. Understanding how combined stressors impact predator-prey dynamics is crucial for predicting and mitigating global change effects on aquatic ecosystems. This study highlights the importance of addressing multiple anthropogenic pressures to preserve freshwater ecosystem health and functionality.

The scent of danger - local adaptation of predator-mediated defences and information transfer disruption in multiply-stressed riverine ecosystems

ECO
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Nicole Ellen Wells; Prof. Dr. Ralph Tollrian; Dr. Linda C. Weiss

Ruhr University Bochum

Predation plays a crucial role in shaping natural biological communities and drives the evolution of different defense or avoidance mechanisms in prey species. Chemical cues (kairomones) released by predator species mediate indirect interactions like drift or hiding behavior between predator and prey. Anthropogenic stressors such as elevated temperature and salt concentration may significantly interfere or inhibit the signal transfer and thereby modify or suppress the defense responses of prey species. Therefore, the effects of predation in freshwater systems under stressor conditions might differ significantly from near-natural conditions. However, the underlying mechanisms of predator perception remain unclear. Building on previous findings, we aim to unravel these underlying mechanisms and how they are influenced by anthropogenic stressors like salt and temperature using the prey species *Gammarus fossarum.* Specifically, we aim to investigate the mechanisms of chemical information transfer and its disruption in *G. fossarum*. We will investigate and identify the neurons that are involved in predator perception. For this purpose, we will monitor the expression of immediate-early genes and components of the evolutionarily conserved mitogen-activated protein kinase pathways. Furthermore, we aim to identify differentially expressed genes involved in the response to biological and anthropogenic stressors. Therefore, this project addresses a critical gap in understanding predator-mediated defenses and responses to anthropogenic stressors.

Small-scale bioassay shows kairomone induced activity changes in *Gammarus* spec.

ECO 541

Lasse Broska; Alexander Julian Rogalla; Nicole Ellen Wells; Prof. Ralph Tollrian; Dr. Linda C. Weiss

Ruhr University Bochum

Behavioural adaptations in the presence of a predator are a widespread mechanism to reduce one's own predation risk. The basis of predator evasion behaviour is sensing the presence of the predator in the first place. Chemical cues are a common way of sensing predator presence. These kairomones are released (involuntarily) by an organism and are beneficial to the recipient. Gammarids, small freshwater amphipods, adapt their behaviour accordingly when sensing the presence of predators like fish. Common behavioural adaptations of gammarids are hiding, drifting or reducing activity. However, strong stressors like elevated temperature or increased salinity were observed to reduce anti-predator responses in aquatic macroinvertebrates. Not sensing potential predators could lead to changes in food web dynamics as stream macroinvertebrates like gammarids experience higher predation pressure. Researching effects on predator-prey interactions often requires elaborate set ups and a great time investment. We established a small-scale bioassay to measure simplified effects of kairomone exposure on gammarid behaviour. Using multiwell cell culture plates, cameras and tracking software we quantified activity of gammarids exposed to a variety of chemical cues. Gammarids were exposed to tab water, water from fish tanks and both gudgeon and stickleback kairomone. Individuals exposed to the stickleback kairomone were less active and covered smaller distances. Gammarids swimming in tab, fish tank or gudgeon kairomone water did not show a significant change in travelled distances. Seemingly, the small-scale set up is sufficient to quickly show simplified kairomone effects without the need of an elaborate set up.

Predator-induced behaviour of *Gammarus pulex*: Effects of predator species, concentration and lighting conditions

ECO
542

Inka Hentschel[1]; Alexander Rogalla; Nicole Ellen Wells; Lasse Broska; Ralph Tollrian; Linda C. Weiss
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Chemical cues released by predators (kairomones) play a crucial role in freshwater ecosystems, especially in mediating predator-prey interactions. Prey species respond to kairomones with behavioural responses such as hiding or entering drift. *Gammarus pulex* is a common benthic arthropod species known to shift behaviour in the presence of its predators. While *G. pulex* is known to alter its behaviour in the presence of predators, the influence of predator identity, cue concentration, and time of day remains poorly understood. In this study, we investigated the behavioural responses of *G. pulex* to chemical cues from two predator species (i.e., *Gasterosteus aculeatus* and *Gobio gobio*) at varying concentrations, under simulated day-night cycles in a controlled flow-channel system. We monitored microhabitat selection and drift activity as indicators of antipredator behaviour. *G. gobio* required higher predator densities than *G. aculeatus* to elicit comparable behavioural shifts. During the day, individuals showed strong microhabitat preferences consistent with a hiding strategy, whereas at night, increased drift suggested a flight response. Our findings reveal that *G. pulex* employs predator-specific and light-dependent avoidance strategies, shaped by both biotic and abiotic factors. This highlights the complexity of predator-induced behavioural plasticity and advances our understanding of how environmental context modulates prey responses in aquatic systems.

Investigation of predator-induced behavioural changes of macroinvertebrates in riverine ecosystems with regard to changing environmental conditions

ECO
543

Alexander J. Rogalla[1]; Nicole E. Wells[1]; Lasse Broska[1]; Inka Hentschel[1]; Dr. Kamil Hupalo[2]; PD Dr. Linda C. Weiss[1]; Prof. Dr. Ralph Tollrian[1]

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Drift is a central mode of locomotion for stream macroinvertebrates, enabling them to forage, colonise new habitats, or escape rapidly when threatened by predators. Human activities, however, are altering riverine environments: rising temperatures and salinity now impose additional stress, potentially impairing prey species' ability to detect predators and mount effective defences. Because such changes can reshape interspecific interactions and reorganise entire freshwater communities, it is vital to understand drift behaviour, the underlying chemical cues, and their sensitivity to environmental drivers.

Our project therefore aims to identify the fish-derived chemical signals that trigger antipredator behaviour in two ecologically important amphipod crustaceans (*Gammarus pulex* and *G. fossarum*) and in the bioindicator mayfly *Baetis rhodani*. We will also determine how elevated temperature and salinisation modulate predator-induced drift in these taxa. To achieve this, we have established experimental indoor flumes that accurately simulate predator presence alongside the targeted stressors.

