



The 12th Polish Evolutionary Conference

16-18 September 2026

Łódź, Poland

PROGRAM & ABSTRACT BOOK



**12TH POLISH EVOLUTIONARY CONFERENCE
UNIVERSITY OF ŁÓDŹ
16-18 SEPTEMBER 2026**

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Faculty of Biology and Environmental Protection, University of Lodz

The Committee of Environmental and Evolutionary Biology, Polish Academy of Sciences



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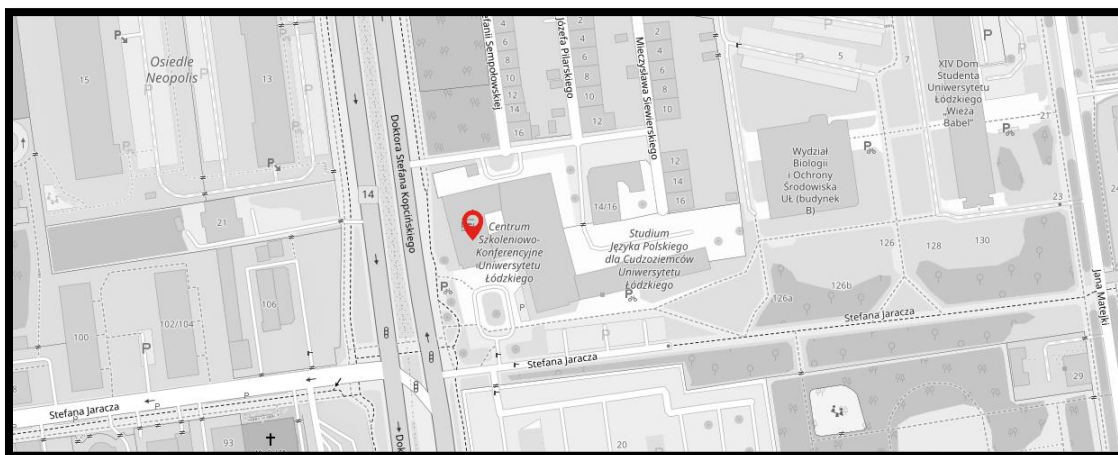
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VENUE

Conference Center of University of Lodz (Kopcińskiego 16/18, 90-232 Lodz).



GETTING THERE

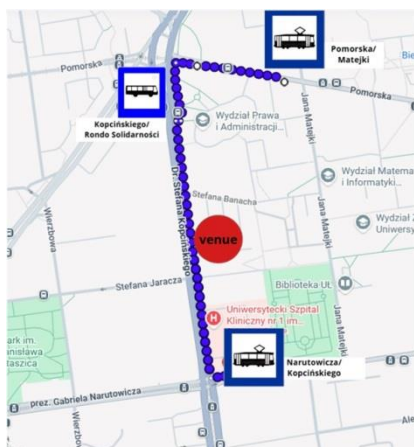
PUBLIC TRANSPORT

The most convenient way to reach the conference venue is by public transport (MPK Łódź).

The nearest stops to the venue are:

- Narutowicza / Kopcińskiego – tram lines: 1, 2, 3, 4, 5, 6, 8, 9, 10A, 10B, 12, 14, 16, 18
- Kopcińskiego / Rondo Solidarności – bus lines: 60A, 60B, 60C, 60D, 70
- Pomorska / Matejki – tram lines: 1, 3, 4, 5, 15, 16, 17, 45; bus lines: 54A, 54B, 87A, 87B

All stops are located within a few minutes' walk from the conference venue.



Tram connections from railway stations:

- From Łódź Fabryczna railway station – tram lines 12 or 18 (or 20 min walk)
- From Łódź Widzew railway station – tram line 9
- From Łódź Kaliska railway station – tram lines 12 or 18

12th Polish Evolutionary Conference programme (Łódź, 16-18.09.2026)

	Wednesday, 16th September	Thursday, 17th September	Friday, 18th September
09:00		Plenary lecture 2 Reto Burri	Plenary lecture 4 Luis-Miguel Chevin
09:30			
10:00			
10:30		Contributed talks: Genomics	Contributed talks: Physiology
11:00			
11:30	Registration	Coffee	Coffee
12:00		Contributed talks: Evolution of reproductive strategies	Contributed talks: Evolutionary ecology
12:30			
13:00			
13:30	Opening	Lunch break	Lunch break
14:00	Plenary lecture 1 Kjetill Sigurd Jakobsen		
14:30		Plenary lecture 3 Courtney Stairs	Contributed talks: Microbial evolution
15:00	Contributed talks: Speciation and hybridization		
15:30		Contributed talks: Comparative evolution	Closing ceremony
16:00	Coffee		
16:30	Contributed talks: Microbiome		
17:00	Ludwik Tomiałojć talk	Poster session	
17:30			
18:00			
18:30			
19:00	Welcome reception - Biedermann's Palace (19.00-22.00)		
...			
22:00			

PLENARY SPEAKERS



Reto Burri

Swiss Ornithological Institute, Sempach, Switzerland

Topic: A mosaic of modular variation at a single gene underpins convergent plumage coloration

Research background and interests: I have a longstanding interest in understanding the molecular bases and evolutionary history of phenotypic and species diversity. To this end, my research makes use of large-scale molecular data to study hybridization and adaptation in avian systems.

Luis-Miguel Chevin

CEFE, University of Montpellier

CNRS, EPHE, IRD, Montpellier, France



Topic: Adapting to fluctuating and complex environments

Research background and interests: I'm interested in the mechanisms and consequences of adaptation to changing environments. My group works on the genetics basis of adaptation, the evolution of plasticity, and eco-evolutionary dynamics, using a combination of approaches: theory, experimental evolution, and analyses of long-term datasets from natural populations. For our experiments we use the halotolerant microalga *Dunaliella salina*, which has fascinating mechanisms of salinity tolerance.



Kjetill Sigurd Jakobsen

Centre for Ecological and Evolutionary Synthesis (CEES)

Dept of Biosciences, University of Oslo, Norway

Topic: Structural genomic variation in an evolutionary perspective

Research background and interests: My research deals with evolutionary genomics - both at the comparative- and population level. A particular interest has been evolution of teleosts (bony fishes), their genome architecture and structural variation in terms of copy number variation, inversions and chromosomal rearrangements. Another focus has been plant evolutionary genomics addressing structural variation in terms of length variation of short tandem repeats and genome architecture effects of hybridisation events. Recently, we have also initiated investigations of bird genomes and their unusual microchromosomes. A large proportion of our current research has been associated with the Earth BioGenome Project (EBP) and European Reference Genome Atlas (ERGA).

Courtney Stairs

Department of Cell and Molecular Biology

Uppsala University, Sweden



Topic: Stealing and dealing: eukaryotic strategies for living without oxygen

Research background and interests: Courtney Stairs explores how microorganisms have evolved to live in anoxic and oxygen-limited environments. Her research focuses on the evolutionary origins and diversification of this anaerobic metabolism in microbial eukaryotes - also known as protists - using a combination of comparative genomics, cell biology, and microbiology.

ABSTRACT BOOK

--- TALKS ---

T1. The genomic predictability of hybridization: nuclear and mitochondrial insights from pine contact zones**Bartosz Łabiszak***, Witold Wachowiak*Department of Plant Ecology and Environmental Protection, Institute of Environmental Biology, Adam Mickiewicz University in Poznan, Poznań, Poland*

* bartosz.labiszak@amu.edu.pl

Hybridization can generate variation, promote adaptive introgression and blur species boundaries. In long-lived forest trees with weak reproductive barriers, replicated hybrid zones allow tests of whether hybridization produces repeatable genomic outcomes or is shaped by local environments. We integrated nuclear and organellar data from contact zones between Scots pine (*Pinus sylvestris*) and the *Pinus mugo* complex in Central Europe. We analysed >1,700 individuals from 29 populations, including three hybrid zones, plus allopatric references of *P. sylvestris*, *P. mugo* and *P. uliginosa*. Nuclear variation was assessed with a custom SNP array targeting transcribed regions. Chloroplast haplotypes traced cytoplasmic inheritance and direction of gene flow. To examine mitochondrial structure, we isolated enriched mitochondrial fractions and used Oxford Nanopore long-read sequencing, enabling reconstruction of the pine mitogenome and tests of parental-like versus recombinant configurations. Hybridization was widespread in all contact zones and dominated by later-generation hybrids and backcrosses, whereas early-generation hybrids were rare. Despite contrasting habitats, nuclear ancestry patterns were consistent, with asymmetric introgression and strong *P. mugo* ancestry. Genome scans and genomic cline analyses identified loci showing non-neutral introgression, indicating ecological effects on admixed genomes. Individuals classified as *P. uliginosa* did not form a distinct genomic lineage, supporting its placement within a hybrid continuum. Mitochondrial analyses revealed a graph-resolved, three-chromosome structure in *P. mugo* and species-informative markers. Overall, pine hybrid zones combine repeatable nuclear-genomic patterns with complex cytoplasmic inheritance. By integrating SNP-based ancestry, chloroplast haplotypes and structurally resolved mitochondrial genomes, this study shows how hybridization shapes species boundaries, adaptive variation and organellar evolution.

T2. Evolution and biogeography of polyploid complex of mountain grasses

Marcin Kiedrzyński^{1*}, Katarzyna M. Zielińska¹, Edyta Kiedrzyńska², Adnan Akbar³, Aamir H. Khan¹

¹*Department of Biogeography, Paleoecology and Nature Conservation, Institute of Ecology and Environmental Protection, Faculty of Biology and Environmental Protection, University of Lodz, Łódź, Poland*

²*Department of UNESCO Ecohydrology and Applied Ecology, Faculty of Biology and Environmental Protection, University of Lodz, Łódź, Poland*

³*Doctoral School of Exact and Natural Sciences, University of Lodz, Łódź, Poland*

* marcin.kiedzynski@biol.uni.lodz.pl

Polyploidy and hybridization are key mechanisms of plant evolution, particularly in mountain systems where climatic oscillations, geographical isolation and habitat heterogeneity promote lineage divergence. We investigate the evolutionary history of the *Festuca amethystina*–*Festuca tatrae* complex, a group of fine-leaved grasses comprising diploid and tetraploid cytotypes with contrasting geographical ranges and ecological niches. *Festuca tatrae* is a narrow-ranging diploid species associated with the Western Carpathians, whereas *F. amethystina* includes diploid and tetraploid lineages distributed across Central and South-Eastern Europe.

By integrating cytogeographical, phylogeographical, ecological and epigenetic evidence, we show that the complex represents a dynamic system of lineage divergence and niche differentiation. Diploid lineages are primarily linked to mountain areas and may reflect refugial components of the complex. In contrast, tetraploid *F. amethystina* occupies a broader climatic, edaphic and geographical space, including lowland and postglacial landscapes. This suggests that polyploidization was associated with increased ecological amplitude and range expansion.

We will present new molecular results supporting the hybrid origin of tetraploid *F. amethystina*, most likely involving diploid *F. amethystina* and *F. tatrae* as parental lineages. This provides evidence that genome merger followed by chromosome doubling contributed to the formation of a successful allotetraploid lineage. In addition, epigenetic analyses reveal differences in global DNA methylation among taxa and cytotypes, suggesting that regulatory changes may have further enhanced the adaptive potential of tetraploids in heterogeneous environments.

The *F. amethystina*–*F. tatrae* complex therefore offers an informative model for understanding how hybridization, polyploidy and epigenetic variation interact to shape diversification, niche evolution and biogeographical patterns in mountain plants.

T3. Theory or myth? Possible ring speciation in flightless beetles around Lake Issyk-Kul, Kyrgyzstan**Barsa Das*** and Lech Karpiński¹*Museum and Institute of Zoology, Polish Academy of Sciences, Warszawa, Poland*

*das.barsa1998@gmail.com

Ring speciation occurs when a population spreads around a geographic barrier (such as a mountain range or body of water) so that neighbouring populations interbreed freely, yet the terminal ends of the "ring" cannot, despite being linked by a chain of intermediate forms. Although conceptually important, well-supported empirical examples remain rare and contested.

The flightless longhorned beetle genus *Dorcadion* belongs to the highly diverse and taxonomically complex tribe *Dorcadionini s.l.*, widely distributed across Central Asia, including Kyrgyzstan, and is characterised by high species diversity, strong interspecific similarity, and often unclear species boundaries (resulting from hybridization and introgression), making it a valuable model for evolutionary studies. Here we investigate a potential case of ring speciation in the *semenovi* species complex distributed around Lake Issyk-Kul, Kyrgyzstan. Of the 12 described subspecies, seven occur around the lake.

A multilocus phylogenetic analysis based on eight markers (three mitochondrial, five nuclear) recovered five well-supported clades. Most show moderate genetic differentiation (ca. 1–2% COI divergence), consistent with gradual divergence along the ring. In contrast, one clade—comprising *D. semenovi alexandrae* and part of *D. semenovi hauseri*—is highly divergent, exceeding 4% COI distance from the remaining lineages. A Mantel test revealed a significant positive correlation between genetic distance and sequential geographic position around the lake ($r = 0.168$, $p = 0.036$), consistent with isolation by distance operating along the ring rather than across it.

This spatial arrangement suggests a ring-like structure in which stepwise divergence culminates in strongly differentiated terminal forms. Parapatric speciation driven by ecological variation may underlie this rare case in flightless beetles, contributing to the broader debate on the prevalence of ring speciation in low-dispersal taxa and invertebrates.

T4. Genomic shifts and ecological opportunity: Driving adaptive radiation in the ancient Lake Ohrid *Gammarus* species flock

Tomasz Mamos^{1*}, Anna Wysocka², Denis Copilaş-Ciocianu³, Lidia Sworobowicz², Serena Mucciolo¹, Sasho Trajanovski⁴, Luiz Felipe de Andrade¹, Walter Salzburger⁵, Klaudyna Królikowska¹, Grzegorz Tończyk¹, Michał Grabowski¹

¹*Department of Invertebrate Zoology and Hydrobiology, University of Lodz, Łódź, Poland*

²*Department of Genetics, University of Gdansk, Gdańsk, Poland*

³*Institute of Ecology, Nature Research Centre, Vilnius, Lithuania*

⁴*Hydro-Biological Institute, Ohrid, North Macedonia*

⁵*Zoological Institute, University of Basel, Basel, Switzerland*

*tomasz.mamos@biol.uni.lodz.pl

Ancient lakes serve as exceptional natural laboratories for studying the evolutionary dynamics of adaptive radiation. Located on the Balkan Peninsula, Lake Ohrid is Europe's oldest lake (~1.3 My) and a major biodiversity hotspot, harboring an extraordinary level of endemism. The local endemic *Gammarus* (Amphipoda, Crustacea) species flock, encompassing over a dozen species, represents a unique model to unravel the mechanisms underlying rapid diversification in a confined lacustrine system. Using an integrative evolutionary approach, we combined extensive COI barcoding, transcriptome sequencing, functional morphology, and genome size estimations across the species flock and its close relatives, with dietary DNA metabarcoding workflows underway. Our results reveal a vertically structured spatial distribution reflecting distinct habitat zonation, highlighting parapatric speciation as a key driver of diversification. We identified two new molecular units representing cryptic species. The onset of the flock's radiation aligns with lake formation, while subsequent speciation events and demographic shifts correlate with Pleistocene glacial water-level fluctuations, depth-range colonization, and spring isolation. Notably, we observed a distinct discrepancy between mitochondrial and nuclear markers. This mitonuclear discordance, coupled with newly discovered variations in genome size across the flock, points toward genomic restructuring and potential hybridization or polyploidization events during the radiation process. Combined with observed morphological divergence, our preliminary findings suggest that the *Gammarus* species flock was shaped by a complex adaptive radiation where ecological opportunity, spatial isolation, and genomic shifts interacted to drive speciation.

T5. Heterogenous landscape of divergence and introgression across the giant genome of the *Lissotriton vulgaris* newt complex**Chmura Jakko^{1,2*}**, Dudek Katarzyna², Nadachowska-Brzyska Krystyna², Babik Wiesław²¹*Jagiellonian University, Doctoral School of Exact and Natural Sciences, Kraków, Poland*²*Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Kraków, Poland*

*jakko.chmura@doctoral.uj.edu.pl

Gene flow between diverging lineages is common and may lead to heterogeneous patterns of genomic divergence and introgression. These processes remain poorly understood in organisms with giant genomes, where low per-megabase recombination rate and abundant repetitive DNA can influence how divergence builds up across the genome. Here, we present an analysis of divergence and introgression across the giant genome of hybridizing newts from the *Lissotriton vulgaris* complex: *L. montandoni*, *L. v. vulgaris*, and *L. v. ampelensis*, focusing on single-copy genomic regions. We analyzed low-coverage (2-3x) whole-genome sequencing data from 24 individuals using a window-based approach to investigate how divergence and introgression vary along chromosomes in this system. The analyzed genomes exceed 27 Gb in size, making them among the largest genomes studied so far in population genomics. To characterize genomic variability, we estimate nucleotide diversity, Watterson's theta, and Tajima's D, which together provide insight into levels of genetic diversity, demographic history, and potential signatures of selection across the genome. We estimate differentiation between taxa using measures of absolute (dxy) and relative (FST) divergence to evaluate how barriers to gene flow are distributed along chromosomes.