By linking chemical ecology with behavioural responses under realistic global-change scenarios, our work will advance mechanistic predictions of how freshwater communities may react to predicted climatic conditions in the coming decades.

Inducible defences of Daphniidae against Odonata larvae

ECO
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Charlotte Emma Westphal; Dr. Linda C. Weiss; Dr. Martin Horstmann; Prof. Dr. Ralph Tollrian

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Species of the cladoceran family Daphniidae play a key role in freshwater ecosystems. While they filter phytoplankton efficiently, they serve as important prey for numerous aquatic predators. In response to such predation pressure, Daphniidae exhibit pronounced phenotypic plasticity, which is often triggered by infochemicals released by predators. These chemical cues enable the early detection of predators and the expression of a range of inducible defense strategies, including morphological changes, behavioural shifts, and alterations in life-history traits. In many species, structural modifications of body shape and accelerated development are well-documented adaptive responses to predation threats. Dragonfly larvae (Odonata) are such a predation threat. They are highly efficient, visually oriented predators that rely strongly on movement and body size when detecting prey. Larger daphniid species are particularly conspicuous and thus subject to strong predation pressure. However, inducible defences against Odonata larvae are undocumented in Daphniidae. In this study, we conducted controlled laboratory experiments in which individuals from multiple daphniid species were continuously exposed to chemical cues from various Zygoptera and Anisoptera larvae using mesh enclosures. The results revealed significant morphological changes: body length, body width, and dorsal spine length (relative to body length) differed significantly in the presence of dragonfly larvae compared to the control group. Additionally, we observed an accelerated development (reduced time to primiparity) and found differences in brood size under predator cue exposure. These findings provide novel evidence for inducible defences in Daphniidae in response to Odonata predation risk, expanding our understanding of predator-prey interactions in freshwater ecosystems.

The effects of the neonicotinoid imidacloprid on workers, larvae and queens after oral exposure

ECO
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Marius Pohl[1]; Dr. Mathias Otto[2]; Dr. Udo Hommen[3]; Dr. Sebastian Eilebrecht[3]; Prof. Dr. Christoph Schäfers[3]; Dr. Benedikt Ringbeck[3]; Dr. Bernd Göckener[3]; Prof. Dr. Jürgen Gadau[1]

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The widespread use of pesticides causes universal contamination of almost all terrestrial ecosystems. Neonicotinoids, the most commonly used broad-spectrum insecticides, affect both target and beneficial non-target insects. Among these, ants (Hymenoptera: Formicidae), as eusocial insects, are worldwide distributed, covering many essential ecosystem services. Despite their ecological relevance, ants are not included in current pesticide risk assessments. To address this, we developed a staged testing scheme using ants as new model organisms by exposing them orally, as the most field-realistic pathway. We assessed pesticide effects at three different levels: (1) workers, (2) larvae and (3) queens.

Using the carpenter ant *Camponotus* maculatus, we observed a clear concentration-dependent worker mortality (LC50= 11.2 mg/L) and behavioral changes, which likely reduced larval exposure but also reduced brood care. Besides mortality, some larvae showed developmental impairments leading to naked pupae, at concentrations where workers appeared unharmed. *Lasius niger* queens, which were exposed to a single dose of imidacloprid, showed significantly reduced brood production and high mite infestation rates (22–78%) compared to the control groups (0% infestation).

Our findings show the feasibility of using ants as test organisms in risk assessments. Given their ecological importance, easy maintenance in laboratory settings and long-lived colonies, ants represent a valuable extension to existing testing protocols. Further research is needed to establish a robust, standardized testing scheme, ultimately contributing to a more effective protection of biodiversity and ecosystems.

Microwear in Marine Mammals: Using DMTA to Differentiate Feeding Patterns in Sympatric Seals

ECO 546

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Understanding feeding strategies in marine mammals is crucial for assessing ecological roles and the impacts of changing prey availability. In this study we apply Dental Microwear Texture Analysis (DMTA) to infer dietary and behavioral differences in two sympatric pinniped species, *Phoca vitulin*a (harbor seal) and *Halichoerus grypus* (grey seal). Microwear textures from >100 teeth of 20 skulls (15 harbor seals, 5 grey seals) collected along the Danish Wadden Sea were analyzed using confocal microscopy, and quantified using standardized surface roughness parameters. The study focused on three tooth positions per jaw, aiming to identify interspecific differences linked to feeding technique and prey type.

Results revealed interspecific variation, particularly in the lower jaw tooth tmp4. Grey seals exhibited smoother enamel with numerous shallow striations, suggesting softer prey and greater reliance on suction feeding. In contrast, harbor seals showed fewer but deeper furrows, indicating that harder food items such as crustaceans were incorporated in their diet, and more frequent use of pierce feeding. Despite overlapping diets, these microwear differences suggest, to some extent, distinct ecological niches and feeding strategies. The findings support prior work using DMTA and highlight the method's potential for reconstructing short-term dietary patterns in marine mammals from museum specimens. This study contributes to understanding dietary partitioning and competition in coexisting seal species and illustrates how microwear analysis can inform conservation and ecosystem monitoring efforts amid changing marine environments.

Protein Reprogramming During Diapause in *Pieris napi*

PHY
631

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Insects in temperate regions rely on diapause—a regulated dormancy involving developmental arrest and metabolic suppression—to survive seasonal adversity. Although shifts in gene expression and metabolite profiles during diapause have been characterised, the underlying molecular regulation, including protein-level changes and their functional consequences, remains largely unresolved. Addressing this gap is crucial for a holistic understanding of diapause physiology and our capacity to predict insect winter performance, particularly under climate change. We conducted a time-series analysis of the complete set of proteins in pupal head tissue of the butterfly *Pieris napi*—a species with a clear diapause phenotype. Individuals were sampled at key stages in diapause and non-diapause pathways. Liquid chromatography-mass spectrometry identified 1,778 proteins across all samples, revealing pathway- and stage-specific protein profiles, indicating protein signatures of diapause-stage transitions. Diapause stage comparisons uncovered 82 unique proteins with significant abundance changes, including metabolic enzymes, time-keeping proteins, and stress-related factors. Protein changes reflect dynamic physiological strategies: early diapause is marked by protein synthesis and structural protection, mid-diapause by increasing lipid metabolism, and late diapause by antioxidant defence, preparing pupae for post-diapause development. These patterns illustrate how *P. napi* reprograms its proteins to balance energy suppression, stress resistance, and developmental timing during prolonged dormancy. This study provides the first comprehensive protein map of diapause in *P. napi*, shedding light on protein-level mechanisms that enable insects to endure and exit dormancy. These findings bridge gene expression and metabolite changes, offering new insights for forecasting insect responses to climate variability and pest control strategies.

First record of the smallest extant brachiopod Gwynia capsula (Jeffreys, 1859) from the German Bight

SYS 731

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Museum für Naturkunde – Leibniz Institute for Evolution and Biodiversity Science

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We describe for the first time the occurrence of the smallest extant brachiopod, *Gwynia capsula* (Jeffreys, 1859), from the island of Helgoland in the German Bight. A single living specimen was found in dredged shell gravel from the Helgoland trench ("Tiefe Rinne"). *G. capsula* was found settling on the fringe of a circular bryozoan colony of *Escharella immersa* (Fleming, 1828) which itself was growing on the inside of a dead shell of the bivalve *Modiolus modiolus*. In order not to destroy this original arrangement, morphological data of the brachiopod were collected using environmental SEM and non-invasive µCT. *Gwynia* was identified through its minute size and its characteristic submarginal ridges on the inside of the dorsal valve supporting the trocholophous lophophore of the animal. Among other localities, populations of *G. capsula* are known from British waters as well as the coasts of France, Belgium and the Netherlands. However, the reproductive biology of the species with only two brooded, lecithotrophic larvae at a time makes it unlikely that developmental stages of *G. capsula* are able to reach Helgoland by natural drift. Thus, the specimen found cannot be the result of a single dispersal event, but part of a larger and possibly stable community of *G. capsula* in Helgoland waters. As with many other marine invertebrates, anthropogenic interference may explain the brachiopod's occurrence on the island since it was a British crown colony throughout most of the 19th century and a hub for ship-based trading between the Empire and the German mainland.

Advances in Nemertean Phylogenomics

SYS
732

Dr. Christina Sagorny; Dr. Ekin Tilic

Senckenberg Gesellschaft für Naturforschung

To date, more than 1,300 species of nemerteans have been described from intertidal waters up to depths of 9,500 m. Nevertheless, the taxonomy of this group is particularly challenging as only few diagnostic morphological characteristics are present. Therefore, recent taxonomical research in nemerteans heavily relies on genetic data. Although mitochondrial genomes are regularly used to reconstruct phylogenetic relationships within Metazoa, the available nemertean mitochondrial genomes have never been collectively analyzed in a phylogenetic context so far. Moreover, most of these mitochondrial genomes represent the neonemertean taxa Heteronemertea and Monostilifera, leaving taxa like basally branching palaeonemerteans and polystiliferous hoplonemerteans vastly underrepresented. Using a genome skimming approach, we strived to increase the amount of publicly available complete mitochondrial genomes in Nemertea and fill in the gaps that still exist within several nemertean taxa. For this purpose, we specifically concentrated on taxa that have been mostly overlooked in the past. Moreover, our goal is to reconstruct a stable nemertean phylogeny based on low coverage whole genome sequencing by not only extracting mitochondrial genomes but also nuclear phylogenetically informative loci, such as single-copy orthologs and protein-coding genes. This approach will greatly advance phylogenomic research in a severely understudies group of marine invertebrates.

Shining a Light on *Spinther* (Annelida): New Species, New Sequences, Same Mystery

SYS
733

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Spinther is a small and enigmatic group of annelids that live in close association with sponges. Their name derives from the Greek word for “spark” or “sparkling,” likely referencing their shimmering appearance. The phylogenetic placement of *Spinther* within the annelid tree of life has remained unresolved. While a transcriptome from an undescribed *Spinther* species from French Polynesia was included in the phylotranscriptomic study of Andrade et al. (2015), the resulting placement was ambiguous and affected by long-branch artifacts.

Here, we present new morphological and genetic data for this previously undescribed species (now formally described, in press), as well as for *Spinther miniaceus* Grube, 1860 — originally described from the Adriatic Sea and later synonymized with *Spinther arcticus* (Sars, 1851). Based on clear morphological differences and geographic separation, we reinstate *S. miniaceus* as a valid species. We redescribe the species based on Grube’s syntypes and designate a lectotype.

Additionally, we provide new molecular resources for *Spinther*, including a near-complete mitochondrial genome of *S. miniaceus* from a topotypical specimen. While the mitogenome lacks three tRNAs and could not be circularized, it includes all protein-coding genes and follows the conserved gene order found in most annelids. However, it offers no further resolution regarding the phylogenetic placement of *Spinther*.

Phylogeography and species diversity of the gecarcinucid freshwater crabs of Sulawesi, Indonesia

SYS
734

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Sulawesi is home to several notable radiations of freshwater invertebrates, particularly within the island's ancient lakes. This is especially true for gecarcinucid freshwater crabs, which are represented on Sulawesi by 21 identified species across five genera (*Migmathelphusa*, *Nautilothelphusa*, *Parathelphusa*, *Sundathelphusa*, *Syntripsa*), with nine species and three genera being endemic to the lakes. The phylogeography and taxonomy of species outside of Sulawesi’s ancient lakes remain largely unknown, partly because the status and distribution of some supposedly widespread species are uncertain, and partly due to sampling gaps.

We sequenced two mitochondrial gene fragments from a large number of new samples collected in previously less-studied regions of Sulawesi. We also included genetic data from type specimens to investigate the phylogeography of gecarcinucids on the island and to gain a better understanding of their species diversity and distributions.