Moreover, we apply the f-statistics framework, both chromosome- and window-based to measure the extent of historical introgression and test its relationship with recombination rate variation inferred from linkage maps. By integrating multiple population genomic statistics, we reveal the genomic determinants of divergence and introgression across a giant genome, and detect pronounced heterogeneity in patterns of genomic differentiation and introgression among the studied lineages.

T6. Linking immunogenetic variation, microbiome and personality.**Magdalena Herdegen-Radwan**

¹*Department of Behavioral Ecology, Institute of Environmental Biology, Adam Mickiewicz University in Poznan, Poznań, Poland*

magher@amu.edu.pl

Personality traits, i.e. individually stable behavioural traits varying across individuals, are ubiquitous across animal species. However, how they arise within populations, and particularly why they often show significant heritability, remains an open question. One of the hypotheses proposes that heritability of personality traits is rooted in polymorphic immunity genes affecting microbiome composition, which in turn may affect personality. Indeed, associations between gut microbiome and behaviours have been reported. Here, I tested the proposed mechanism by integrating behavioural (boldness), gut microbial, and immune (MHC class II) diversity in a laboratory population of guppies. I found support for the effects of both specific MHC alleles and allelic divergence on individual gut microbiome diversity and composition. Variance in boldness was significantly associated with a secondary gradient in microbial community composition, while it was not affected by MHC attributes. These results suggest that heritable immune diversity may exert some control over microbial communities in the host gut, and this relationship translates into a detectable, albeit subtle effect on boldness in guppies.

T7. Living with few or many: contrasting microbiome strategies in Greenland insects**Diana Rojas Guerrero^{1,2*}**, Piotr Łukasik¹¹*Institute of Environmental Sciences at the Faculty of Biology, Jagiellonian University, Kraków, Poland*²*Doctoral School of Exact and Natural Sciences, Biology, Jagiellonian University, Kraków, Poland*

*diana.rojas-guerrero@doctoral.uj.edu.pl

Symbiotic bacteria play important roles in host biology and evolution, influencing traits that enable organisms to persist in rapidly changing environments. In Arctic ecosystems like Greenland, extreme climatic conditions fluctuate across seasons raising the question of whether microbial symbionts contribute to host success in such environments. Although microbial partners may provide benefits such as nutrient supplementation and protection against biotic or abiotic stressors, little is known about their diversity, distribution, and potential roles in Arctic ecosystems.

Here, we investigated microbial associations across populations of two widespread insect groups in Greenland: mosquitoes (Culicidae), which are extremely abundant insects in the region, and hoverflies (Syrphidae) some of the most diverse pollinators on the island. Using multi-target amplicon sequencing, we simultaneously characterized host identity and their bacterial communities to examine how microbial associations vary among host taxa and to identify symbiotic bacteria.

We found striking differences between the two insect groups. The two mosquito species present in Greenland harboured diverse but low-abundance bacterial communities, with little evidence for stable or dominant symbiotic associations. In contrast, hoverflies exhibited simple yet abundant microbiota and emerged as the most diverse hosts of the bacterial endosymbiont *Wolbachia* identified among Greenland insects. *Wolbachia* infection patterns varied substantially among hoverfly lineages, suggesting a complex history of host-symbiont associations. Together, these findings suggest that while some species appear to thrive with sparse and transient microbial communities, others maintain abundant and lineage-specific associations with bacterial symbionts. Understanding the ecological and evolutionary consequences of these contrasting microbiome strategies will provide insights into how insects persist and survive in harsh environments.

T8. Genetic rescue increases long-term fitness despite elevating putative genetic load

Jonathan M. Parrett, Mateusz Konczal, Marta Kulczak & **Jacek Radwan***

¹*Evolutionary Biology Group, Faculty of Biology, Adam Mickiewicz University, Poznań, Poland*

*jacek.radwan@amu.edu.pl

Genetic rescue is a potentially powerful conservation strategy to restore fitness in small genetically depauperate populations, however, long-term effectiveness, impact of rescuer traits and introduced variation on population persistence remains uncertain. Using a male-dimorphic mite we tested whether males that differ in their expression of a condition-dependent sexually selected weapon, previously shown to shape genetic variation in populations and influence reproductive competitiveness, influences the efficacy of genetic rescue. Here we show that introductions from either male morph increased genetic diversity and putative load similarly, indicting even less sexually competitive males can still be effective rescuers. Yet, fitness benefits of rescue by male morphs differed over time, suggesting additional effects not captured by our estimates of genetic load exist. Despite populations being forced to remain small and introductions of males increasing segregating putative load, fitness benefits were sustained for 20 generations—increasing fecundity in benign conditions and reducing extinction risk under thermal stress—likely because genetic variation remained high and deleterious effects largely remaining masked. Overall, these results provide experimental evidence that maximising genome-wide variation via genetic rescue can yield long-lasting benefits to populations facing environmental change, even when rescuers are in lower condition and many presumed deleterious mutations are introduced.

T9. Repeatome evolution in giant genomes across a speciation continuum in newts**Zuzanna Nowak^{1,2*}**, Matias Rodriguez¹, Katarzyna Dudek¹, Wiesław Babik¹¹*Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Kraków, Poland*²*Doctoral School of Exact and Natural Sciences, Jagiellonian University, Kraków, Poland*

*zuzanna.nowak@doctoral.uj.edu.pl

Repetitive elements, primarily transposable elements (TEs) and satellite DNA, constitute most of the genome in many eukaryotes, profoundly shaping genome structure and function. This impact is magnified in giant genomes, defined as those exceeding 10 billion base pairs (Gb). However, while the mechanistic basis of genomic enlargement via TE proliferation is well documented, its evolutionary consequences remain poorly understood. All salamanders (Urodela) exhibit widespread genomic gigantism, making them ideal models to investigate these dynamics. We focus on five evolutionary lineages within the *Lissotriton vulgaris* species complex, which diverged within the last 6 million years, and which form a speciation continuum. Their genome sizes range from 27.5 to 30.5 Gb, a difference amounting to the size of the entire human genome. We compare the genomic landscape of repetitive sequences within and between *L. vulgaris* complex lineages to test whether genome size differences are due to differences in the abundance of particular TE or satellite families, as predicted by some theories of repeatome evolution, or rather due to a generalised expansion/contraction of diverse categories of repetitive elements. We use low coverage (2-3 x) whole genome sequencing of multiple individuals within all five.

T10. Genomic signatures of host-parasite coevolution in the bank vole - nematode system**Dawid Sadkowski***, Abosede Olarewaju, Agnieszka Kloch¹*University of Warsaw, Faculty of Biology, Institute of Ecology, Department of Animal Ecology and Evolution, Warszawa, Poland*

*d.sadkowski2@uw.edu.pl

Parasites play a crucial role in the evolution of their hosts. Variation in parasite prevalence, genetic diversity, and community composition among host populations can generate spatially heterogeneous selection pressures, potentially promoting local adaptation and genomic differentiation in their hosts. On the other hand, host populations are equally diverse, leading to local, host-parasite arms race visible at the genetic level. This co-evolution has been comprehensively described from the host perspective, yet little is known about the parasite adaptations to the host defense. Moreover, all studies up to date focused on SNP variance, neglecting structural variation which is an underexplored yet potentially critical component of adaptive evolution. In the project, aim to fill this gap using bank vole *Myodes glareolus* - nematode *Heligmosomum mixtum* system to study the role of structural variants, in particular inversions, in host-parasite evolutionary interplay. Using samples collected along a geographical cline (Finland-Poland-Czech Republic) and a temporal cline (2005-2025), this study aims to detect structural variants from RAD-seq data using window PCA, with the goal of distinguishing recent mutations linked to ongoing climate change from those that arose during the last glaciation.

T11. Uncovering the evolution and roles of somatic piRNAs

Dominik Robak, Takahisa Yamashita, Krystian Komenda, Rafał Miłodrowski, Szymon Szrajer, Tomasz Gaczorek, **Guillem Ylla***

¹*Laboratory of Bioinformatics and Genome Biology, Faculty of Biochemistry, Biophysics and Biotechnology, Jagiellonian University, Kraków, Poland*

*guillem.ylla@uj.edu.pl

PIWI-interacting RNAs (piRNAs) are classically defined by their role in maintaining genome integrity through transposable element silencing within the animal germline. While recent studies have reported somatic piRNA expression in select species, the evolutionary scale and functions of non-gonadal piRNAs remain enigmatic. This knowledge gap is partially due to the lack of standardized, automated tools capable of identifying piRNA loci across non-model organisms. To streamline and standardize the detection, annotation, and study of piRNA clusters and secondary piRNA signatures across animal species, we developed piRAT (piRNA Annotation Tool), which requires only small RNA-seq mapped against a genome assembly. With this strategy, we analyzed 168 public small RNA sequencing datasets spanning 17 diverse arthropod species, determining that non-gonadal somatic piRNA expression is not an isolated anomaly, but a widespread feature conserved across major lineages of the phylum Arthropoda. Furthermore, we knocked down genes involved in the piRNA biogenesis pathway in multiple tissues of our two insect models (*Blattella germanica* and *Gryllus bimaculatus*). These knockdowns, coupled with small RNA-seq and lncRNA-seq, confirmed the presence of both biogenesis pathways in multiple somatic tissues, identified the targets of the piRNAs, and revealed insights into their potential functional roles. These findings challenge the old paradigm of gonad-restricted piRNA functionality in animals, and show that non-gonadal piRNA expression is common in different lineages, where they can play important regulatory roles.

T12. Domestication of mobile DNA in bacterial genomes – the case of virulence plasmids of bacteria of the genus *Cronobacter***Zofia Owczarzak^{1*}**, Kamil Krakowski², Anastazja Tasinkiewicz¹, Dariusz Bartosik¹¹*Institute of Microbiology, Faculty of Biology, University of Warsaw, Warszawa, Poland*²*Institute of Evolutionary Biology, Faculty of Biology, University of Warsaw, Warszawa, Poland*

*z.owczarzak@uw.edu.pl

Bacterial survival depends on the ability to adapt to changing environmental conditions. One of the major mechanisms underlying prokaryotic adaptation is horizontal gene transfer (HGT), which enables the acquisition of exogenous DNA and novel traits, including antibiotic resistance. Among HGT mechanisms, plasmid-mediated DNA transfer is particularly important. Plasmids are autonomously replicating mobile genetic elements that drive bacterial evolution and phenotypic diversification. However, due to their mobility and temporary occurrence in individual strains, it is difficult to trace their long-term co-evolution with particular hosts, and define the processes leading to mutual adaptation of plasmids and bacteria. In-depth analysis of different families of bacterial plasmids has identified a group of highly related non-transferable virulence plasmids of bacteria of the genus *Cronobacter*, which provide an excellent model for studying the phenomenon of domestication of bacterial plasmids. These replicons are likely to have been associated with this genus throughout its evolutionary history. Thus, they have accompanied the genetic differentiation of individual strains and their subsequent speciation, which is thought to have started around 45–68 million years ago (i.e. at the beginning of the Cenozoic Era). This unprecedented linkage of one structural type of plasmid with a narrow group of related species raises important questions about the causes and effects (at the molecular and physiological levels) of such a close long-term association. We performed a comprehensive analysis of these plasmids, with particular emphasis on their genetic cargo, including systems that mediate antagonistic interactions between bacteria. These systems may have played a pivotal role in the evolutionary history of their hosts by shaping interbacterial competition, adaptation, and genome evolution.

T13. Assortative mating by plumage colour traits: validation using a covariance partitioning approach in a long-term data set

Katarzyna Janas^{1,2*}, Barbara Class³, Amélie Fargevieille³, Arnaud Grégoire³, Anne Charmantier³, Céline Teplitsky³, Claire Doutrelant³

¹*Museum and Institute of Zoology, Polish Academy of Sciences, Warszawa, Poland*

²*Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland*

³*Centre d'Ecologie Fonctionnelle et Evolutive, Univ. Montpellier, CNRS, Montpellier, France*

*kjanas@miiz.waw.pl

Assortative mating, a pattern of mate choice based on phenotypic similarity, has important evolutionary implications, particularly for local adaptation and speciation. It is widespread in birds and has been documented for behavioural, morphological, and colour traits. A commonly used method for estimating assortative mating relies on within-pair phenotypic correlations; however, recent studies have shown that this approach may lead to overestimation. An alternative approach, based on covariance partitioning, allows for discrimination between intrinsic (i.e. unbiased) assortative mating and resemblance caused by confounding factors: shared environment or measurement error. While this method has been applied to behavioural and morphological traits, colour traits have not yet been evaluated in this context. Here, we used covariance partitioning to assess the strength of intrinsic assortative mating in the blue tit (*Cyanistes caeruleus*) plumage traits. We analysed a 19-year dataset from two long-term study populations (Pirio, Corsica, and Rouvière, mainland France). We fitted bivariate mixed models for two colour traits (crown UV chroma and breast carotenoid chroma) and compared them with models for morphometric traits (tarsus length, wing length, body mass). Despite high within-pair phenotypic correlations for all traits, our models revealed significant intrinsic assortative mating only for tarsus length. To determine whether this result was driven by high lability of colour traits, we conducted a simulation study which showed that low within-trait repeatability, typical of colour traits, substantially reduces the power to detect intrinsic assortative mating. Taken together, our results suggest that examining assortative mating based on strongly condition-dependent traits requires careful study design to ensure adequate statistical power.

T14. Mimicry and formation of host specific lineages in the shining bronze-cuckoo *Chalcites lucidus***Alfredo Attisano***, Roman Gula, Jörn Theuerkauf¹*Museum and Institute of Zoology, Polish Academy of Sciences, Warszawa, Poland*

*aattisano@miiz.waw.pl

Antagonistic coevolutionary interactions between avian brood parasites and their hosts can promote selection for discrimination of the parasite by the hosts via acoustic and visual signals. Nestlings of brood parasites are therefore under selection to evolve visual and acoustic mimicry of the host nestlings to avoid discrimination by host parents. An outstanding question is whether mimicry of the host can lead to host specialisation and species diversification in brood parasites. The shining bronze-cuckoo *Chalcites lucidus* has three subspecies distributed in geographically separated regions of the South Pacific (Australia, New Caledonia, New Zealand). The cuckoo parasites exclusively hosts in the family Acanthizidae and each cuckoo subspecies specialises on a single host in each region. No hosts discriminate the cuckoo egg, but some discriminate the parasite nestling. We found evidence that host discrimination in these systems has promoted selection for remarkable multimodal mimicry in cuckoo nestlings. These closely resemble visual and acoustic features of their specific host's nestlings and each cuckoo subspecies resembles more closely the respective unrelated host rather than any of the phylogenetically related cuckoo subspecies. Furthermore, the accuracy of acoustic and visual mimicry covary with host defences and acceptance rates of the cuckoo nestlings across the range. Our research shows that a parasitic lifestyle can promote phenotypic variation in brood parasites as a strategy to decrease rejection rates by the host. Furthermore, host specialisation overcomes phylogenetic constraints promoting selection for diversification and formation of distinct evolutionary units in the shining bronze-cuckoo.

T15. The role of extra-pair copulation in nestling colour in a host-parasite system

Xinrou Huang*, Roman Gula, Jörn Theuerkauf, Alfredo Attisano

¹*Museum and Institute of Zoology, Polish Academy of Sciences, Warszawa, Poland*

*xinrou.huang@bioplanet.edu.pl

Extra-pair copulation in birds can increase offspring fitness and genetic diversity, but also potentially result in intra-nest phenotypic variation in offspring. Hosts of avian brood parasites rely on intra-nest uniformity to discriminate a parasite in the nest, therefore increased intra-nest phenotypic variation can decrease the discrimination ability of the parasite. In New Caledonia, the fan-tailed gerygone (*Gerygone flavolateralis*) discriminates nestlings of the brood parasitic shining bronze-cuckoo (*Chalcites lucidus*). However, the gerygone has two nestling phenotypes (bright, dark) occurring in monomorphic and polymorphic broods, which can potentially decrease the ability to discriminate the parasite nestling. We used three populations of fan-tailed gerygone from two habitats with contrasting relative proportions of bright/dark nestlings to investigate whether extra-pair paternity is linked to phenotypic variation in nestlings and broods. Using 17 microsatellite markers on 75 gerygone families (126 adults and 138 nestlings), we found that extra-pair paternity occurred in 36% of the broods and that 25% of the offspring were sired by extra-pair males. The rates of extra-pair paternity were similar across populations, even though the relative proportions of bright/dark nestlings differed among populations. We found that extra-pair paternity was more likely when nests were built in denser vegetation and when females had a partner in poorer body condition. The results indicate that the mating system in this host is affected by ecological factors, however it does not affect the relative occurrence of nestling and brood phenotypes.