Our phylogenetic analysis uncovers several novel findings, most notably that:

(I) the range of *Parathelphusa* extends into the northern part of Sulawesi; (II) the strong geographic structure in the genetic data can only be partially linked to the island’s paleogeography and recent catchments; (III) the actual distribution of most more widespread *Parathelphusa* species differs significantly from current beliefs; and (IV) the number of mtDNA lineages (n = 32) is nearly twice the number of recognized species (n = 17) within *Parathelphusa* s.l. (including the three ancient lake genera). Overall, a comprehensive, integrative taxonomic revision of Sulawesi gecarcinucids is required to fully comprehend their diversity and distribution on the island.

Museomics and phylogenomics of tropical golden moles (Afrosoricida, Chrysochloridae)

SYS
735

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Due to their cryptic lifestyle, high endemism, and low abundance, golden moles (Chrysochloridae) are among the least-studied placental mammals. Their center of diversification lies in the (semi)arid regions of southern Africa, but two species occur in tropical central Africa. Stuhlmann's golden mole (*Kilimatalpa stuhlmanni*) is particularly noteworthy, being restricted to geographically distant and isolated Afrotropical mountain forest "islands" from Cameroon to Tanzania. Phylogenetic and phylogeographic analysis of such a rare and widely scattered animal is challenging.

In this study, modern and historical tissue samples were used to reconstruct mitochondrial genomes from 48 golden mole specimens spanning six genera and all six known distribution areas of *K. stuhlmanni*. Museomic and phylogenetic approaches were applied to gain insights into the evolutionary relationships within this poorly known group.

The resulting phylogenetic trees reveal a monophyletic *K. stuhlmanni* group, composed of at least eight lineages clustering into three deeply divergent clades. These clades correspond to the Tanzanian highlands, Mount Oku in Cameroon, and the Albertine Rift including the Kenyan and Ugandan mountains. Divergence time estimates suggest a deep split 8–11 million years ago, consistent with the breakup of the ancient pan-African rainforest. Genetic distances indicate that some lineages may represent distinct species or subspecies, while the three main clades likely correspond to different genera.

These findings provide new insights into the diversity and evolution of golden moles and demonstrate the value of museomic approaches for phylogenetic and biogeographic studies of rare and elusive species.

Systematic status of the giant land snail species *Bertia pergrandis* and *Bertia setzeri* from Vietnam (Gastropoda: Dyakiidae)

SYS
736

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The land snail genus *Bertia*, which belongs to the stylommatophoran family Dyakiidae, is endemic to Vietnam and Cambodia. All three recognised *Bertia* species are characterised by exceptionally large, sinistral shells. The type species of the genus, *Bertia cambojiensis*, which has been considered extinct and was rediscovered only in 2012, has been studied in more detail over the last years. Knowledge on the other two species, *Bertia pergrandis* and *Bertia setzeri*, however, remains very limited and their systematic status has not yet been confirmed by molecular data. Based on recently collected material from Vietnam, we examined the phylogenetic relationships of *B. pergrandis* and *B. setzeri* utilising DNA sequence data. Our phylogenetic analysis confirms the affiliation of both species to the genus *Bertia*, while a clade containing both, *B. pergrandis* and *B. setzeri*, forms the sister group of *B. cambojiensis*. Furthermore, we present data on the reproductive anatomy of *B. pergrandis* and *B. setzeri*. Our findings contribute to a better understanding of one of the most conspicuous land snail genera in Southeast Asia.

First record of the non-native slug species *Deroceras laeve* (Agriolimacidae) in southern Vietnam

SYS 737

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[1] Museum für Naturkunde – Leibniz Institute for Evolution and Biodiversity Science
[2] Senckenberg Museum of Natural History Görlitz

Bidoup-Nui Ba National Park is located on the Da Lat Plateau in southern Vietnam. In April–May 2022, a survey of the park's terrestrial gastropod fauna was carried out as part of the German-Vietnamese biodiversity research project VIETBIO. Among the gastropods collected were six individuals of the non-native agriolimacid slug *Deroceras laeve*, the first record of this species in southern Vietnam. The specimens were found in disturbed habitat around a ranger station located at the eastern edge of the park at ca. 1,640 m a.s.l. Species identity was confirmed by anatomy and DNA sequencing. The species exhibits a penis polymorphism, but all our individuals were aphallic. The four sequenced specimens yielded three different COI haplotypes, of which two were identical with sequences published from other continents. *Deroceras laeve* is presumably native to the Holarctic region, but has been introduced widely, also to the tropics. Its remarkable ecological flexibility allows it to thrive from subarctic tundra to tropical rainforest, lowland to high mountains, and also at synanthropic sites. Locally, it is considered as agricultural and horticultural pest, and mass occurrences in greenhouses have been reported. In Southeast Asia, the species was recorded for the first time in 2018 from the Hoang Lien mountains in northern Vietnam, over 1,200 km from Bidoup-Nui Ba National Park. The newly discovered population might originate from nearby large-scale greenhouse facilities. The transport of plant material and soil might pose the risk of further introductions.

The microbiome of kleptoplasty

SYS
738

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Uniwersytet im. Adama Mickiewicza w Poznaniu

Marine gastropod molluscs of the family Plakobranchidae and genus Elysia exhibit a rare phenomenon known as kleptoplasty - the retention of functional chloroplasts from algal cells. Kleptoplasts become incorporated into the epithelium of the digestive tract and can remain photosynthetically active for extended periods, depending on the species. This adaptation enables these marine slugs to partially or even fully meet their nutritional needs through photosynthesis. While the mechanisms underlying kleptoplasty are still not fully understood, one hypothesis suggests that associated microorganisms may contribute to the maintenance of photosynthetic processes within host tissues.

This study focuses on laboratory-bred *Elysia viridis* and aims to identify and characterize the gut microbial community inhabiting the intestines of *E. viridis* individuals. Our research aims to elucidate the potential role of the gut microbiome in sustaining kleptoplasty, particularly its involvement in maintaining chloroplast functionality within the digestive system of specimens. This is the first phase of a broader project. In subsequent phases, the gut microbiome will also be compared with that of wild populations of *Elysia viridis*, and later with wild and laboratory-maintained populations of *Elysia rubeni*, a pseudo-cryptic species closely related to *Elysia viridis*. This will provide deeper insight into the environmental and biological factors influencing kleptoplasty in molluscs. The project is conducted in collaboration with the Autonomous University of Madrid.

SYS
739

Breaking *Salmacina* (Serpulidae, Annelida) Out of the Tube: A Case for Integrative Taxonomy

Hannah Annika Cremer; Dr. Ekin Tilic
Senckenberg Gesellschaft für Naturforschung

Salmacina setosa Langerhans, 1884, was originally described from Madeira based on an account consisting of only eight sentences. This limited diagnosis poses significant challenges for confident species-level identification by modern standards. Here, we present an integrative redescription of *Salmacina cf. setosa* based on specimens collected off the Mauritanian coast—geographically close to the type locality. Morphological features were examined using stereomicroscopy, light microscopy, and scanning electron microscopy (SEM), with detailed documentation of chaetal structure, body morphology, and reproductive forms across various life stages. We also document asexual reproduction by budding, as well as anterior regeneration, based on morphological evidence captured in SEM imagery.

Sequencing the standard barcoding gene COI is notoriously difficult—if not impossible—for many Serpulidae, including *Salmacina*. This longstanding challenge has limited molecular work across the group. To address this, we employed high-throughput genome skimming to recover mitochondrial and other phylogenetically informative sequences. As genomic resources for *Salmacina* are currently sparse, our dataset represents a novel contribution that may enable the design of genus-specific primers and facilitate future barcoding efforts. While sequence data from Madeira are still needed to confirm species identity, our combined morphological and molecular analyses provide a robust foundation for future taxonomic and systematic work on *Salmacina setosa* and related taxa.

Assessing the adaptive potential of German pollinators through comparative population genomics

SYS
740

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Pollinators are vital to ecosystem function by supporting both wild flowering plant reproduction and agricultural productivity. In Germany, as in much of Europe, many pollinator taxa and other flying insects are undergoing marked declines in abundance, diversity, and distribution. These losses, driven by land-use change, pesticide exposure, climate change, and emerging diseases, raise urgent questions about the evolutionary capacity of pollinators to persist under accelerating environmental pressures. To address this, our study applies comparative population genomics to assess the genetic health and adaptive potential of common pollinator species across Germany. Using whole-genome resequencing, we will characterize patterns of genetic diversity, population structure, and gene flow in nine common pollinator species (three each of bees, butterflies, and hoverflies) across five major regions (Berlin, Hamburg, Stuttgart, Cologne/Bonn, and Munich). Furthermore, we will reconstruct the deep historical change in population size to determine what trajectory each species is currently undergoing. Lastly, using museomics, we will characterize change in genetic diversity over the past century by comparing modern and historical DNA in two cities: Berlin and Stuttgart. This will allow us to directly observe recent change in genetic diversity and determine whether this change is local or observed across other parts of Germany. By integrating genomic data across multiple taxa and timescales, we aim to identify general, species-specific, or region-specific patterns and trajectories. Our findings will not only contribute to a deeper understanding of pollinator evolution but also support evidence-based conservation strategies tailored to Germany’s changing landscapes.

Experience-independent development of chirping in brown ghost knifefish

BEH
831

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In general, communication signals can fall within a large continuum between innate cues, directly referenced to internal states, and more abstract signals, referring to more complex subjects and learned through experience. While the former have the prerogative to trigger innate and stereotyped responses, the latter require repeated experience through which signals tune to more advanced forms.

The weakly electric knifefish, *Apteronotus leptorhynchus* (brown ghost), produces a sinusoidal electric organ discharge (EOD), with frequencies varying across individuals and often containing transient frequency modulations, known as chirps. Chirps of different types have been widely considered communication signals used in different behavioral contexts (e.g., aggression, courtship). Whether chirps are referenced to internal states or external objects or whether social experience is required for their emission is unknown.

Our work focuses on age-related differences, comparing chirping activity between juvenile and adult subjects. By stimulating freely swimming fish with EOD mimics of varying intensity and frequency, we examined response sensitivity to playback signals. We also assessed the effects of social experience by comparing isolated and group-housed juveniles.

The results show a general dependency of chirping on signal intensity and frequency. Neither age nor social isolation significantly altered the production of any of the four chirp types considered, although socially isolated individuals tend to emit more chirps.

These findings indicate that chirps are independent of social experience and are therefore likely to be innate signals referenced to internal states, the nature of which is yet to be determined.

Effects of heat exposure on male condition, mating behavior and fertility in a spider

BEH
832

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Climate change is intensifying the frequency and severity of heat waves, presenting challenges to wildlife, including ectothermic organisms. While research on thermal stress has focused on survival limits, we have little understanding of how sublethal temperatures affect mating behavior and reproductive success. Sublethal temperatures can impact fitness almost as significantly as survival, as insect sperm fertility decreases far below the critical thermal maximum. This study examined the effects of acute heat exposure on male nursery web spiders (*Pisaura mirabilis*), a common species in Central European grasslands. Males produce nuptial gifts from captured prey and present them to females before mating. We tested the impact of 4-hour exposure to 37°C (when spiders exhibit behavioral changes) or 40°C (as a sublethal temperature) on males and compared these to a control group at 25°C. We investigated whether acute heat exposure affects male physiological condition. By pairing them with untreated females, we explored heat treatment effects on courtship behavior and reproductive success. Heat exposure reduced male body mass and condition in both heat treatments compared to controls. However, prey acceptance, nuptial gift production, copulation probability, and copulation duration did not differ between treatments. All females oviposited and spiderling hatching proportion was unaffected by treatment. We conclude that, although heat exposure impairs male physiological condition, mating behavior and reproductive success in *P. mirabilis* are not compromised by short-term thermal stress, unlike insects. This resilience may be due to the immobility and encapsulation of spider sperm, making them more resistant to heat stress than insect sperm.