T16. The evolution of an individual-like dispersive stage in colonial siphonophores**Maciej Mańko^{1*}**, Catriona Munro², Lucas Leclère²¹*University of Gdansk, Gdańsk, Poland*²*Sorbonne Université, Paris, France*

*maciej.manko@ug.edu.pl

Many sedentary colonial animals reproduce by releasing a dispersive stage, a larva or detached zooids (e.g., medusa), that enables gene flow and range expansion. Pelagic colonial siphonophores (Cnidaria: Hydrozoa) have taken a different and evolutionarily unique route: in certain species, reproduction proceeds through colony fragmentation, whereby an entire terminal cluster of zooids breaks away as a single dispersive unit, the eudoxid, rather than shedding individual reproductive zooids. Despite being built from several functionally specialized zooids, the eudoxid acts as one cohesive individual, hinting at an evolutionary transition in individuality. Until now, how eudoxids form and where they originated evolutionarily had remained obscure. Combining live imaging, immunohistochemistry, and pharmacological inhibition, we reconstruct the mechanistic basis of eudoxid formation. We show that a dedicated muscle governs eudoxid release and that the process entails substantial tissue remodeling, yielding a physiologically integrated dispersive unit with its own distinct behaviors. Our reconstructions indicate that eudoxids arose a single time, via a coordinated overhaul of colony architecture alongside the modification of zooid structures. We further demonstrate that eudoxids and their parental colonies frequently occupy different distributions, pointing to niche partitioning between the two life-cycle stages. Together, these results illustrate how muscle evolution and structural reorganization of the colony gave rise to a novel, individual-like dispersive stage, helping explain the ecological success of siphonophores across marine environments.

T17. Meta-analytic evidence for growth-reproduction trade-offs in woody plants

Barczyk M.^{1*}, Bogdziewicz M.¹, Drobnia Sz.², Bogdańska M.¹, Eichert U.¹, Foest J.¹, Journé J.⁴, Kondrat K.³, Szymkowiak J.¹, Hacket-Pain A.⁴

¹*Forest Biology Center, Adam Mickiewicz University in Poznan, Poznań, Poland*

²*Department of Synthetic Evolutionary Ecology, Institute of Environmental Sciences Jagiellonian University, Kraków, Poland*

³*Department of Organic Chemistry, Faculty of Chemistry, University of Lodz, Łódź, Poland*

⁴*University of Liverpool, Liverpool, England*

*maciejkbarczyk@gmail.com

Growth and reproduction draw on a common resource pool, yet empirical studies of woody plants report widely differing relationships between seed production and somatic growth. Here we synthesize 685 estimates from 78 studies covering 79 woody species to test how growth–reproduction correlations vary across time, species, and environments. Growth and reproduction measured within the same year were negatively correlated, suggesting an immediate cost of reproduction. Lagged growth–reproduction relationships further suggest that reproduction incurs delayed constraints on growth beyond the year of investment. The strength and direction of growth–reproduction correlations showed no detectable phylogenetic signal and were not systematically related to functional traits and climate. Instead, trade-offs were strongest in species with high interannual variability in seed production and weakened markedly over recent decades in these species. Together, these results show that growth–reproduction trade-offs in woody plants are common but not fixed, and that shifts in reproductive variability under environmental change can alter how trees balance growth and reproduction, with consequences for long-term forest functioning.

T18. Late adaptive immune system development in salamanders: a life-history trade-off?**Magdalena Migalska***, Katarzyna Dudek, Wiesław Babik¹*Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Kraków, Poland*

*magda.migalska@uj.edu.pl

The adaptive immune system (AIS) of jawed vertebrates is a major evolutionary innovation that enables recognition of diverse pathogens and provides immunological memory. However, establishing a broad anticipatory repertoire of immune receptors is developmentally costly, potentially creating trade-offs during early life. These constraints may be especially pronounced in small amphibian larvae, which hatch into pathogen-rich environments. In addition, metamorphosis extensively remodels tissues and alters the antigenic landscape of “self”, potentially reducing the value of AIS repertoires established during larval stages. Consistent with this idea, studies in *Xenopus* suggest that full AIS development may be delayed until after metamorphosis. Yet little is known about the developmental trajectories of AIS across amphibians, including in salamanders, where existing evidence is mostly based on an atypical, neotenic laboratory model, the axolotl. Here, we investigate AIS development across 18 species from four salamander families: Hynobiidae, Salamandridae, Ambystomatidae, and Plethodontidae. Using comparative transcriptomics, we examine developmental expression patterns of key AIS components: major histocompatibility complex (MHC) genes and T-cell receptors (TCRs). In most taxa, except larger-bodied species, TCR expression appears limited prior to metamorphosis, whereas MHC genes (particularly MHC-I), are expressed earlier. Smallest plethodontid salamanders exhibit comparatively low TCR expression even in adulthood, despite apparently typical MHC expression levels. We further explore phylogenetic diversity of MHC genes and TCR α gene segments (TRAV and TRAJ), as well as developmental changes in TCR α repertoire diversity. Together, these analyses provide new insights into the timing, capacity and evolutionary diversification of amphibian AIS across a broad phylogenetic framework – knowledge urgently needed as emerging amphibian pathogens pose escalating threats.

T19. The role of global wind regimes in avian body size and shape evolution**Federica Bordogna***, Rafał Martyka, Arkadiusz Fröhlich¹*Institute of Nature Conservation, Polish Academy of Sciences, Kraków, Poland*

*bordogna@iop.krakow.pl

Wind is a major agent of thermoregulation, yet it remains unknown whether it could affect the evolution of avian body form. Here, we test whether global wind regimes, together with temperature, could be involved in ecogeographic rules across all the world's birds, while controlling for phylogeny and migratory habits, and using different measures of climatic seasonality. We expected an increase in body mass (Bergmann's rule) and a decrease in unfeathered appendages, such as beak and tarsus (Allen's rule), with environmental wind speed (additive model: Temperature + Wind). We also expected these effects to be stronger at lower rather than higher ambient temperatures (interactive model: Temperature × Wind). We found a prominent increase in body mass with wind speed that was independent of temperature, particularly during the hottest months. The wind–temperature interaction best explained appendage lengths, with wind-related elongation being more prominent in colder environments; this pattern was best attributable to the coldest seasons for beak length and to the hottest seasons for tarsus length. Our study opens a new perspective on multiple climatic agents constraining the diversity of animal body forms through evolution.

T20. Microhabitat structure predicts eye presence in bryophyte-dwelling tardigrade communities**Yelyzaveta Matsko^{1,2*}**, Krzysztof Miler³, Izabela Poprawa¹, Daniel Stec³¹*Institute of Biology, Biotechnology and Environmental Protection, Faculty of Natural Sciences, University of Silesia, Katowice, Poland*²*Doctoral School at the University of Silesia in Katowice, Katowice, Poland*³*Institute of Systematics and Evolution of Animals of the Polish Academy of Sciences, Kraków, Poland*

*yelyzaveta.matsko@us.edu.pl

Tardigrades often vary in eye presence among closely related taxa, yet the ecological drivers of this variation remain poorly understood. Because visual structures are commonly linked to environmental conditions, we investigated factors that may influence eye occurrence in bryophyte-dwelling tardigrades. Specifically, we tested whether eye presence is associated primarily with broad-scale light availability or with fine-scale microhabitat characteristics related to bryophyte structure. Bryophyte samples were collected in the Italian Alps. We selected a subset of 75 samples balanced across transects, elevation, light exposure, and bryophyte life and growth forms. From each sample, 30–40 tardigrade individuals were examined for eye presence using light microscopy. Fixed effects, including sample exposure to sunlight, bryophyte light indicator value, and morphological complexity, quantified from traits such as shoot size, life form, and growth form, were analysed using mixed-effects models. Eyes were present in 2,459 individuals, representing 88.5% of all examined specimens, and absent in 319 individuals, representing 11.5%. Among all eyeless specimens, 52% occurred in only ten samples, indicating strong patchiness at the microhabitat scale. Both bryophyte light indicator value and morphological complexity significantly predicted eye presence. However, morphological complexity was the strongest predictor, accounting for approximately 40% of the explained variance. The probability of eye presence decreased significantly with increasing structural complexity of the bryophyte patch. These findings indicate that microhabitat characteristics are associated with the distribution of visual traits in limno-terrestrial tardigrade communities and highlight the importance of fine-scale environmental filtering in shaping sensory trait variation in microscopic animals.

T21. Rethinking Claw Reduction in Tardigrades: Hidden Phylogenetic Complexity Revealed in Isohypsibioidea (Tardigrada).

Jędrzej Warguła^{1*}, Wiktoria Dmuchowska¹, Adrian Wieczorek¹, Daniel Stec², Andrzej Węgiel³, Łukasz Kaczmarek¹

¹*Department of Animal Taxonomy and Ecology, Adam Mickiewicz University in Poznań, Poznań, Poland*

²*Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Kraków, Poland*

³*Poznań University of Life Sciences, Faculty of Forestry, Poznań, Poland*

*jedwar@amu.edu.pl

Water bears (Tardigrada) are a phylum of microinvertebrates characterized by high morphological plasticity and a large capacity for the adaptation to diverse environments, including mosses, lichens, leaf litter, and soil. Soil-dwelling species are particularly noteworthy, as they often exhibit a significant reduction of claws, and in some cases, their complete loss on some or on all legs. This reduction is interpreted as an adaptation facilitating movement between soil particles and represents a case of convergent evolution across several eutardigrade families. Given the crucial taxonomic importance of claw morphology in tardigrades, the phylogenetic relationships of many soil-dwelling taxa have remained unresolved. Morphological and molecular analyses (COI, ITS-2, 18S rRNA, and 28S rRNA) of eutardigrade taxa from Ethiopia, Uganda and the Republic of South Africa, including the discovery of three new genera, altogether with examination of historical specimens from Mozambique and Australia, have provided new insights into the phylogeny of soil-dwelling eutardigrades from the superfamily Isohypsibioidea. Our results revise current view on evolutionary relationships within the superfamily and suggest that some morphological characters previously regarded as phylogenetically informative may, instead, reflect convergent adaptations to the constraints of the soil environment, whereas other traits may better capture the evolutionary history of the Eutardigrada. This study demonstrates how the integration of morphological and molecular data can refine our understanding of the evolutionary relationships and taxonomic diversity of soil microfauna.

T22. Evolution and Anhydrobiosis and: Evolutionary consequences of metabolism slowing down or complete stop**Łukasz Kaczmarek^{1*}**, Jędrzej Warguła¹, Wiktoria Dmuchowska¹, Duygu Berdi², Bartłomiej Gołdyn³¹*Department of Animal Taxonomy and Ecology, Adam Mickiewicz University in Poznan, Poznań, Poland*²*Department of Biology, Ankara University in Ankara, Turkey*³*Department of General Zoology, Adam Mickiewicz University in Poznan, Poznań, Poland*

*kaczmar@amu.edu.pl

Water availability is one of the most important ecological factors and evolutionary pressures on terrestrial life. Nevertheless, some microorganisms, plants and animals are able to survive desiccation even with complete or almost complete loss of body water. The dried organisms may stay in this form without serious damage for a long time and resume active life immediately when water appears in the environment. This state of suspended animation is named anhydrobiosis. Among animals anhydrobiosis, present at each stage of life i.e., eggs, juveniles and adults, is known in roundworms (Nematoda), wheel animals (Rotifera) and water bears (Tardigrada). Anhydrobiosis may affect not only the life history of individual specimens (survival, reproduction, aging) but, when common or evolutionarily persistent, may influence the life-history strategy of entire species. For example, anhydrobiosis has a strong influence on animal aging and fitness which is illustrated by “Sleeping Beauty” model. According to this hypothesis, anhydrobiotic organisms do not age while in the anhydrobiotic state and display improved overall fitness, a trait that is also evident in their offspring. However, anhydrobiosis may influence not only aging processes, but also species diversification. As it was shown in tardigrades and rotifers, species/groups of species e.g. living in permanent water environments and not capable to anhydrobiosis are much more morphologically divaricated in comparison to closely related groups capable to anhydrobiosis and inhabiting temporary habitats. Summarizing, the process of anhydrobiosis may from one side slow down or stop aging which is beneficial for the individuals and, on the other hand, slow down the evolutionary processes, what may be unfavorable for the species in general. In present talk we will discuss all potential evolutionary consequences i.e. pros and cons of anhydrobiosis and how it influences biology, ecology and biogeography of anhydrobiotic taxa.

T23. Parental senescence effects in an annual fish**Milan Vrtílek^{1*}**, Malahat Dianat¹, Anna Kromerová², Dagmar Čížková¹, Miloslava Fojtová², Jiří Fajkus²¹*Czech Academy of Sciences, Institute of Vertebrate Biology, Brno, Czech Republic*²*Masaryk University, CEITEC, Brno, Czech Republic*

*vrtilek@ivb.cz

Senescence occurs across multiple life functions and traits but not synchronously. Evolutionary theory of senescence predicts for example that decline in parental effects and fertility may develop along divergent trajectories. In the short-lived turquoise killifish (*Nothobranchius furzeri*), we focused on how senescence of parents affects viability of their offspring. We monitored parental senescence at both performance and cellular level in a longitudinal laboratory study. Using factorial breeding design, we aimed at testing if older parents also produce biologically “older” offspring. Such offspring would be inferior in stiff post-hatching competition with the offspring of young parents. We observed clear signs of parental reproductive senescence and age-related telomere shortening at the population level. The negative impact of advanced parental age fell most severely on survival of offspring during incubation and their hatching. The offspring that eventually hatched, however, grew at a similar rate irrespective of parental age. Shorter telomeres of the aged parents were also not transmitted to the next generation. This suggests that turquoise killifish parents trade off quality of their offspring for the number. This may extend their scope for bet-hedging in the unpredictable natural environment of ephemeral ponds.

T24. Cooling for the night: zebra finches modify their hypothermic curve when facing an energetic challenge**Małgorzata M. Lipowska^{1*}**, Jakub P. Płachta^{1,2}, Ulf Bauchinger^{1,3}, Edyta T. Sadowska¹¹*Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Kraków, Poland*²*Doctoral School of Exact and Natural Sciences, Jagiellonian University, Kraków, Poland*³*Nature Conservation Station Unterelbe, State Agency for Bird Conservation, Freiburg/Elbe, Germany*

*malgorzata.lipowska@uj.edu.pl

Birds employ hypothermia during their resting phase, which conserves energy at the cost of rapid rewarming back to active-phase level. We hypothesized that modulation of both the rate of cooling and hypothermia depth could simultaneously augment energy savings and lessen the severity of the eventual rewarming phase when an animal is facing an energetic challenge. Here, we continuously recorded body temperature of fed and fasted zebra finches (*Taeniopygia guttata*) resting in ambient temperatures below (15 or 25°C) and within their thermoneutral zone (30°C), and tested how these compounding challenges affected the shape of their hypothermic curves. The fed birds displayed a similar hypothermia pattern regardless of ambient temperature, whereas the effect of fasting was more pronounced in lower temperatures. During initial cooling phase, fed birds reduced their temperature by 2.9°C, 3.5°C or 3.0°C (warmest to coldest ambient). Fasted birds exhibited a deeper decline (3.3°C, 4.2°C and 4.9°C, respectively) but cooled more slowly (12%, 22% and 57%). During the maintenance phase following the initial cooling, the body temperature further decreased by approximately 0.1°C/h in fed birds, whereas in fasted ones it stabilised, or even steadily increased by 0.1°C/h in the coldest ambient conditions. Consequently, the temperature difference between fasted and fed birds decreased with time, indicating a redistribution of energetic costs across the night. These findings suggest that birds can increase total overnight energy savings while mitigating the peak energetic demands of rewarming, potentially through a combination of moderated hypothermia depth and reduced passive heat loss.

T25. Does selection of laboratory mice for high basal metabolic rate increase their susceptibility to high ambient temperature?**Piotr Roszkowski^{1*}**, Julita Sadowska², Andrzej Gębczyński², Paweł Brzęk²¹*Doctoral School of the University of Białystok, Białystok, Poland*²*Faculty of Biology, University of Białystok, Białystok, Poland*

*p.roszkowski@uwb.edu.pl

Global climate change has emphasized the importance of understanding of thermal stress biology, as increasing ambient temperature can impose physiological challenge on animals. Basal metabolic rate (BMR) quantifies the minimal energetic cost of maintaining an endothermic organism under thermoneutral conditions and is a key determinant of physiology in mammals. Since BMR represents an unavoidable cost of body maintenance it can constitute relative larger part of total energy expenditure at higher ambient temperature when thermogenic needs are reduced. As a result, individuals with higher BMR may be more strongly affected by higher ambient temperatures due to impaired heat dissipation. Here, we investigated the effect of housing temperature on reproduction and development in two lines of laboratory mice divergently selected for high (H-BMR) and low (L-BMR) BMR. Animals were acclimated to 23 °C or 30 °C, bred, and their offspring were reared to maturity under the same conditions. Our preliminary results reveal that 30 °C reduced reproductive output more strongly in H-BMR than in L-BMR females, confirming that individuals with higher BMR are more affected by high ambient temperature. Housing temperature exerted a significant and complex effect on the between-line difference in the growth of young mice. The effect of BMR on most physiological traits and morphometrics studied in adult mice was not affected by housing temperature. However, adult L-BMR mice were heavier than H-BMR mice when reared at 30 °C but not at 23 °C. Sex affected several studied traits, but its effect was largely independent of housing temperature. We conclude that individuals with higher BMR can indeed be more affected by increasing ambient temperature. This study was supported by the National Science Centre, Poland, grant 2023/49/B/NZ8/00725 (JK).

T26. Age - related changes in immune functions in laboratory mice divergently selected for basal metabolic rate**Sylwia Szymborska***, Aneta Książek, Sebastian Maciak, Marek Konarzewski¹*Faculty of Biology, University of Białystok, Białystok, Poland*

*s.buczynska@uwb.edu.pl

Aging is associated with thymic (tissue for T cell maturation) atrophy, reduced production of naïve immune cells, and alterations in the numbers of T-helper (Th) and T-cytotoxic (Tc) lymphocytes. This process, known as immunosenescence, leads to a progressive decline in immune responsiveness. According to the Life History Theory, maintaining immune function is energetically costly; therefore, metabolic rate may be one of the factors driving the rate of immune system aging. To investigate this putative relationship, we conducted an experiment in which we assessed immunity markers every 2 months (between the 18th and 66th weeks of age). We monitored the total number of (i) mature T lymphocytes, (ii) including Th and Tc lymphocytes, (iii) recent thymic emigrants (RTEs, representing naïve T-cells) in blood, and (iv) the level of anti-KLH IgM antibodies in serum. In the study, we used male laboratory mice selected for a high (H-BMR) or low (L-BMR) Basal Metabolic Rate (BMR). To induce antibody production, mice were immunized with the KLH antigen (keyhole limpet hemocyanin), while controls received PBS. At no point was there a between-line type difference in age-related thymic atrophy rate; but all markers in blood were higher in the L-BMR than in the H-BMR mice. In both line types, aging was associated with a decline in the total number of mature T cells, Th and Tc cell subsets, and RTEs; however, only the numbers of Tc and RTEs declined more strongly in the L-BMR mice. Interestingly, anti-KLH IgM antibody production increased slightly with age in both lines, and, irrespective of age, it was higher in the immunized H-BMR line. Our findings suggest that BMR may differentially influence the rate of immunosenescence and reflect a trade-off between immune function and lifespan, potentially linking BMR with longevity. Importantly, a humoral immune response (as measured by anti-KLH IgM antibody levels) appears to be more dependent on T cell function than on their abundance.

T27. Ecological niche dynamics and trophic interactions predict future invasion impacts under climate change**Ali Serhan Tarkan^{1*}**, Dagmara Błońska¹, Sadi Aksu²¹*Department of Ecology and Vertebrate Zoology, Faculty of Biology and Environmental Protection, University of Lodz, Łódź, Poland*²*Vocational School of Health Services, Eskişehir Osmangazi University, Eskişehir, Türkiye*

*serhantarkan@gmail.com

Climate change and biological invasions are among the major drivers of contemporary biodiversity change, altering species distributions, trophic interactions, and community structure. Understanding how these processes interact is essential for predicting future ecological impacts and ecosystem responses. Here, we developed an integrative framework to assess how climate change may modify the ecological impacts of an invasive predator across native and non-native ranges. Using the European perch, *Perca fluviatilis* as a model species, we combined stable isotope data describing trophic position, temperature-dependent functional response data quantifying predation strength, and ecological niche models estimating spatial overlap with potential prey species. These complementary components were integrated to estimate invasion impact and generate spatially explicit projections under current climatic conditions and future climate scenarios (2050 and 2100). Our results indicate that the current ecological impact of *P. fluviatilis* is greatest across temperate regions of the Northern Hemisphere, including Europe, northern Asia, and parts of North America. Future projections revealed a poleward shift and expansion of impact hotspots under climate warming. In invaded regions, ecological impacts were concentrated in southern South America, southern Australia, and New Zealand, with projected increases in impact intensity through both 2050 and 2100. These findings demonstrate that the ecological consequences of biological invasions are dynamic and strongly influenced by climate-driven changes in species distributions and trophic interactions. More broadly, our framework provides a mechanistic approach for linking niche dynamics, predator–prey interactions, and climate change to improve predictions of invasion impacts across space and time.

T28. The eco-evolutionary dynamics of an adaptive radiation**Dawid Żegota^{1,2*}**, Eliza Szczerkowska-Majchrzak², Carl Smith², Grzegorz Zięba²¹*BioMedChem Doctoral School of the University of Lodz and the Institutes of the Polish Academy of Sciences in Lodz, Łódź, Poland*²*Faculty of Biology and Environmental Protection, University of Lodz, Łódź, Poland*

*dawid.zegota@edu.uni.lodz.pl

Eco-evolutionary dynamics link ecological change to evolutionary responses and their reciprocal ecological consequences. We tested this framework in an adaptive radiation of the three-spined stickleback (*Gasterosteus aculeatus*) across 21 replicated lochs on North Uist, Scotland (7 basic, 7 acidic with fish, 7 fishless acidic). Surveys in autumn 2025 and spring 2026 quantified pH, water absorbance, macroinvertebrate/zooplankton productivity, stickleback gut fullness, body size, lateral plate counts, relative abundance (CPUE), competitor (nine-spined stickleback) and predator (brown trout) densities, as well as loch size, elevation and distance to the marine source of the ancestral population. Bayesian spatial models and structural equation modelling revealed that low pH and high water absorbance reduced productivity and food availability, selecting for smaller fish with fewer lateral plates. Reduced body size and armour, together with lower fecundity in acid lochs, interacted with competitor and predator densities to constrain three-spined stickleback population size, driving evo-to-eco feedbacks. Non-metric multidimensional scaling showed discrete macroinvertebrate and fish communities structured by pH. This replicated natural experiment demonstrates how abiotic gradients drive rapid morphological evolution that feeds back to population and community dynamics. Our findings illustrate the mechanistic basis of adaptive radiation and highlight eco-evolutionary processes governing biodiversity across an environmental gradient.

T29. Preferences for the colour of artificial nest material in a cavity nesting songbird**Adrian Surmacki**¹*Adam Mickiewicz University in Poznan, Poznań, Poland*

adrian@amu.edu.pl

Tits (Paridae) are known to use anthropogenic materials for nest building, although the mechanisms governing such behaviour remain unclear. We conducted two experiments in which Great Tit females could choose among four colours of artificial nest material for nest lining. In the first experiment (2022), the material consisted of acrylic fibres, whereas in the second (2024), it was natural wool worsted. The studies were performed in a woodland population of Great Tits nesting in nest boxes. Samples, each containing all four colours, were distributed evenly before the nest-building period. The use of each colour was assessed from photographs and expressed as the percentage of nest area covered by a given colour. Great Tits used acrylic fibres more frequently than wool worsted, which were found in 82% and 23% of nests, respectively. Females showed significant preferences for particular colours, although these preferences were only partially consistent between the two experiments. Red and white were the most preferred colours in the acrylic fibre experiment, whereas white clearly dominated in the wool worsted experiment. In both experiments, blue was the least preferred colour. These results underline the importance of considering both colour and material structure in nest-material choice experiments.

T30. Food composition of Great Tit nestlings in a gradient of urbanization**Patrycja Piotrowska^{1*}**, Marta Szulkin², Michela Corsini³¹*Adam Mickiewicz University in Poznan, Poznań, Poland*²*Institute of Evolutionary Biology Faculty of Biology, University of Warsaw, Warszawa, Poland*³*Institute for Alpine Environment Eurac Research, Bolzano, Italy*

*piotrowskap15@gmail.com

Great Tits constitute a valuable model species in urban ecology studies, as they rear their offspring in habitats with varying levels of urbanization. They, however, tend to experience reduced breeding success in cities, which has recently been linked to the increased level of impervious surface area (ISA) in the environment. This finding raises questions about the impact of urbanization on various factors that may contribute to breeding success, including the diet composition of nestlings. I investigated the diet of urban Great Tits nestlings in relation to the percentage of impervious surface (ISA) and tree cover around the nest, as well as the influence of parental sex and time of day on the prey composition delivered. My data were collected through the analysis of videos recorded in 2018 and 2019 inside 26 Great Tit nestboxes distributed in a gradient of urbanization in Warsaw. I found that caterpillars were the main component of nestling diet, and that their proportion in the diet was negatively correlated with the amount of impervious surfaces around the nest. An increasing amount of impervious surfaces also resulted in a decreased proportion of spiders and increased proportion of adult Lepidoptera in nestling diet. The proportion of spiders was also positively affected by tree cover percentage. I did not observe any sex- or time-dependent differences in prey composition. Although further studies are necessary, my results suggest that the urban diet may contribute to impaired breeding parameters of Great Tits, as it is poorer in nutritious invertebrate taxa. Information on feeding frequency, prey abundance in urban environments, and the dietary requirements of nestlings is essential for obtaining a comprehensive understanding of food availability for growing passerines in urban areas.

T31. *Wolbachia*-Host Co-evolution in *Drosophila* Clonal Cell Lines**Navina Mable Francis^{1,2*}**, Ewa Chrostek^{1,3}¹*Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Kraków, Poland*²*Jagiellonian University, Doctoral School of Exact and Natural Sciences, Kraków, Poland*³*Department of Evolution, Ecology and Behaviour, Institute of Infection, Veterinary and Ecological Sciences, University of Liverpool, UK*

*navina.francis@doctoral.uj.edu.pl

Wolbachia, an intracellular maternally transmitted bacterial symbiont, is known for its diverse effects on host organisms, including reproductive manipulations and antiviral protection. As *Wolbachia* cannot be cultured outside the host cells, *Wolbachia*-infected insect cells have been widely used to study *Wolbachia* phenotypes. JW18 is an embryo-derived *Drosophila melanogaster* cell line widely used in *Wolbachia* research. It has been employed to study viral replication dynamics, cell-to-cell transmission of *Wolbachia*, and to screen for *Wolbachia*-targeting drugs. However, *Wolbachia* abundance in JW18 varies between individual cells and across passages. Additionally, this cell culture is morphologically heterogeneous. This variability suggests that any treatment applied to a JW18 culture could select for sub-populations of cells, effectively altering the culture composition, rather than directly affecting the physiology of the cells. To address this heterogeneity and reduce experimental variability, we cloned JW18 and generated monoclonal cultures from the parental JW18 cell line. We demonstrate that these monoclonal cultures exhibit distinct proliferation rates and *Wolbachia* infection statuses. To investigate the genomic basis of this variation and its evolutionary dynamics, we performed whole-genome sequencing of both host cells and *Wolbachia* across the monoclonal cultures. By sequencing the same clones one year apart, we aim to capture evolutionary trajectories in both the host and symbiont, and to test whether *Wolbachia* undergoes adaptive divergence within the distinct cellular environments. This system offers a rare opportunity to observe host-symbiont co-evolution under controlled, replicated conditions, and to identify the genomic determinants of symbiotic compatibility. The monoclonal cultures will help pinpoint the characteristics of intracellular environments that are either hospitable or hostile to *Wolbachia* academic contexts. Students can document AI-supported assignments, teachers can define transparent rules for coursework, authors can generate structured AI-use statements for papers and proposals, and journal editors or reviewers can assess disclosures consistently. AldIT demonstrates how structured, app-based disclosure can make AI-assisted academic work more transparent, accountable, and easier to evaluate across institutional and publishing contexts.

T32. New branches on the evolutionary tree of *Wolbachia* - Ancient sexual manipulators in tiny, enigmatic flies

Karol Hubert Nowak^{1*}, Monika Prus¹, Mateusz Buczek¹, Dylan Shropshire², Emily Hartop³, Piotr Łukasik¹

¹*Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland*

²*Department of Biological Sciences, Lehigh University, Bethlehem, Pennsylvania*

³*Leibniz Institute for Evolution and Biodiversity Science, Germany*

*karol.hubert.nowak@doctoral.uj.edu.pl

Nearly half of known insect species host an intracellular bacterial symbiont called *Wolbachia*, which can profoundly alter their hosts' biology through various forms of reproductive manipulation, modulation of behaviour and preferences, nutritional provisioning and anti-viral protection. Yet despite its ecological and evolutionary relevance, the taxonomic and functional diversity and distribution of *Wolbachia* remain poorly understood. Among traditionally recognised *Wolbachia* lineages, supergroups A and B are known relatively well thanks to their broad distribution and high prevalence in model organisms. However, the strains associated with rarely explored insect clades have been largely overlooked.

Our goal was to characterise the *Wolbachia* diversity, phylogenetic relations, and functions in natural communities of scuttle flies (Diptera: Phoridae) using high-throughput sequencing techniques. Amplicon sequencing data from 1842 phorids, representing >180 species, revealed >250 distinct *Wolbachia* genotypes, displaying host-specific distribution patterns. For most of these fly-*Wolbachia* genotype combinations, we generated metagenomic data that provided genome-level phylogeny and preliminary insight into symbiont functions.

We identified four main supergroup-level clades of *Wolbachia*, including two novel and clearly distinct supergroup-level clades, provisionally named "Pho-1" and "Pho-2", broadly distributed across taxonomically diverse phorids. Phylogenomic analyses revealed rampant and possibly recent host-shift events within Phoridae. Preliminary amplicon-based screening suggests "Pho-2" clade may have a host range extending beyond phorids, including parasitoids from the order Hymenoptera and other Diptera species. Based on the elevated prevalence and abundance in females, we also speculate on the reproductive manipulation effects. We are currently reconstructing functional genes of the newly discovered clades to assess their broader ecological relevance.

T33. Quiescence as an eco-evolutionary process: bet-hedging and within-state diversity under fluctuating environments**Dominika Włoch-Salamon***, Fatemeh Rabbani, Monika Opatek, Bogna Smug¹*Jagiellonian University, Kraków, Poland*

*dominika.wloch-salamon@uj.edu.pl

How populations persist under unpredictable environmental fluctuation is one of the central questions in evolutionary biology. Where plasticity tracks predictable change, bet-hedging spreads risk across phenotypes when the future cannot be anticipated. Using the single-celled fungus *Saccharomyces cerevisiae*, we study this strategic evolutionary trade-off through the transition into and out of the quiescent (G0) state — a near-universal but underexplored axis of phenotypic diversification. Our earlier work showed that heterogeneity within starved yeast populations behaves as a bet-hedging strategy — heritable, evolvable, and favouring different phenotypes depending on the duration and complexity of environmental stress. We now explore how diversity is structured within the quiescent state itself, distinguishing rapid- and slow/deep-quiescent fractions that differ markedly in transcriptome, metabolism, and re-entry kinetics — alternative bets along a survival-versus-regrowth axis that diverges with a population's evolutionary history. This suggests quiescence is not a single endpoint but a continuum of evolved strategies, best understood not as a static state but as a temporal process whose adaptive value emerges only across fluctuating environments and evolutionary time. The framework of “process ontology” links mechanisms of phenotypic diversification to population-level eco-evolutionary dynamics, offering a bet-hedging counterpart to plasticity under complex, unpredictable conditions.

T34. Less Is More: Adaptive Gene Loss in *Mycobacterium leprae*Ajay Raj Singh¹, Szymon Kaczanowski^{2*}¹*Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Kraków, Poland*²*Institute of Biochemistry and Biophysics of the Polish Academy of Sciences, Warszawa, Poland*

*szymonkaczanowski@gmail.com

Loss-of-function (LOF) mutations are increasingly recognized as a general mechanism of evolutionary adaptation. Such mutations arise in both experimental and natural populations and are often adaptive; however, it remains unclear whether most LOF mutations are truly beneficial. In our previous work, we demonstrated that LOF mutations are major drivers of adaptation in *Saccharomyces cerevisiae* during short-term experimental evolution. We developed a modified dN/dS framework in which the rate of nonsense mutations (dNonsense) serves as a direct measure of selection acting on gene inactivation, an assumption validated experimentally. Here, we test the hypothesis that LOF mutations also play an important role in evolution under natural ecological conditions. We address this question using genomic sequences of the pathogen *Mycobacterium leprae*, a species whose evolutionary history is characterized by extensive gene decay. We identified 16 nonsense mutations segregating in extant populations. Analysis using the dNonsense/dS framework revealed signatures of positive selection for all 16 mutations, indicating that adaptive gene loss continues to shape the evolution of this pathogen and supporting a broader role for LOF mutations in adaptation in natural populations.