Impact of partner loss on brood care in the biparental cichlid fish *Pelvicachromis taeniatus*

BEH
833

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In species with biparental care, the loss of one parent, e.g. due to predation, is a realistic scenario under natural conditions. The remaining parent can facultatively increase brood care to compensate for care of the missing parent, show no compensation or abandon the offspring. The decision is expected to be sex-specific because of usually higher reproductive investment of females. To test these hypotheses, *Pelvicachromis taeniatus*, an African cichlid fish with biparental brood care and colour ornamentation in both sexes, were used. The free-swimming fry are guarded by both parents. For the experiment, breeding pairs were arranged in standardized tanks. In case of a successful reproduction, at free-swimming stage, the broods were split and placed into a new tank each, together only with the mother (uniparental female care) or together only with the father (uniparental male care). As control, both parents were placed together with the brood to a new tank (biparental care). The brood size was standardized. Parental brood care were then video recorded on 10 days with every observation lasting 30 minutes. Additionally, photographs of the fish were taken to relate the intensity of colour ornaments with brood care efforts. The results of this study could give new insight on sexual conflict over care and the reliability of colour ornaments as indictor of brood care quality.

Do urban red squirrels (*Sciurus vulgaris*) have a different sense of risk than their rural conspecifics?

BEH
834

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Urbanization challenges wildlife with habitat fragmentation, altered predator communities, and increasing anthropogenic pressures. Behavioural plasticity is a key trait that enables species to cope with these challenges. This study investigates whether Eurasian red squirrels (*Sciurus vulgaris*; thereafter 'squirrels') can differentiate between other mammals – including humans – as sources of mortality risk, as just a disturbance or even an opportunity for food, and whether such responses differ in urban-adapted individuals who adjusted to the presence of humans. Using camera trap data collected along an urban-rural gradient in Berlin, Germany, during autumn 2021 and autumn 2024, we analysed hourly activity patterns of squirrels along with their natural predators (raccoons *Procyon lotor*, martens *Martes* spec.) and domestic pets (cats *Felis catus*) representing risk, non-predatory mammals (wild boar *Sus scrofa*) and humans representing disturbances or humans as potential food source, as squirrels are commonly fed in urban areas. We analysed the temporal activity overlap between squirrels and these different species groups and assessed whether squirrels adjust their activity in response to these interactions. Additionally, we analysed whether these adjustments differ along the urban-rural gradient. The findings will provide insights into the behavioural flexibility of squirrels, particularly their ability to balance risks and opportunities in human altered environments with their activity timing. By understanding how squirrels navigate interspecies interactions and human influence, the study contributes to a broader understanding of how urban wildlife adjusts to novel environments.

A crustacean's chemical shield: quinoline-derivates protect *Porcellio scaber* woodlice from spider predation

BEH
835

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In evolutionary time, aquatic crustaceans colonized land and faced new terrestrial predators such as spiders and ants. We tested the hypothesis that the crustacean terrestrial woodlouse *Porcellio scaber* produces defensive metabolites that provide protection against terrestrial predators. When attacked by a predator, *P. scaber* discharges proteinaceous secretions from its tegumental glands. Analyses of gland secretion extracts by gas chromatography-mass spectrometry and by liquid-chromatography-mass spectrometry revealed four metabolites: methyl 8-hydroxy-quinoline-2-carboxylate, methyl 8-hydroxy-4-methoxy-quinoline-2-carboxylate, methyl 8-(sulfooxy)quinoline-2-carboxylate, and methyl 4-methoxy-8-(sulfooxy)quinoline-2-carboxylate, the latter three being natural products not previously known. In behavioural experiments, *Steatoda grossa* spiders readily preyed on *Tenebrio molitor* beetles but avoided chemically well-defended *P. scaber*. When beetles were rendered chemically well-defended by topical applications of either *P. scaber* gland secretion extract or synthetic metabolites identified in these extracts, spiders rejected the beetles as prey. Our data support the hypothesis that *P. scaber* produces defensive metabolites that provide protection against terrestrial predators. We show that the crustacean *P. scaber*, like many insects, is chemically defended against predators.

Neophobia and innovative problem-solving in Eurasian red squirrels (*Sciurus vulgaris*) along an urban - rural gradient in Berlin

BEH
836

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Urbanisation creates novel habitats that pose new challenges to wildlife. While some species decline or disappear, others seem to thrive in the city. Eurasian red squirrels (*Sciurus vulgaris*) are widespread and common in cities such as Berlin, where we investigated personality traits and cognitive performance of squirrels. Specifically, we tested object neophobia and innovative problem-solving, particularly in terms of persistence in solving food-extraction tasks and the success rate of doing so, while accounting for individual differences. We hypothesised that squirrels would show varying levels of neophobia, success rates, and persistence depending on the degree of urbanisation at different study sites.

We placed two experimental boxes at three study sites in Berlin with differing degrees of urbanisation in autumn 2024. Squirrels could enter the boxes freely. Novel objects and problem-solving tasks were placed in the boxes individually and in a random order on four consecutive days over a four-week period. Individuals were filmed and time spent fully inside the box, solving latency, and the number of successes were measured. We used zero-inflated GLMMs to relate the time spent fully inside the box to the type of treatment.

First results show that the time squirrels spent in the boxes significantly increased when problem-solving tasks were present and at higher temperatures. Furthermore, squirrels were significantly less likely to enter boxes with novel objects inside, indicated by an increased probability of structural zeros. Additionally, at sites with a lower degree of urbanisation, fewer individuals entered the boxes, and those that did entered less frequently. These findings indicate that chirps are independent of social experience and are therefore likely to be innate signals referenced to internal states, the nature of which is yet to be determined.