ABSTRACT BOOK

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P1. A review of the lateral line organ in amphipods with emphasis on the *Gammarus* species flock from ancient Lake Ohrid

Luiz F. Andrade

¹*Department of Invertebrate Zoology and Hydrobiology, University of Lodz, Łódź, Poland*

²*Hydro-Biological Institute – Ohrid, Macedonia*

luiz.felipe.de.andrade@biol.uni.lodz.pl

The lateral line organ is an intriguing sensory structure of gammarids, presumed to function as chemo-, mechano-, and/or electro-receptors. This organ is composed of two rows of dorsal and lateral units that are spread along the body. These structures are often found on each somite and telson, and each unit is characterized by a nearly straight or curved excavation on the cuticle with an arrangement of flattened microtrichs inserted within a rounded concentric “ring”. Despite some previous studies shedding light on the lateral line organ, many aspects of its composition and function are still unclear. As such, our study aims to investigate the structure and variation of this organ in amphipod crustaceans from diverse habitats and modes of life, with emphasis on the *Gammarus* species flock from the ancient Lake Ohrid. Preliminary analyses of species of 40 amphipod families from a broad geographic range show remarkable differentiation of the lateral line structure, making it possible to assume it as a potential morphological marker of adaptive radiation. As a study case, specimens collected from Lake Ohrid across a depth gradient from 5 to 240 meters were compared with sister species living in local springs and streams, all exposed to varied water current intensities, predation pressure and chemical composition. For the initial analysis, 10 males and 10 females of similar sizes from five species (*Gammarus parechiniformis*, *G. roeselii*, *G. sketi*, *G. solidus* and *G. stankokaramani*) were selected, coated with gold, and analyzed through Scanning Electron Microscopy. The results show that there are clear interspecific differences in the morphology of the lateral lines, including the degree of curvature of the excavations and the number of microtrichs of species from the same sampling site. Additionally, size- and sex-specific changes were observed. Based on these observations, we hypothesize that, in different environmental conditions, even the conspecific individuals might show divergent patterns in the structure of the lateral line. Furthermore, other analyzed peracarid orders did not present the organ. This could suggest that the organ is unique to amphipods, being a specialized and adaptable structure, helping the gammarids in spatial orientation. This work was supported by the National Science Centre, Poland, under the MINIATURA-7 call, project number 2023/07/X/NZ8/01443.

P2. Losing Identity? The Rise of a Hybrid Swarm in Mixed Populations of Syrian and Great Spotted Woodpeckers in Central Europe

Antonii Bakai^{1*}, Bartłomiej Kusal¹, Zuzanna Pochłopeni¹, Nermeen Amer¹, Petr Veselý², Martin Černý³, Alena Fišerová², Eliška Šlapanská³, Gerard Gorman⁴, Łukasz Kajtoch¹

¹*Institute of Systematics and Evolution of Animals Polish Academy of Sciences, Kraków, Poland*

²*Department of Zoology Moravian Museum, Brno, Czech Republic*

³*Faculty of Science University of South Bohemia, České Budějovice, Czech Republic*

⁴*Hungarian Woodpecker Working Group, Budapest, Hungary*

*bakai@isez.pan.krakow.pl

Hybridization is an important evolutionary force shaping biological diversity, yet its role in natural populations remains underestimated. In woodpeckers, interspecific hybridization has been documented in approximately 20% of species, although genetic evidence remains scarce. Here, we focus on two closely related species that have recently become sympatric in Europe following the expansion of the Syrian Woodpecker *Dendrocopos syriacus* (SW) from the Middle East. In Europe, SW occupies synanthropic woodlands, where it co-occurs with the widespread Great Spotted Woodpecker *D. major* (GW). Although the two species compete for resources, they are also capable of hybridizing. Reports of hybrid individuals have increased in recent years, largely due to citizen science records. Using a panel of single nucleotide polymorphisms (SNPs) generated through ddRADseq, we investigated genetic structure and admixture in woodpeckers from southern Poland and Moravia (SW = 29, GW = 34, and 19 presumed hybrids). SNP analyses confirmed the hybrid status of most adults showing intermediate plumage characteristics. In contrast, most juveniles identified as putative hybrids were not genetically confirmed, indicating that young SWs and GWs are difficult to distinguish morphologically. Overall, about 20% of the examined individuals exhibited mixed ancestry, with backcrosses predominating. Our results reveal the existence of a hybrid swarm comprising SWs, GWs, and their descendants, indicating ongoing gene flow between the species. Beyond its evolutionary significance, widespread hybridization has important implications for woodpecker monitoring and research, which typically overlook hybrid detection. Ongoing introgression may also affect the conservation of the SW, a rare and declining species of conservation concern in the European Union.

P3. Does experimental brood size manipulation affect natal dispersal in blue tits?

Julia Barczyk^{1*}, Katarzyna Janas^{1,2}, Aneta Arct¹, Anna Dubiec², Lars Gustafsson³, Mariusz Cichoń¹, Szymon M. Drobnik¹

¹*Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland*

²*Museum and Institute of Zoology, Polish Academy of Sciences, Warszawa, Poland*

³*Department of Animal Ecology/Ecology and Genetics, Uppsala University, Uppsala, Sweden*

*julia.barczyk@uj.edu.pl

While many factors have been associated with natal dispersal in animals, the mechanisms shaping this behaviour in wild populations are still not fully understood. Long-term ecological studies provide valuable opportunities to explore these processes. In this study, we tested whether experimental manipulation of early-life conditions can influence natal dispersal in a natural bird population. We analysed data spanning more than 20 years from a nest-box population of blue tits (*Cyanistes caeruleus*) on the island of Gotland, Sweden. We found that individuals raised in experimentally enlarged broods, and therefore likely exposed to less favourable rearing conditions, were more likely to disperse beyond their natal plots compared to those from unmanipulated broods. However, brood size manipulation had no effect on natal dispersal distance. Although we did not detect sex-specific differences in dispersal probability, females dispersed over longer distances and were more likely to leave their natal plots than males. In addition, hatching date was positively associated with natal dispersal distance. Our findings suggest that early-life conditions may play an important role in shaping dispersal decisions in wild populations.

P4. Visual guidance of prey-capture decisions in naïve euryphagous jumping spiders

Maciej Bartos

*Department of Biodiversity Studies and Bioeducation, Faculty of Biology and Environmental Protection,
University of Lodz, Łódź, Poland*

maciej.bartos@biol.uni.lodz.pl

The ability to detect and interpret environmental stimuli is essential for survival and is shaped by natural selection. For visually hunting predators, efficient recognition of relevant cues can improve prey-capture success, whereas inaccurate assessment may reduce hunting performance. Jumping spiders are an important model for studying visually guided behaviour in arthropods. Despite compact nervous systems, they possess high-resolution eyes and make precise predatory decisions. However, it remains unclear how visual cues contribute to prey identification and capture, especially in euryphagous species. While some jumping spiders are specialized predators that respond selectively to particular stimuli, most species hunt a broad range of arthropods. Such generalists must detect prey and assign diverse prey types to functional categories associated with appropriate attack tactics. This task may be especially demanding for naïve individuals, which must make effective predatory decisions without experience. To investigate how naïve generalist jumping spiders classify prey, I studied *Yllenus arenarius*, a euryphagous species known for prey-specific predatory tactics. Freshly hatched, prey-naïve spiders were presented with virtual prey models on a miniature screen. The stimuli differed in body length, movement type, number of details, and their position on the prey model. The results indicate that naïve *Y. arenarius* use different visual cues for different predatory tasks. They rely primarily on general features, such as body length and movement pattern, to classify prey into categories associated with escape risk. In contrast to specialized jumping spiders, this generalist species does not appear to base its decisions mainly on detailed morphological traits. These findings suggest that general visual cues may allow naïve euryphagous predators to efficiently assign diverse prey to functional categories despite the limited capacity of a compact nervous system.

P5. First DNA Barcode Data for Turkish Tardigrades: An Integrative Taxonomic Assessment

Duygu Berdi^{1,2*}, Ahmet Altındağ², Emre Keskin^{3,4}, Işıl Çelik³, Zeynep Ece İmamoğlu⁵

¹*Department of Animal Taxonomy and Ecology, Adam Mickiewicz University in Poznan, Poznań, Poland*

²*Department of Biology, Ankara University in Ankara, Turkey*

³*AgriGenomics Hub, Animal and Plant Genomics Research Innovation Centre in Ankara, Turkey*

⁴*Evolutionary Genetics Laboratory (eGL), Department of Fisheries and Aquaculture, Agricultural Faculty, Ankara University in Ankara Turkey*

⁵*Graduate School of Natural and Applied Sciences, Ankara University in Ankara Turkey*

*duyber@amu.edu.pl, dberdi@ankara.edu.tr

Tardigrades are microscopic invertebrates inhabiting terrestrial, freshwater, and marine environments. Despite their broad global distribution, the diversity and distribution of many tardigrades taxa remain insufficiently understood, particularly in regions where genetic data are scarce. Owing to its unique geographic position between Europe and Asia and its high biodiversity, Turkey represents interesting area in case of tardigrade fauna. Genetic data on Turkish tardigrades remain limited. In this study, moss heterotardigrades collected in three provinces of Turkey in 2023 were investigated using an integrative taxonomic approach. Morphological and genetic analyses confirmed the presence of four heterotardigrade species i.e. *Echiniscus testudo*, *Echiniscus merokensis*, *Echiniscus blumi*, and *Echiniscus granulatus*. In addition, one specimen assigned to the genus *Pseudechiniscus* could not be reliably identified at the species level. The present study provides first DNA barcode data for Turkish heterotardigrades and highlights the importance of integrating morphological, morphometric, and genetic evidences in tardigrade taxonomy. The results further emphasize the need for reliable reference sequence databases linked to morphologically verified voucher specimens.

P6. Evolutionary history and phylogeographic structuring of freshwater crustaceans in the Periadriatic region

Karolina Biniek^{1*}, Aleksandra Jabłońska², Tomasz Mamos², Mišel Jelić³, Krešimir Žganec⁴, Vladimir Pesic⁵, Michał Grabowski²

¹*Doctoral School of Exact and Natural Sciences, University of Lodz, Łódź, Poland*

²*Department of Invertebrate Zoology and Hydrobiology, Faculty of Biology and Environmental Protection, University of Lodz, Łódź, Poland*

³*Varazdin City Museum, Varaždin, Croatia*

⁴*Department of Teacher Education Studies in Gospić, University of Zadar, Croatia*

⁵*Department of Biology, University of Montenegro, Podgorica, Montenegro*

*karolina.biniek@edu.uni.lodz.pl

The Periadriatic region represents a key Mediterranean biodiversity hotspot, ideal for exploring how paleogeographic and macroevolutionary processes have shaped current genetic structures. This study investigates the phylogeography and diversification histories of widespread malacostracan lineages with contrasting ecological traits, specifically amphipods (*Gammarus balcanicus*), isopods (*Asellus aquaticus*), mysids (*Diamysis*), and caridean shrimps (*Atyaephyra* and *Palaemon antennarius*), across a geographic gradient.

By integrating multimarker molecular datasets from more than 2000 individuals from the region, we reconstructed three major phases of faunal evolution. The earliest phase, initiated during the Miocene, was driven by the continentalization of Europe and tectonic uplift of the Alps, Dinarides, and Hellenides, establishing deep genetic splits between Balkan and Apennine lineages. The second phase relates to the Messinian Salinity Crisis and the subsequent Lago Mare episode, which facilitated habitat reconfigurations and faunal exchange across newly connected basins. The final phase spans Pleistocene glaciations, during which sea level regressions unified hydrological networks into the expansive Mega Po river system, prompting recent colonisation.

Our comparative approach reveals a pronounced phylogeographic structuring across all examined taxa, highlighting deep genetic divergence within the studied region. These findings underscore the role of the Periadriatic region as a critical evolutionary center, where recurrent geological barriers and historical land bridge connections have driven the accumulation of high genetic variability. Ultimately, the established molecular reference library provides a fundamental framework for understanding and preserving Mediterranean freshwater biodiversity.

P7. The acute inflammation-endurance exercise interplay: the opposite effect in laboratory mice selected for the high basal and maximum metabolic rate

Joanna Błońska*, Aneta Książek and Marek Konarzewski

Faculty of Biology, University of Białystok, Białystok, Poland

*j.blonska@uwb.edu.pl

Immune function requires substantial energetic investment. Basal Metabolic Rate (BMR) reflects the energy expenditure required to maintain routine physiological processes, including the immune system's readiness to respond. However, Maximum Metabolic Rate (MMR) is expected to constrain the dynamics of an acute immune response, as it determines the capacity for rapid energy mobilization and utilization. Because a high MMR is a key determinant of endurance exercise performance, this question is directly linked to the suggested beneficial effects of high-intensity interval training (HIIT) on immune functions. We investigated how genetically determined variation in BMR and MMR affects an acute immune response. We used female laboratory mice (*Mus musculus*) randomly selected for high and low BMR (H-BMR and L-BMR line types), a line type selected for high MMR, and randomly bred control mice. The innate immune system of females was induced with lipopolysaccharide (LPS), an antigen that mimics bacterial infection and is widely used to induce acute inflammation. We measured plasma levels of granulocyte-macrophage colony-stimulating factor (GM-CSF), a cytokine produced early in the inflammatory response. Our pilot study showed that LPS-dose females responded markedly more strongly to the LPS antigen than PBS-injected control females ($p < 0.0001$). In the LPS-dose group, the highest GM-CSF level was observed in H-BMR mice, whereas the lowest level was observed in females from the high MMR line type ($p = 0.008$). The strongest response of the H-BMR mice suggests that a high investment in immune readiness provides a substantial advantage during an acute bacterial infection. The reduced GM-CSF production in the high MMR mice contrasts with expectations derived from the HIIT predictions, according to which enhanced metabolic capacity for energy mobilization should facilitate a higher inflammatory response. This unexpected result represents an intriguing topic for further investigation.

P8. Metabolic-Behavioural Allocation and Oxidative Stress in Hibernating Marsupial During the Active Season

Jan S. Boratyński^{1*}, Karolina Iwińska¹, Carla Toledo², Isidora Camus² and Roberto Nespolo²

¹*Mammal Research Institute, Polish Academy of Sciences, Białowieża, Poland*

²*Instituto de Ciencias Ambientales y Evolutivas, Austral University of Chile, Valdivia*

*jan.boratynski@gmail.com

The performance model predicts that proactive behaviours coevolve with the supporting metabolic system. Even low-maintenance metabolism results in the production of reactive oxygen species (ROS), and therefore, energetically costly behaviours are associated with an additional oxidative stress risk. When not mitigated by an effective antioxidant system, ROS cause fatal consequences for an organism, shortening life span. We thus hypothesized that among-individual positive covariation between behavioural activity and metabolism must be associated with a sufficient antioxidant system. Alternatively, because the production or acquisition of antioxidants can be challenging under natural conditions, we expect that individuals will balance oxidative stress by allocating resources between competing functions. We studied maintenance metabolism, aerobic capacity, oxidative stress markers in blood serum, and activity behaviour in the male free-ranging marsupial Monito del monte, *Dromiciops gliroides*. As a long-living hibernating animal, this species should prioritize oxidative balance maintenance even during the energetically expensive mating period. None of the studied traits consistently differed among individuals, and no correlation was found at the among-individual level. Within-individual changes in behavioural activity were positively correlated with ROS-related DNA damage, which itself was correlated positively with total oxidant level, and accompanied by an undetectable antioxidant level. The metabolic scope was associated with increased DNA damage, while the maintenance and exercise metabolism itself were not. Maintenance metabolism correlated with behaviour: individuals who increased maintenance metabolism at the same time reduced behavioural activity. This study suggests that oxidative stress provides an important physiological context for a flexible allocation mechanism underlying behaviour-metabolism plasticity. Jan S. Boratyński was financially supported by Bekker 2024 (decision No. BPN/BEK/2024/1/00319/DEC/1) program of Polish National Agency for Academic Exchange.

P9. Diversity and distribution of bacterial microbiota in European *Delphacini* planthoppers with obligate fungal symbionts

Igor Boruta^{1*}, Veronika Adriienko¹, Adam Stroiński³, Piotr Łukasik², Anna Michalik¹

¹Department of Developmental Biology and Invertebrate Morphology, Institute of Zoology and Biomedical Research, Faculty of Biology, Jagiellonian University, Kraków, Poland

²Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Kraków, Poland

³Museum and Institute of Zoology, Polish Academy of Sciences, Warszawa, Poland

*igor.boruta@student.uj.edu.pl

Planthoppers harbor diverse microbial symbionts that affect various aspects of their biology, including nutrition and reproduction. The ancestral obligate symbionts of Fulgoromorpha - Sulcia and Vidania have co-evolved with their hosts for app. 270 Mya supplying essential amino acids lacking in their diet. While these ancient symbionts have been retained in many planthopper lineages, in some of them, including delphacids from Delphacinae subfamily, they have been replaced by *Ophiocordyceps* fungi. *Delphacinae* planthoppers are also characterized by wing polymorphism, with populations comprising both macropterous and brachypterous individuals.

To characterize the microbiota composition of *Delphacini* planthoppers we analyzed 912 individuals belonging to 32 species collected from 78 localizations in northern Europe and Greenland. Multitarget amplicon sequencing revealed presence of *Ophiocordyceps* fungi in all examined individuals, confirming the obligatory nature of this association. Despite the absence of obligate bacterial symbionts, these hoppers harbor a variety of facultative bacteria, including *Wolbachia*, *Rickettsia*, *Cardinium*, *Arsenophonus*, and *Spiroplasma*. Facultative symbionts were detected in all examined species; however, their taxonomic composition varied among populations, and their prevalence ranged from stable, highly persistent associations to more variable and apparently unstable infections. Our results reveal considerable diversity in facultative symbiont communities within European *Delphacini* and highlight the potential evolutionary significance of these associations. The widespread occurrence and variable prevalence of facultative symbionts suggest that they may contribute to ecological adaptation and potentially influence traits such as wing polymorphism, an important determinant of dispersal and population structure. The work was supported by NCN Opus 21 grant No. 2021/41/B/NZ8/04526.

P10. How does *Aegeritella* infect ants? New light on the ant-fungal interaction 50 years after the species description

Zofia Bulanda^{1*}, Marta Wrzosek²

¹Botanic Garden, Faculty of Biology, University of Warsaw, Warszawa, Poland

²Botanic Garden, University of Warsaw, Warszawa, Poland

*z.bulanda@student.uw.edu.pl

Aegeritella superficialis is known as an ectoparasitic fungus, primarily found on ants from the *Formica rufa* group. First reported in 1974 by Bałazy and Wiśniewski from mounds located in Wielkopolski National Park (Poland). Recent genetic studies classify *A. superficialis* in the order Capnodiales, which consists mainly of epiphytic fungi associated with honeydew and sap-sucking insects. *Formica* ants form mutualistic interactions with sap-sucking aphids, tending them and harvesting honeydew. This taxonomic and ecological context raises new questions concerning the life cycle and transmission mechanisms of *A. superficialis* and suggests a possible role of honeydew and aphids in this ant–fungal interaction. The aim of this study was to explore the occurrence of *A. superficialis* in *F. polyctena* colonies and to determine the influence of environmental surroundings and mound size on its prevalence.

For this purpose, we collected data from 92 *F. polyctena* nests located in Wielkopolski National Park, calculating the percentage of *Aegeritella*-infected ants based on around 30 individuals from each nest and noting where on the ants body the infection occurred.

We found that the mean *A. superficialis* prevalence (ca. 23%) was approximately twice as high as reported by Bałazy. Colonization levels varied significantly between mounds (SD~23%), and between three examined forest types, with highest percentages noted in the deciduous forest. Furthermore there is a positive association between mound size and infection prevalence. These results indicate that local environmental factors may shape transmission dynamics of this fungus and suggest a complex interaction shaped by multiple factors. Additionally we found that *Aegeritella* was located mostly on the mesosoma, gaster, and third leg pair of the studied ants.

Further studies on seasonal variation are needed to fully understand this ecological interaction.

P11. Family-wide mitogenomic phylogeny of Heptageniidae (Ephemeroptera) and the first draft nuclear genome of the Balkan endemic *Ecdyonurus puma* Jacob & Braasch 1986

Wiktoria Cechowicz^{1*}, Roman Hodunko^{1,2}, Tomasz Mamos¹

¹*Department of Invertebrate Zoology and Hydrobiology, Faculty of Biology and Environmental Protection, University of Lodz, Łódź, Poland*

²*Biology Centre of the Czech Academy of Sciences, Institute of Entomology, 37005, České Budějovice, Czech Republic*

*wiktoria.cechowicz@edu.uni.lodz.pl

The Balkan Peninsula is a major European biodiversity hotspot where complex geological history has driven intense diversification. Mayflies (Ephemeroptera) are among the oldest winged insects. Within it, Heptageniidae is a species-rich family found in fast flowing streams. Despite being important bioindicators, their global genomic resources remain scarce, with only two reconstructed genomes published to date. Moreover, molecular databases are severely underrepresented for Balkan taxa. The study addresses a critical gap by generating the first nuclear genome and complete mitogenome for *Ecdyonurus puma*, a rare, narrow-range endemic known exclusively from Montenegro. Larvae of *E. puma* were collected from the Morača River and genomic DNA was sequenced using the Illumina platform. The complete mitochondrial genome was assembled de novo using GetOrganelle, yielding a circular molecule of 15,541 bp containing 37 genes. Notably, we confirmed a duplication of the Methionine tRNA gene (trnM1 and trnM2) within the IQM region, establishing a robust diagnostic synapomorphy for the Ecdyonurinae subfamily. To reconstruct a time-calibrated phylogeny of Heptageniidae, we analyzed 71 mitogenomes (including 62 accessible GenBank sequences and 8 outgroups) using a partitioned relaxed molecular clock in BEAST, supported by multi-fossil calibrations from Baltic (~38 Ma) and Burmese (~98.7 Ma) ambers. Simultaneously, the nuclear genome was reconstructed and reference-guided (RagTag) against *E. torrentis*. Genomic profiling via GenomeScope and RESPECT revealed a highly complex, repetitive architecture, with 2.70% heterozygosity and a repeat content of about 62%. Despite these genomic challenges, the final scaffolded assembly reached a total length of 547.5 Mb with exceptional macro-contiguity, BUSCO analysis confirmed high gene-set completeness at 85.5%.

P12. Landscape-driven immunogenetic differentiation in a common waterbird

Amelia Chyb^{1*}, Radosław Włodarczyk¹, Joanna Drzewińska-Chańko¹, Jan Jedlikowski², Piotr Minias¹

¹*Faculty of Biology and Environmental Protection, Department of Biodiversity Studies and Bioeducation, University of Lodz, Łódź, Poland*

²*Faculty of Biology, Biological and Chemical Research Centre, University of Warsaw, Warszawa, Poland*

*amelia.chyb@biol.uni.lodz.pl

Bird populations from human-dominated areas are often exposed to altered, urban-related pathogen pressure, which may require genetic adaptation in pathogen-recognition components of the immune system. Here, we aimed to investigate landscape-related variation of innate (Toll-like receptors, TLRs) and adaptive (MHC) immune genes in a common waterbird, the Eurasian coot *Fulica atra*. For this purpose, we conducted country-scale sampling and genotyped nearly 300 coots from four pairs of urban and nonurban populations. In general, urban populations were characterized by reduced diversity (allelic richness) in both TLRs and MHC genes, which may suggest removal of disadvantaged allelic variants from human-dominated environment via purifying selection. At the same time, we identified a set of allelic variants and supertypes showing higher frequencies in urban than in nonurban populations. Our results also revealed significant immunogenetic differentiation between two types of landscape (urban vs. nonurban), as well as among particular urban populations. Finally, the level of differentiation was significantly higher at immune (MHC-II and TLR1LB) than neutral markers (microsatellites), suggesting adaptation. Our study shed the new light on the microevolutionary processes acting on the avian immune system in urban ecosystem. In particular, our results suggest that the immunogenetic differentiation between urban and nonurban habitat may be shaped not only by colonization history and genetic drift, but also by natural selection.

P13. Diversity and Evolutionary Stability of Bacterial Symbionts in *Philaenus spumarius*

Pola Demczak^{1*}, Veronika Andriienko¹, Michał Kolasa²

¹Jagiellonian University, Faculty of Biology, Institute of Zoology and Biomedical Research, Department of Developmental Biology and Invertebrate Morphology, Kraków, Poland

²National Research Institute of Animal Production, Department of Farm Animal Biodiversity Conservation and Horse Breeding, Balice, Poland

*pola.demczak@student.uj.edu.pl

Symbiosis with microorganisms enabled Auchenorrhyncha to exploit a nutrient-poor diet of plant sap and likely contributed to their evolutionary success. This association originated approximately 270 Mya, when the last common ancestor of Auchenorrhyncha acquired the Bacteroidetes bacterium *Sulcia muelleri*, which was later supplemented by a betasymbiont. While the association with *Sulcia* has remained remarkably stable and is retained in most extant Auchenorrhyncha, associations with betasymbionts are more dynamic and have undergone multiple replacement events.

One such replacement occurred in a spittlebug *Philaenus spumarius* - the focus of this study. We analyzed 679 individuals from 93 populations across 18 European countries. Host genetic diversity and microbial community composition were assessed using multitarget amplicon sequencing and individuals were assigned to colour morphotypes to test for associations between phenotype and microbiome structure. Analyses of 16S rRNA revealed three main bacterial symbionts: *Sulcia*, *Sodalis* and *Wolbachia*. *Sulcia* was detected in all individuals, represented by a single zOTU. In contrast, *Sodalis* exhibited high strain-level diversity, with one dominant zOTU and multiple low-abundant zOTUs suggesting multiple infections. *Wolbachia* showed lower diversity and less consistent distribution than *Sodalis*. It was present in northern populations, but absent from southern ones. Both *Sodalis* and *Wolbachia* displayed population-level structuring, with variants associated with geographic regions; however, no correlation with colour morphotype was detected. We additionally sequenced metagenomes from selected individuals, enabling the reconstruction of symbiont genomes and the characterization of their metabolic capabilities.

This study highlights the evolutionary complexity of *Philaenus spumarius* microbial communities and provides new insights into the roles of phenotype and geography in shaping host-microbiome interactions.

P14. Claws in the Genus *Macrobiotus* (Eutardigrada, Macrobiotida): It is not Always a Good Phylogenetic Signal

Wiktoria Dmuchowska*, Jędrzej Warguła, Łukasz Kaczmarek

Department of Animal Taxonomy and Ecology, Adam Mickiewicz University in Poznań, Poznań, Poland

*wiktoria.dmuchowska@amu.edu.pl

Tardigrada (water bears) are microscopic invertebrates characterized by considerable claw variability and the ability to inhabit diverse environments, including mosses, lichens, leaf litter, and soil. For a long time, claw shape, size, and configuration were considered strong phylogenetic characters for classifying eutardigrades into higher taxonomic units such as genera and families. However, recent molecular studies based on markers such as COI, ITS-2, 18S rRNA, and 28S rRNA have shown that claw morphology does not always reflect evolutionary history. The genus *Macrobiotus* C.A.S. Schultze, 1834 provides a good example of this phenomenon. Species of the *Macrobiotus xerobiotus* group exhibit varying degrees of claw reduction, whereas members of the *Macrobiotus ariekammensis* group possess extremely elongated claws. In this study, we conducted genetic analyses of the rare African species *Macrobiotus drakensbergi* Dastych, 1993, confirming its placement within the genus *Macrobiotus*. Morphological examination revealed a previously undescribed claw morphology, further expanding the known range of claw variation within the genus. The evolutionary significance of such extensive claw diversity remains unclear, but it may represent adaptations to specific microhabitats. This is supported by members of the *Macrobiotus xerobiotus* group inhabiting dry soils, where claw reduction is a well-documented adaptation in Eutardigrada. Our results demonstrate that substantial morphological divergence may occur without corresponding genetic differentiation and highlight the need to integrate morphological and molecular data when reconstructing evolutionary relationships within Tardigrada.

P15. Capital or income breeding during biological invasions?

Maciej J. Ejsmond

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

*Centre for Ecological and Evolutionary Synthesis, Department of Biosciences, Faculty of Mathematics
and Natural Sciences, University of Oslo, Oslo, Norway*

maciek.ejsmond@gmail.com

Biological invasions and climate-induced range shifts threaten global biodiversity and incur significant economic costs. A key step in reducing their negative impact is understanding the traits that underpin successful colonization. In this study, I use theoretical modelling to investigate if storing of internal reserves for reproduction by animals can facilitate biological colonization. Capital breeders reproduce using reserves, whereas income breeders rely on concurrent resource acquisition for reproduction. According to the existing theory, capital breeding is expected to slow down population growth. Nevertheless, there are many examples of invasions by capital breeders, as well as fascinating evolutionary transitions towards capital breeding during biological invasions. The presented theoretical model finds the Evolutionarily Stable Strategy (ESS) in response to various population expansion scenarios and seasonal variations in conditions. The model predicts that income breeding is favored in aseasonal environments, whereas capital breeders have a selective advantage in environments with strong seasonal fluctuations. While income breeders outcompete capital breeders in rapidly expanding populations, capital breeding can be crucial for the establishment of alien species in seasonal environments. This work enhances our understanding of the adaptive value of capital and income breeding in growing populations. The presented theory enables predictions to be made about colonization events based on how alien animal species utilize their reproductive reserve.

P16. Minimally destructive DNA extraction recovers genomic data from century-old Blattodea specimens

Nuria Farrus* and Guillem Ylla

Faculty of Biochemistry, Biophysics and Biotechnology, Jagiellonian University, Kraków, Poland

*nuria.farrus@uj.edu.pl

Natural history museums house millions of arthropod specimens collected all over the world, representing an invaluable source of biological information for taxonomic and systematic research. Recent advances in DNA sequencing technologies have revived interest in museum collections, unlocking possibilities for studying evolution, adaptation, and population genomics. However, working with museum samples presents challenges. First, many specimens are unique or irreplaceable, so it is essential to recover ancient DNA (aDNA) while minimizing morphological damage. Second, aDNA in historical specimens is often highly degraded, characterized by fragmentation, base damage, and low amounts of total DNA. Third, many museum collections remain either not digitized or only partially, limiting access to historical material.

In this study, we created a global museum database of the German cockroach *Blattella germanica*, one of the most important urban insect pests worldwide. The database comprises more than 1,000 museum specimens from collections across the world, half of them digitized by us through museum visits. From this dataset, we selected historical specimens more than 100 years old to extract genomic DNA using a minimally destructive extraction protocol, in which pinned specimens were incubated directly in a mild lysis buffer without pin removal and with minimal manipulation.

Our results demonstrate that genomic DNA can be successfully recovered without amputating any body parts of the specimen, yielding more than 100 ng in total in some cases. The extracted DNA was used for DNA library preparation and Illumina sequencing. These results contribute to the improvement of museomics practices by preventing the destruction of this irreplaceable material while linking specimens with genomic data.

P17. Wood decay and birds: a hidden arena of niche evolution across the avian tree of life

Arkadiusz Fröhlich^{1,2*}, Ziemowit Kosiński³, Łukasz Kajtoch⁴, Michał Ciach⁵, Marcel Klaassen², Matthew R.E. Symonds²

¹*Institute of Nature Conservation, Polish Academy of Sciences, Kraków, Poland*

²*Centre for Integrative Ecology, School of Life and Environmental Sciences, Deakin University, Burwood, Victoria 3125, Australia*

³*Department of Avian Biology and Ecology, Institute of Environmental Biology, Faculty of Biology, Adam Mickiewicz University in Poznań, Poznań, Poland*

⁴*Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Sławkowska 17, 31-016 Kraków, Poland*

⁵*Department of Forest Biodiversity, Faculty of Forestry, University of Agriculture in Kraków, al. 29 Listopada 46, 31-425 Kraków, Poland*

*frohlich@iop.krakow.pl

Wood decay underpins major ecosystem services and a large fraction of biodiversity, yet wood-decay biodiversity remains poorly understood beyond fungi, insects, woodpeckers and temperate or boreal systems. Using birds as a globally documented model, we show that saproxylic niches are not marginal specializations but widespread, underestimated and evolutionarily recurrent associations with decaying wood and its derivative microhabitats. A systematic review and global handbook survey identified 1,816 saproxylic species across 116 families and 25 orders. These species use standing, lying and crown deadwood, exposed roots, cavities formed by excavation, decay or abiotic processes, tree injuries, epixylic structures, insect nests and sap runs for nesting or foraging. Bias-corrected models suggest that saproxylic species may comprise 29% of all birds (SE = 4%). Avian saproxyly is structured by phylogeny, yet has also appeared repeatedly across unrelated lineages and biogeographic regions, producing woodpecker-like convergent niches worldwide. Across biomes, temperate and boreal forests showed heightened saproxylic propensity. Although saproxylic birds were not globally more threatened than others, extinction risk was elevated overall in tree-injury users and regionally in nest-camouflaging species in the Nearctic, standing-deadwood users in savannas and tropical forests, and saproxylic nesters in the Neotropics and Australasia. These overlooked guilds warrant stronger attention.

P18. Genomic footprints of adaptation to the cave environment in *Loboptera* cockroaches from the Canary Islands

Tomasz Gaczorek^{1*}, Mateo Alvarado¹, Piotr Michnal¹, Xavier Bellés², Pedro Oromí³, Heriberto López⁴ and Guillem Ylla¹

¹Laboratory of Bioinformatics and Genome Biology, Faculty of Biochemistry, Biophysics and Biotechnology, Jagiellonian University, Kraków, Poland

²Institute of Evolutionary Biology, CSIC-Universitat Pompeu Fabra, Barcelona, Spain

³University of La Laguna, Tenerife, Canary Islands, Spain

⁴Institute of Natural Products and Agrobiology, CSIC, Tenerife, Canary Islands, Spain

*tomasz.gaczorek@uj.edu.pl

Cave habitats are characterized by harsh external conditions, including complete darkness and limited food availability. Species living in such conditions often display distinctive features such as loss of pigmentation, reduction of eyes, limited oviposition, extension of distal body parts and altered behavior. Although the morphological characteristics are well understood, revealing the underlying genomic patterns requires a direct genome-level comparison between cave dwellers and their surface-dwelling relatives.