Watch me move: Sublethal effects of Imidacloprid on reproduction and behavior of *Nicrophorus vespilloides*

BEH
837

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The use of neonicotinoid insecticides, such as Imidacloprid in crop production has greatly increased in the last two decades. While effective against pests, these insecticides can have adverse effects on non-target organisms. Previous studies suggest not only increased mortality when exposing beetles to Imidacloprid, but also sublethal effects which impair behavior. In this study we examined the effects of Imidacloprid on reproductive success and behavior in *Nicrophorus vespilloides*, a burying beetle known for parental care. Adult beetles were exposed to one of eight concentrations and observed individually for 48h to assess individual responses. They were then paired and provided a mouse carcass to initiate reproduction. After the larvae hatched, when activity is known to be highest, parental behavior was recorded using cameras. The survival and weight of larvae and adults was noted at multiple timepoints during brood care. Preliminary results indicate that the beetles that were exposed to higher amounts of Imidacloprid exhibited more behavioral anomalies than the beetles exposed to lower doses. This included erratic movements in the 48h after poisoning, as well as overall more movement – and because of this a possibly higher predation risk – in the individuals given higher doses of Imidacloprid. Despite this, *N. vespilloides* showed a much higher tolerance and greater recovery after the administration of the insecticide than was originally assumed. This highlights the importance of considering not only mortality, but sublethal effects when evaluating ecological risks of pesticides.

Toxic vibes – the effects of imidacloprid on the stridulation activity of *Nicrophorus vespilloides*

BEH
838

Emily Zenger[1]; Dr. Magdalena M Mair[1]; **Dr. Taina Conrad**[2]

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The use of imidacloprid, a neonicotinoid, is a widely used pest control method in agriculture. Although lethal effects on target and non-target species are well known, far less is known about possible sublethal effects, especially on non-target species. Burying beetles of the genus *Nicrophorus* are likely to be exposed to imidacloprid as they use small vertebrate carcasses, which are often found in and around fields, for brood care.

We investigated the influence of external imidacloprid exposure on both survival and reproduction of the beetle species *Nicrophorus vespilloides* as well as changes in their acoustic communication, known to be elemental in their brood care.

The effects of eight different imidacloprid concentrations (0-300 ng/µl) were examined by applying 1 µl of each concentration to the abdomen of eight pairs of *N. vespilloides*. Mating pairs were then induced to breed. Stridulations were recorded during brood care, when activity is known to be high. To investigate the impact of each treatment, the weight of the beetles was measured several times and offspring fitness was recorded. One hour of acoustic data of each pair was analysed using Raven Pro 1.6. No significant effect on beetle survival was observed after a single treatment with imidacloprid. However, preliminary results show that a higher concentration of the neonicotinoid is associated with an increase in stridulation communication.

Effective communication contributes significantly to the success of biparental care of *N. vespilloides*. Therefore, contact with imidacloprid may negatively affect the beetles' fitness, even if the exposed individual survives.

Boldness and Niche Similarity Shape Spatial Interactions in a Natural Rodent Community

BEH
839

Dr. Jonas Stiegler[1]; Dr. Annika Schirmer[1]; Prof. Dr. Florian Jeltsch[1]; Prof. Dr. Jana Eccard[1]; Prof. Dr. Melanie Dammhahn[2]

[1] Universität Potsdam
[2] Universität Münster

Consistent behavioral differences among individuals shape species interactions and promote coexistence. These individual-level traits help characterize ecological niches, particularly under varying intensities of interspecific competition. Yet, most studies focus on species-level mean traits, often overlooking the ecological significance of within-species behavioral variation. In a natural rodent community of four co-occurring species, we tested whether boldness predicts space use and spatial proximity to conspecifics and heterospecifics of similar and dissimilar ecological niches. In all study species, boldness was positively associated with core area, home range size, and ground cover use, and negatively with vegetation height, indicating general behavioral type-dependent space use. In one ecological similar species pair (omnivorous bank voles and striped field mice), fewer conspecifics, but more heterospecifics of similar ecological niches, were present near bolder individuals. Contrarily, in the second ecological similar species pair (granivorous common and field voles), only the conspecific pattern could be observed. We found no relationship with heterospecifics from dissimilar niches, and no effect of sex in either species. The differences in spatial interaction patterns are likely due to the different strengths of interspecific competition within the ecologically similar species pairs. Our results demonstrate that boldness influences spatial interactions, dependent on the ecological niche similarity and the strength of interspecific competition. Behavioral type-dependent space use may promote individual niche differentiation and facilitate species coexistence, especially under strong interspecific competition.

Individual differences in zebra finches - The long way of selection lines

BEH
840

Dr. Sabine Kraus

Bielefeld University

Inter-individual differences in behaviour that are consistent over time and/or contexts, i.e. animal personality, are a widespread phenomenon in nature with ecological and evolutionary implications. Since this recognised consistent inter-individual variation in behaviour is contrary to the previous expectation of flexibility and selection towards a mean optimal phenotype with little variance, the questions arise how such stable variation is generated, maintained and what underlying mechanisms drive this variation?

To dive deeper into these questions artificial selection experiments can provide a powerful tool for identifying co-selected traits, to understand the general evolvability of traits and to uncover the genetic architecture of complex traits.

We established a long-term selection line project with two replicates on wild-type zebra finches (*Taeniopygia guttata*) bi-directionally selected for three different personality traits: aggression, exploration and fearlessness.

Our results so far show a clear response to selection in bidirectionally selected lines for fearlessness and aggression, but not for exploration. In line with these results, estimates of heritability using parent-offspring regression suggested heritable variation in aggression and fearlessness. Furthermore, the behavioural traits as well as the hormonal levels of corticosterone and testosterone were repeatable and within the range described for behavioural and physiological traits.

In further steps, we will investigate the effects on fitness associated with interindividual differences in behaviour. Additionally, we check whether certain behavioural traits are associated with individual variations in gut microbiota as a potential source of individual variation.

Does artificial light at night (ALAN) affect foraging behavior and corticosterone release in barn owls?