To study the genomic footprints of cave adaptation in hemimetabolous insects, we examined three species of *Loboptera* cockroaches that inhabit Tenerife, Canary Islands: *L. subterranea*, *L. troglobia*, and *L. decipiens*. The surface-dwelling *L. decipiens* serves as the reference group. The other two species, *L. subterranea* and *L. troglobia*, which are endemic and adapted to cave habitats independently, exhibit different levels of morphological adaptations. Notably, *L. troglobia* has undergone the most extreme modifications, including the complete loss of eyes.

For the purpose of this study, we utilized long genomic reads (ONT), HiC and mRNA-seq data generated by ERGA to perform a de novo genome assembly and annotate the genomes of all three species. Based on the obtained annotations, we performed comparative genome analyses, including the analysis of gene family expansions and contractions and quantitative molecular evolutionary analysis. We believe that the provided genetic resources and detected signals of adaptation can serve as a valuable resource for comparative studies related to adaptation to extreme environments.

P19. Thermoneutral Zone Shifts in Lactating Mice Selected for Divergent Basal Metabolic Rate

Andrzej K Gębczyński*, Julita Sadowska

Faculty of Biology, University of Białystok, Białystok, Poland

*andgebcz@uwb.edu.pl

The issue of defining and selecting the most appropriate housing temperature for laboratory animal facilities is becoming a more widely discussed factor, and rightly so. Ambient temperature affects a plethora of metabolic and behavioral traits, thus potentially causing chronic thermal stress, whether by setting T_a too low or too high, which can impact the physiology, individual performance, and animal welfare. However, the same ambient thermal conditions can affect an individual differently depending on the animal's physiological state. A prime example is lactation, a highly exothermic and energetically demanding period. Using mice artificially selected for high or low Basal Metabolic Rate (BMR) that also inherently differ in their thermoregulatory capacities and thermoneutral zone (TNZ) ranges, we studied how lactation at standard housing conditions affects their TNZ. Our results demonstrate that the lower critical temperature (LCT) setpoint of the thermoneutral zone in mice shows some plasticity during the highly exothermic period of lactation to ease the process of heat dissipation, and the magnitude of this plastic response is associated with the individual's genetically determined BMR and inherent thermoregulatory profile.

P20. Oxidative status during breeding season in females of long-living relict marsupial species - monito del monte

Karolina Iwińska^{1,2*}, Jan S Boratyński², Carla Toledo³, Isidora Camus³ and Roberto Nespolo³

¹*Mammal Research Institute, Polish Academy of Sciences, Białowieża, Poland*

²*Doctoral School of University of Białystok, Białystok, Poland*

³*Instituto de Ciencias Ambientales y Evolutivas, Austral University of Chile, Valdivia, Chile*

*iwinska.karolina@gmail.com

Reproduction is considered to increase oxidative stress (OS), but studies on these physiological costs have yielded inconsistent results. Many report the opposite trend—lower OS during lactation, the most energetically expensive period for eutherian mammals. However, no studies have yet investigated the OS during breeding in marsupials that diverged from their common ancestor 150Mya. Moreover, marsupial reproductive strategies differ from eutherians - short gestation and lower daily energetic demands, sustained over a much longer breeding period. Here, we studied OS during reproduction in the marsupial, the monito del monte *Dromiciops gliroides*, a long-living iteroparous mammal that should invest in protective self-maintenance mechanisms to mitigate the negative consequences of OS for future reproductive potential. Monito del monte is also a 'living-fossil', thus studying this model species can provide insights into how ancestral animals managed OS risk during reproduction. We compared total oxidant status (TOS), total antioxidant status (TAS), and oxidative DNA damage marker in pregnant, lactating, and non-reproducing free-ranging females through an active season. The TOS and related DNA damage in blood serum did not differ between females of different reproductive status. We found that pregnant females exhibited higher TAS than lactating and non-reproducing individuals. This suggests that marsupials prepare for reproduction by upregulating antioxidant defense mechanisms during gestation. Moreover, our results indicated that the slope of the relationship between TAS and TOS differed significantly between pregnant and other groups of females. The negative relationship between TAS and TOS during gestation suggests that, despite enhanced protection, during this short period, females face the highest disruption of OS balance. Conversely, the positive relationship between TAS and TOS in lactating and non-reproducing females indicates successful mitigation of OS costs.

P21. Disruption of an Essential Symbiosis: Effects of *Bacillus subtilis* on Aphid-Associated Microbiota

Aleksandra Janik^{1*}, Kamil Tylek¹, Diego Castillo Franco¹, Jagoda Kamińska¹, Martyna Materowska², Roma Durak², Anna Michalik¹

¹*Department of Developmental Biology and Invertebrate Morphology, Institute of Zoology and Biomedical Research, Jagiellonian University, Kraków, Poland*

²*University of Rzeszow, Faculty of Biology, Nature Protection and Sustainable Development, Rzeszów, Poland*

*aleksandra.m.janik@student.uj.edu.pl

Symbiotic microorganisms play a central role in insect ecology and evolution, influencing host nutrition, development, stress tolerance, and adaptation. In aphids, the obligate symbiont *Buchnera aphidicola* provides essential amino acids absent from plant sap, whereas facultative symbionts may enhance resistance to environmental stressors, natural enemies, and pathogens.

In this study, we investigated the effects of three *Bacillus subtilis* strains on the microbiota of three aphid species: *Myzus persicae*, *Acyrtosiphon pisum*, and *Macrosiphum rosae*. We focused on changes in the abundance and morphology of obligate and facultative symbionts following bacterial infection. Spray treatments were particularly effective against *A. pisum* and *M. rosae*, in which high levels of *B. subtilis* were detected within host tissues.

Infection resulted in a marked reduction in the abundance of the obligate symbiont *Buchnera aphidicola* and induced progressive degeneration of symbiont cells. Microscopic analyses revealed extensive structural alterations, including cytoplasmic reorganization, cell shrinkage, disruption of the perisymbiotic membrane, and the formation of fragmented, amorphous, or crescent-shaped cells. In contrast, the facultative symbiont *Serratia* appeared unaffected by *B. subtilis* infection.

The observed effects are likely mediated by antimicrobial secondary metabolites, particularly surfactin, produced by all analyzed *B. subtilis* strains. Our results demonstrate that obligate nutritional symbionts are highly susceptible to antagonistic interactions with entomopathogenic bacteria and may represent a critical target in host–microbe–microbe interactions. These findings highlight the importance of considering symbiont-mediated mechanisms in studies of insect ecology and evolution and suggest that disruption of essential symbioses may contribute to the effectiveness of biological control agents.

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P22. How stable are relict populations? Spatial and temporal dynamics of genetic structure in an endangered steppe species

Łukasz Kajtoch^{1*}, Miłosz Mazur², Radosław Ścibior³, Nermeen Amer¹, Rama Krovi¹, Daniel Kubisz¹

¹*Institute of Systematics and Evolution of Animals of the Polish Academy of Sciences, Kraków, Poland*

²*Institute of Biology, University of Opole, Opole, Poland*

³*Department of Zoology and Animal Ecology, University of Life Sciences in Lublin, Lublin, Poland*

*lukasz.kajtoch@gmail.com

Steppe species exhibit phylogeographic patterns opposite to those of temperate-zone taxa, as their present-day distributions are largely restricted to so-called warm-stage refugia. This makes them particularly vulnerable to environmental and climatic changes. Among European steppe relicts, an especially interesting species is *Cheilotoma musciformis*, a colorful leaf beetle occurring in the Pontic and Pannonian steppes as well as in isolated populations in Central Europe, including Poland, where it is represented by an endemic evolutionary lineage. In Poland, the species' range has contracted by approximately 40% over the last decade (only approx. 20 sites left), raising concerns about the long-term persistence of its populations. Using a set of single nucleotide polymorphisms (SNPs) generated through ddRADseq, we investigated population structure and genetic connectivity in two time periods (2010 and 2025). The analyses revealed higher genetic diversity and gene flow in the earlier period, followed by reduced genetic variation and increased population isolation in the later period. These results suggest that ongoing habitat changes—including shrub encroachment, transformation of xerothermic grasslands, and excessively intensive active management through grazing that removes host plants—are contributing to genetic erosion and restricting dispersal among populations. Our findings provide important guidance for the recently initiated conservation programme for this species in Poland. As *C. musciformis* is both a charismatic and an indicator species of xerothermic habitats, safeguarding its populations may contribute to more effective conservation planning and management of xerothermic reserves and Natura 2000 sites.

P23. Coping with microclimatic extremes: physiological tolerance in an isolated tropical summit amphibian

Marlena Kapuściak^{1,2*}, Bruno B. Wisse³, Philippe J. R. Kok¹

¹*Department of Ecology and Vertebrate Zoology, Faculty of Biology and Environmental Protection, University of Lodz, Łódź, Poland*

²*BioMedChem Doctoral School of the University of Lodz and Lodz Institutes of the Polish Academy of Sciences, Łódź, Poland*

³*Unaffiliated, The Netherlands*

*marlena.kapusciak@edu.uni.lodz.pl

Tepui summits of the Pantepui region are isolated sandstone table mountains characterised by strong winds, intense solar radiation, and pronounced temperature and humidity fluctuations. For amphibians, ectotherms with highly permeable skin, such environments impose coupled thermal and hydric constraints. The endemic toad *Oreophrynella quelchii* is a direct developer that occurs in very large populations on Roraima-tepui, shows limited dispersal, and frequently uses exposed sandstone substrates where thermal and desiccation stress may occur. We investigated whether the physiological profile of *O. quelchii* is consistent with activity in this extreme summit environment. In a field laboratory on Roraima-tepui, we quantified upper and lower thermal limits, voluntary thermal avoidance threshold, dehydration tolerance, and evaporative water-loss dynamics during progressive heat–desiccation exposure. Limited observations from the frog *Pristimantis aureoventris* provided ecological context. *O. quelchii* exhibited high critical thermal maxima (mean CT_{max} = 32.6°C ± 1.51) and low critical thermal minima (CT_{min} = 0.46°C ± 1.22) and a broad thermal tolerance breadth. Dehydration-tolerance trials further showed high critical activity points, reaching up to 47.7% body mass loss. During dynamic heat–desiccation trials, evaporative flux covaried with increasing body temperature and vapour pressure deficit, approaching passive evaporation rates, yet individuals recovered fully after rehydration. In contrast, the limited *P. aureoventris* dataset suggested narrower thermal tolerance breadth, lower dehydration tolerance, and lower evaporative flux. Together, these results suggest that *O. quelchii* appears to rely on restricted movements, microhabitat use, behavioural avoidance, and tolerance to acute coupled heat and water stress. More broadly, our study shows how organismal physiology can contribute to understanding adaptation and resilience in isolated tropical montane environments.

P24. Genomic footprints for drought tolerance in *Festuca grasses*

Aamir Hamid Khan^{1*}, Adnan Akbar^{1,2}, Bushra Bibi³, Muhammad Kashif Naeem^{*3}, Marcin Kiedrzyński¹

¹*Department of Biogeography, Paleoecology and Nature Conservation, Faculty of Biology and Environmental Protection, University of Lodz, Łódź, Poland*

²*Doctoral School of Exact and Natural Sciences, University of Lodz, Łódź, Poland*

³*National Institute for Genomics and Advanced Biotechnology (NIGAB), NARC, Park Road, Islamabad-45500, Pakistan*

*aamir.hamid.khan@biol.uni.lodz.pl

Grasses (Poaceae) are among the most resilient plants and can survive prolonged desiccation in semi-arid regions with seasonal rainfall. Among the grasses Fescue (*Festuca L.*) is remarkably divers, containing around 600 species and ranking as most species rich group within the grass family. However, in the recent years, drought environment hindered its largescale plantation. So, it is necessary to improve its performance in water deficit conditions by studying the response mechanisms of *Festuca* during the drought conditions. In current study, we performed a genome-wide association analysis using *F. tatrae* (2x, n = 10), *F. amethystina* (2x, n = 10) and *F. amethystina* (4x, n = 20) species to identify single nucleotide polymorphism (SNPs) that contribute to drought tolerance. The experiment was performed in the glasshouse for two years and phenotypic data of plant height, plant width, the chlorophyll content and soil moisture condition were estimated in 2023 and 2024. These 40 accessions were genotyped using SLAF-seq method, further De Novo assembly, NGS, SNP calling and quality control analyses generated 28,685 high quality single nucleotide polymorphisms (SNPs) for further analysis. GWAS identified 37 significant SNPs across all traits over the two years. SNP annotation identified the four candidate genes including, Antagonist of Like Heterochromatin Protein1 (ALP1), F-box/LRR-repeat protein 14-like, Wall-associated receptor kinase 2 and Vernalization1 associated with drought stress. Further validation of these SNPs and functional characterization of associated genes will be essential to optimize their application in improving fescue's adaptability to climate challenges as well opening avenue for further drought study in *Festuca tatrae* and *F. amethystina* (2x, 4x).

P25. Sensitivity to human gaze among wintering corvids in an urban environment

Maja Kosieradzka*, Adrian Surmacki

Adam Mickiewicz University in Poznan, Poznań, Poland

*majkos3@st.amu.edu.pl

The aim of this study was to test whether corvid species are sensitive to human gaze and whether this sensitivity is species-specific. Gaze sensitivity was assessed using two variants of the flight initiation distance (FID) test. In the first treatment, the observer approached the bird while looking directly at it, whereas in the second treatment the observer approached with an averted gaze. In both treatments, the observer faced the bird. The experiments were conducted in Poznań, Poland, between November and February on wintering populations of rooks, jackdaws, magpies, and hooded crows. All species initiated escape at greater distances (i.e., exhibited longer FIDs) when approached by an observer maintaining direct gaze. However, no significant interspecific differences in sensitivity to human gaze were detected. Neither the distance from the city centre nor the date of observation significantly affected FID.

P26. Substrate type filters bryophytes according to their life strategy

Marcin T. Mazurkiewicz^{1*}, Sylwia Wierzchowska², Bogdan Jaroszewicz¹

¹*University of Warsaw, Warszawa, Poland*

²*Wroclaw University of Environmental and Life Sciences, Wrocław, Poland*

*mt.mazurkiewicz@uw.edu.pl

Bryophytes are not only pioneer organisms colonizing newly available habitats, but also highly specialized species restricted to particular forest microhabitats. Some bryophytes are limited to a single microhabitat type, meaning the occurrence of multiple specialist species in a small area can be considered an indicator of high habitat diversity and heterogeneity. The aim of our study was to investigate the patterns of bryophyte distribution on three major substrate types: dead wood, bark of living trees, and soil and litter. We investigated how these substrates modulate functional composition of bryophyte communities by recording their occurrence across 151 ha of natural forest and 144 ha of managed forest in the Białowieża Forest. We assessed taxonomic and functional diversity of bryophytes using life strategy, life form, growth form, spore and body size, vegetative propagule production, capsule position, and hemeroby. Our analyses revealed the highest species richness and Shannon diversity in bryophyte communities associated with dead wood in natural forests, while the lowest diversity was found on soil and litter of managed forests. Similar results were obtained when examining the functional richness index. Functional divergence and dispersion indices likewise identified epixylic communities as the most functionally diverse. However, the functional evenness index was the highest in bryophyte communities associated with dead wood in natural forests, and with living trees and dead wood in managed forests. Bryophyte communities associated with different substrate types also differed significantly in their functional composition and dominant life strategies. Our results highlight the key role of dead wood in maintaining both taxonomic and functional diversity of forest bryophytes and demonstrate that forest management affects not only species richness but also the functional structure of bryophyte communities.

P27. Characterization of chemical profiles and microbiome composition in femoral glands of male sand lizards (*Lacerta agilis*)

Joanna Michalska-Madej^{1,2*}, Aneta Woźniakiewicz³, Michał Woźniakiewicz³, Alejandro Ibáñez¹

¹Department of Ecology and Vertebrate Zoology, Faculty of Biology and Environmental Protection, University of Lodz, Łódź, Poland

²BioMedChem Doctoral School of the University of Lodz and Lodz Institutes of the Polish Academy of Science, University of Lodz, Łódź, Poland

³Department of Analytical Chemistry, Laboratory for Forensic Chemistry, Faculty of Chemistry, Jagiellonian University, Kraków, Poland

*joanna.michalska.madej@edu.uni.lodz.pl

Chemical communication is a widespread mode of information transfer in animals, mediating species and sex recognition, mate choice, competition, and signalling of individual quality or reproductive status. In lizards, femoral gland secretions are an important source of chemical signals, yet the factors shaping their composition remain poorly understood. This study provides the first attempt to examine the potential link between the microbiome and chemical composition of femoral gland secretions in the sand lizard (*Lacerta agilis*). For that purpose, we captured male sand lizards during the mating season and sampled femoral gland secretions. From each individual, we obtained samples for microbiome analysis (using NGS sequencing of the V3-V4 region of the prokaryotic 16S rRNA gene) as well as for chemical analysis (using GC-MS). GC-MS analysis indicated the presence of a rich mixture of lipophilic compounds that is qualitatively similar to other lacertid lizards. Among the most common chemical classes there were carboxylic acids, alcohols, tocopherols and steroids. Key compounds included α -tocopherol, saturated fatty acids such as dodecanoic acid (C12:0), tetradecanoic acid (C14:0), and hexadecanoic acid (C16:0), as well as cholesterol, campesterol, and 5 α -cholestan-3 β -ol. Microbiome analysis revealed that femoral glands contained diverse microbial communities. The dominant bacterial phyla included Bacillota, Pseudomonadota, Actinomycetota, and Bacteroidota. Among the bacterial genera detected, we highlight *Pseudomonas*, *Burkholderia-Caballeronia-Paraburkholderia*, *Escherichia-Shigella*, *Sphingomonas*, *Paracoccus*, and *Methylobacterium* which could be relevant for chemical signalling. These results indicate that femoral gland secretions in *L. agilis* are a complex chemo-biological systems harbouring diverse microbial communities. Our study highlights the need to integrate GC-MS and NGS analyses to understand the potential role of the microbiome to reptile chemical communication.