BEH
841

Jana-Marie Cordes[1]; Anne-Caroline Heintz[2]; Prof. Dr. Alexandre Roulin[3]; Dr. Pierre Bize[2]; Dr. Bettina Almasi[2]

[1] University of Münster
[2] Swiss Ornithological Institute
[3] University of Lausanne

With global human population growth, anthropogenic pollution has intensified, including the rapid expansion of artificial light at night. As an environmental stressor, artificial light at night disrupts behavioral and physiological processes across a wide range of species. However, its impact on nocturnal, synanthropic birds of prey remains poorly understood. This study investigated how short-term artificial light near the nest box entrance, simulating a streetlamp, affected parental behavior and physiology in breeding barn owls (*Tyto alba*) in western Switzerland. Using a multi-method approach combining GPS tracking, camera traps, a perch-weighing system, and corticosterone measurements as an indicator of physiological stress, we found that light exposure influenced both behavior and physiology in barn owls, with effects varying with sex and pheomelanin-based plumage coloration, a trait linked to personality. Darker pheomelanic males showed increased nest box attendance under light exposure compared to their whiter conspecifics. Food provisioning trips increased in whiter females and redder males when exposed to light. Corticosterone concentrations were elevated following light exposure, especially in whiter individuals. Additionally, males exposed to light showed a decrease in body mass, with the most pronounced reduction observed in reddish individuals. These findings provide experimental evidence that even short-term exposure to artificial light at night can alter behavioral and physiological traits in a nocturnal predator in a color- and sex-specific manner. They highlight the importance of integrating individual variation into research on anthropogenic environmental change and support the need for conservation strategies to reduce the ecological impacts of light pollution in human-dominated landscapes.

MONDAY

8. - 12.
September
2025

117th annual meeting
German Zoological Society

SATELLITE SYMPOSIA

09:30 - 20:00
Evolutionary & Behavioural Biology
Wildlife in Urban Spaces - Adaptations and Human Perceptions

09:00 - 20:00
Physiology
Advances in Membrane Physiology

Mo 14:00 - 20:00 I Di 09:00 - 12:00
Developmental Biology
Network Analysis

TUESDAY

EXCURSIONS

13:45 - 15:45
Medizinhistorisches Museum Charité

14:00 - 15:30
Erinnerungsort Ihnestraße

14:00 - 16:00
Zoologischer Garten

14:00 - 16:00
Tierpark

15:00 - 16:30
Botanischer Garten - Saatgutbank

15:00 - 16:30
Botanisches Museum - Hinter den Kulissen

14:00
DZG BOARD | DZG SPEAKER

15:15
DZG ADVISORY BOARD

19:30 ICEBREAKER - SAURIERSAAL
Nadia Fröbisch
`From Fossils to Flies - Evolutionary Biology Research at the Museum für Naturkunde`

WEDNESDAY

09:00 PLENARY
Ellen Decaestecker
The Role of the Microbiome in Eco-Evolutionary Interactions

10:00 PLENARY
Johanna Mappes
Ecological and Genetic Factors Driving Antipredator Defense Strategies in Lepidoptera

coffee break

SGCT	ECO	EVO	MOR	BEH
11:30	508	223	317	816
11:45	515	225	311	809
12:00	514	226	305	821
12:15	503	211	307	810
12:30	512	220	302	814
12:45	507	204	315	803

SUBJECT GROUP MEETING 11:30 NEU

SUBJECT GROUP MEETING 12:15 PHY

lunch break

13:15
DFG - Info Event

INVITED GROUP TALKS

14:00	M. Mair	M.T. Aguado
14:30	J. Jeschke	K. Gray
	ECO	SYS

coffee break

SGCT	EVO	MOR	DEV	SYS
15:30	219	319	103	704
15:45	202	318	108	706
16:00	201	308	101	708
16:15	208	316	102	707
16:30	210	313	104	710

SUBJECT GROUP MEETING 15:30 ECO

17:00 POSTERSESSION

POSTERS &
SNACKS & DRINKS

THURSDAY

09:00 PLENARY
Marta Szulkin
Anthropocene Biology in Eastern Europe and Beyond

10:00 PLENARY
Mirjam Knörnschild
Bats in Transition

coffee break

SGCT	EVO	ECO	NEU	DEV
11:30	213	518	402	105
11:45	224	513	401	106
12:00	228	519	406	109
12:15	215	509	404	111
12:30	218	501	403	107
12:45	212	502	405	110

SUBJECT GROUP MEETING 11:30 BEH

SUBJECT GROUP MEETING 12:15 SYS

lunch break

INVITED GROUP TALKS

14:00	M. Dominguez	M. Vogt
14:30	R. Archer	J. Beetz
	EVO	NEU

INVITED GROUP TALKS

15:00	N. Grunstra	N. Ullrich
15:30	J. Wolff	A. Vilcinskas
	MOR	PHY

coffee break

SGCT	ECO	MOR	SYS	BEH
16:30	510	306	714	820
16:45	511	301	713	812
17:00	522	304	709	804
17:15	504	303	703	808

SUBJECT GROUP MEETING 16:30 EVO

17:35 **Michael Ohl**
The DZG's Dream: Cataloging All Species

18:15 AWARDS

Werner-Rathmayer-Award
Award of the Horst-Wiehe Foundation
Walther-Arndt-Research-Award

FRIDAY

09:00 PLENARY
Ute Hentschel Humeida
Can sponges differentiate between microbial friend or foe?

10:00 PLENARY
Silke Sachse
Neurobiology & Genetics

coffee break

SGCT	EVO	ECO	BEH	PHY
11:30	209	516	807	601
11:45	227	506	805	602
12:00	205	521	817	606
12:15	216	505	815	604
12:30	222	520	813	603
12:45	203	517	806	605

SUBJECT GROUP MEETING 11:30 DEV

SUBJECT GROUP MEETING 12:15 MOR

lunch break

INVITED GROUP TALKS

14:00	D. Rößler	O. Roth
14:30	E. Frank	J. Colgren
	BEH	DEV

coffee break

SGCT	MOR	EVO	BEH	SYS
15:30	312	214	811	701
15:45	310	217	819	702
16:00	314	207	818	711
16:15	320	221	801	712
16:30	309	206	802	705

17:00
DZG GENERAL MEETING

18:15 PUBLIC LECTURE
Sophia Kimmig
„Tiere in der Stadt"

19:30 CLOSING EVENT
Conference Dinner at **Luise Dahlem**
Student Awards

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