P28. When nothing means something: hidden patterns in bumblebee microbiota

Bartłomiej Molasy^{1,2*}, Veronika Andriienko^{1,2}, Michał Robert Kolasa³, Anna Michalik⁴

¹*Department of Developmental Biology and Invertebrate Morphology, Institute of Zoology and Biomedical Research, Jagiellonian University, Kraków, Poland*

²*Doctoral School of Exact and Natural Sciences, Jagiellonian University, Kraków, Poland*

³*Department of Biodiversity Protection and Horse Breeding, National Research Institute of Animal Production, Kraków, Poland*³*Varazdin City Museum, Varaždin, Croatia*

⁴*Department of Developmental Biology and Invertebrate Morphology, Institute of Zoology and Biomedical Research, Jagiellonian University, Kraków, Poland*

*bartlomiej.molasy@doctoral.uj.edu.pl

Long-term symbiotic relationships have evolved between bumblebees and their gut-associated bacteria, resulting in highly specialized microbial communities that contribute to host nutrition, pathogen defence, and digestion. Despite the existence of a conserved core microbiota, these symbioses remain dynamic, as microbial taxa can be acquired from the environment and may respond to ecological and host-related factors. To investigate the relative importance of host identity, sex, and environment in structuring bumblebee-associated microbial communities, we analyzed the gut microbiota of 150 individuals representing 15 bumblebee species collected in Sweden, Estonia, and Greenland (Zackenbergl Valley). We combined multitarget amplicon sequencing, metagenomics, fluorescence in situ hybridization (FISH), and Hierarchical Modeling of Species Communities (HMSC) to characterize bacterial and fungal communities and identify factors associated with microbiome variation. Core bacterial taxa, including *Gilliamella*, *Snodgrassella*, *Bombiscardovia*, and *Lactobacillaceae*, were detected in most samples. However, microbiome composition varied substantially among host species and regions, particularly at the ASV level. HMSC analyses revealed significant associations between microbial community structure and host species, sex, and habitat. A striking pattern emerged in Greenland populations, where amplicon sequencing failed to detect *Gilliamella*, a key member of the core bumblebee microbiota. Metagenomic analyses and FISH subsequently confirmed its presence, demonstrating that the apparent absence of this taxon reflected methodological limitations rather than true symbiont loss. Our results highlight the importance of integrating complementary approaches when studying host-associated microbiomes. They also suggest that extreme environmental conditions may destabilize host-microbe associations, particularly during prolonged diapause or periods of reduced immune function.

P29. The Invisible Allies: Microbial Communities Shaping Parasitic Hymenoptera

Shayan Naeem*, Piotr Łukasik

Institute of Environmental Sciences at the Faculty of Biology, Jagiellonian University, Kraków, Poland

*Shayan.naeem@doctoral.uj.edu.pl

Symbiotic microorganisms can shape insects' nutrition, reproduction, defense, and other traits, yet we know little about their diversity beyond a few model clades. For example, in Hymenoptera, microbiota research has strongly focused on two clades, bees and ants, while the remainder of the order's diversity, which primarily comprises parasitoids, remains poorly studied. In this study, we aim to characterize bacterial and fungal symbioses across hymenopteran parasitoid taxa comprehensively. Specifically, we asked (1) how bacterial diversity and abundance vary across hymenopteran parasitoid taxa; (2) how geography shapes microbiota within and among species; and (3) whether we may identify common and region-specific partners that might influence host nutrition, immunity, or reproduction. To do this, we used an innovative approach – the simultaneous sequencing of insect, bacterial, and fungal genes, including microbiota quantification – applied to a collection of more than 3,000 diverse parasitic Hymenoptera collected from Greenland, Sweden, and Madagascar and analyzed several individuals from different habitats.

Our data reveals massive variation in bacterial abundance and community composition among the surveyed wasps. Many species harbor very low bacterial loads – are virtually sterile. On the other hand, the microbiota of others is dominated by abundant facultative endosymbiotic bacteria such as *Wolbachia*. Broadly, we found little evidence for the common presence of abundant, specialized microbial communities comprising taxa other than endosymbionts. In my presentation, I will explain how these patterns vary among taxonomic groups and biogeographic regions.

P30. Evaluating Outlier Detection Methods in Ecological Data Using Virtual Species

Maria Piasecka*, Lechośław Kuczyński

Population Ecology Lab, Faculty of Biology, Adam Mickiewicz University in Poznan, Poznań, Poland

*marytonina@wp.pl

Ecological monitoring data are crucial for understanding biodiversity change and supporting conservation efforts. However, these datasets can be affected by errors, including observer bias, species misidentification or recording mistakes. Such errors may appear as outliers and, if not detected, can strongly influence ecological analyses. However, due to inherent complexity of biodiversity monitoring datasets, this task is particularly challenging. These datasets are structurally hierarchical, spatially and temporally autocorrelated and contain substantial random variation between species and locations. As a result, methods developed for other types of data may not be equally effective when applied to ecological monitoring data. The aim of this study is to evaluate the effectiveness of selected outlier detection methods using simulated ecological datasets generated with a virtual species approach. Multiple virtual species, each with different ecological characteristics, are used to create realistic monitoring scenarios. Controlled anomalies are then introduced into the data to compare the different detection methods. The comparison focuses on the ability of the methods to correctly identify anomalous observations while minimizing false detections. The expected outcome is the identification of reliable approaches for detecting anomalous observations in ecological datasets. These results will improve the quality control procedures used in biodiversity monitoring programmes and provide the basis for developing an R package dedicated to outlier detection in ecological monitoring data.

P31. Anthropogenic materials in bird nests: testing the adaptive value of cigarette butts in Great Tits

Maria Pietrala^{1,2*}, Michał Gładalski¹, Sandra Sowa¹, Iwona Demeško¹, Adam Kaliński¹, Marcin Markowski¹, Joanna Skwarska¹, Jarosław Wawrzyniak¹, Agnieszka Wojciechowska¹, Jarema Wódka^{1,3}, Piotr Zieliński⁴ & Jerzy Bańbura¹

¹*Faculty of Biology and Environmental Protection, Department of Experimental Zoology and Evolutionary Biology, University of Lodz, Łódź, Poland*

²*BioMedChem Doctoral School of the University of Lodz and Lodz Institutes of the Polish Academy of Sciences, Łódź, Poland*

³*Doctoral School of Exact and Natural Science, University of Lodz, Łódź, Poland*

⁴*Faculty of Biology and Environmental Protection, Department of Ecology and Vertebrate Zoology, University of Lodz, Łódź, Poland*

*maria.pietrala@edu.uni.lodz.pl

Urban habitats expose birds to a wide range of novel materials, including different types of anthropogenic waste. Observations from recent years indicate that some urban-dwelling tits incorporate cigarette butts into their nests, and in certain cases even build nests directly inside ashtrays intended for cigarette disposal. Because tobacco (*Nicotiana sp.*) is known for its insect-repellent and insecticidal properties, such behaviour may have adaptive significance. Self-medication behaviour has been documented in tit species. Under natural conditions, blue tits *Cyanistes caeruleus*, which are closely related to great tits *Parus major*, are known to line their nests with freshly collected aromatic plants that can reduce parasite loads through the release of bioactive compounds. Since parasites negatively affect host condition (especially during nesting phase) and reproductive success, life-history theory predicts that they act as a strong selective pressure. In this study, we tested whether the presence of cigarette butts in great tit nests (treatment A), or the replacement of the original nest with a sterilized artificial nest composed of moss and cotton wool (treatment B), influences nestling condition (including treatment C – control group). These manipulations were carried out three times during the nestling phase, on days 4, 8, and 11. Physiological condition was assessed by measuring hemoglobin concentration and hematocrit in 13-day-old nestlings, and both experimental groups were compared with an unmanipulated control group (treatment C). Our results show that nestlings from both experimental (A and B) treatments had higher hemoglobin but not hematocrit levels, indicating improved physiological condition relative to control individuals.

P32. Urbanization promotes endoparasite load in feral pigeon

Weronika Pietrzak^{1,2*}, Aleksandra Szymańska³, Alina Lorenz³, Maciej Kamiński¹

¹*Faculty of Biology and Environmental Protection, Department of Biodiversity Studies and Bioeducation, University of Lodz, Łódź, Poland*

²*Doctoral School of Exact and Natural Sciences, University of Lodz, Łódź, Poland*

³*Faculty of Biology and Environmental Protection, Univeristy of Lodz, Łódź, Poland*

*weronika.pietrzak@edu.uni.lodz.pl

Urbanized environment in a large city is profoundly transformed and greatly differs from the natural habitats. Among other, they differ in the composition, diversity, and abundance of pathogen communities. Urban animals must adapt to such environmental changes. Moreover, urban animals tend to live in higher population densities, compared to natural populations. Elevated population density can facilitate transmission of parasites and other pathogens. Thus, the immune system of urban animals should adjust to face a novel set of challenges. The feral pigeon *Columba livia domestica* is one of the most successful urban bird species, notorious for its high population density. Here, we investigated the associations of host population density and local degree of habitat urbanization with endoparasite load in feral pigeons. Furthermore, we examined the relationship between endoparasite load and the activity of natural antibodies (NAbs), a proxy of constitutive humoral immunity. In our study, we sampled 150 adult feral pigeons caught at 10 study sites in Łódź, Poland. The sites differed in their level of urbanization and pigeon population density. Endoparasite eggs in faecal samples were counted using the faecal flotation method, with counts performed with a McMaster chamber under a light microscope. The NAbs activity was assessed with a haemagglutination assay, based on the capability of plasma to agglutinate foreign cells. The associations were analyzed using mixed-effects models that included sex, sampling date, and study site as the random factor. The parasite load increased with the level of urbanization, but it was not related to pigeon population density. At the same time, birds with higher parasite egg counts had lower haemagglutination scores. These results show that fine-scale differences in the degree of urbanization within a city may be more important for endoparasite pressure than local host density. The negative relationship between endoparasite loads and haemagglutination scores may suggest an immunosuppressive effect of endoparasite infection. Our results, however, do not show which of these factors affects the other, but they point to a link between the intensity of endoparasite infections and constitutive humoral immunity.

P33. Saving energy, investing in protection: Rest-phase hypothermia mobilises antioxidant defences in zebra finches during an energetic challenge

Jakub P. Płachta^{1,2*}, Małgorzata M. Lipowska¹, Ulf Bauchinger^{1,3}, Edyta T. Sadowska¹

¹*Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Kraków, Poland*

²*Doctoral School of Exact and Natural Sciences, Jagiellonian University, Kraków, Poland*

³*Nature Conservation Station Unterelbe, State Agency for Bird Conservation, Freiburg/Elbe, Germany*

*jakub.plachta@doctoral.uj.edu.pl

Entering rest-phase hypothermia may help birds survive energetic crises, yet its consequences for oxidative balance remain poorly understood. In particular, it is still unclear whether deeper hypothermia protects birds from oxidative stress by reducing reactive oxygen species (ROS) production or instead impairs antioxidant defences needed to counter the burst of ROS during rewarming. We studied how thermoregulation and metabolic suppression during the resting phase correspond to oxidative status across the hypothermic curve. We performed rest-phase metabolic rate (MR) and body temperature (T_b) measurements in 96 male and female zebra finches, which were either fed or fasted for 24 hours. We sampled blood at three stages: before the onset of the resting phase, during hypothermia, and during rewarming. We quantified oxidative status using plasma antioxidant capacity (OXY), uric acid concentration (UA), and oxidative damage (dROMs). Fasting amplified metabolic suppression, resulting in deeper hypothermia. However, oxidative markers were more strongly associated with T_b than MR. Deeper hypothermia increased UA, whereas OXY remained unchanged. At the same time, dROMs declined. Notably, higher concentrations of both plasma antioxidant markers were associated with higher dROMs, pointing towards mobilisation of antioxidant defences in response to increased oxidative challenge. Our results demonstrate that simultaneous assessment of T_b and MR is necessary for understanding oxidative dynamics during hypothermia. While metabolic activity is the primary source of ROS production, oxidative status appears more closely linked to body temperature. We suggest that deeper hypothermia entails increased mobilisation of antioxidant defences, limiting oxidative damage overnight and buffering the oxidative challenge during rewarming. Rest-phase hypothermia seems more than an energy-saving strategy, supporting oxidative balance through lower metabolic demands and enhanced defences.

P34. Older zebra finches maintain lower body temperatures rather than increasing heat production during cold exposure

Dawid K. Pszczoła^{1*}, Jakub P. Płachta^{1,2}, Małgorzata M. Lipowska¹, Ulf Bauchinger^{1,3}, Edyta T. Sadowska¹

¹*Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Kraków, Poland*

²*Doctoral School of Exact and Natural Sciences, Jagiellonian University, Kraków, Poland*

³*Nature Conservation Station Unterelbe, State Agency for Bird Conservation, Freiburg/Elbe, Germany*

*dawid.pszczola@student.uj.edu.pl

Thermoregulation is a key physiological process in birds, particularly in small passerines that experience high rates of heat exchange with the environment and therefore face substantial energetic costs of maintaining body temperature in cool conditions. Age-related physiological deterioration is expected to impair thermoregulatory performance, yet empirical evidence remains limited.

We investigated age-related variation in body temperature (T_b), resting metabolic rate (RMR), and thermal conductance in zebra finches (*Taeniopygia guttata castanotis*). Measurements were conducted in 88 individuals aged 1–6 years at ambient temperatures (T_a) of 15, 25, and 28°C. RMR was quantified using flow-through respirometry, while T_b was continuously monitored using implanted PIT tags. Thermal conductance was calculated from RMR and the body-to-ambient temperature gradient for each T_a.

As expected, mass-adjusted RMR increased markedly as T_a decreased. Surprisingly, however, age had no detectable effect on RMR. In contrast, T_b declined significantly with age, while thermal conductance tended to increase with age. Consequently, older birds maintained lower body temperatures despite metabolic rates comparable to those of younger individuals.

Our results suggest that ageing alters thermoregulatory performance independent of concomitant changes in resting metabolic rate. The combination of preserved RMR and lower T_b in older individuals may indicate either a strategic adjustment of thermoregulatory set points or an age-related decline in the capacity to defend high body temperatures under cool conditions. From an evolutionary perspective, this pattern may reflect age-dependent adjustments in energy allocation, potentially reducing thermoregulatory costs through maintenance of a smaller body-to-environment temperature gradient, albeit at the expense of physiological performance.

P35. Convergent evolution of quiescence phenotypes in *S. cerevisiae* shaped by starvation duration

Fatemeh Rabbani*, Dominika Włoch-Salamon

Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Kraków, Poland

*fatemeh.rabbani@doctoral.uj.edu.pl

Quiescence is a reversible non-proliferative cellular state observed across organisms from microorganisms to multicellular eukaryotes. Although it is important for stress survival stem cell maintenance and cancer persistence its evolutionary dynamics remain poorly understood. In *Saccharomyces cerevisiae* nutrient depletion induces quiescence but cells show heterogeneity in entry and exit with some forming deeper quiescent states associated with delayed re-entry into proliferation. To study evolution of quiescence phenotypes we performed experimental evolution under recurrent starvation. Yeast populations were exposed to two starvation regimes 7 and 21 days and two conditions spent growth medium and distilled water. After each starvation period viable cells were transferred to fresh medium at 10^5 cells per mL and the cycle was repeated for 20 transfers reaching 200 generations. Viability was assessed using propidium iodide staining and GFP fluorescence from a TDH3 integrated reporter.

Across both regimes dead cell proportion decreased over time indicating adaptation to starvation. In the 7 day regime populations evolved toward a GFP positive PI resistant phenotype with improved viability compared to ancestors. In the 21 day regime early transfers showed GFP positive and GFP negative subpopulations while later transfers converged to a mainly GFP positive population indicating selection for a more uniform state.

Microscopy showed increased budding after both regimes in evolved populations and cell size heterogeneity increased over time. Overall repeated starvation selects for quiescence phenotypes that enhance survival and adaptation.

P36. The ecological and developmental foundations of brood parasitism in a catfish

Martin Reichard^{1,2*}, Matej Polačik², Radim Blažek², Lukas Koch², Tomáš Suchánek³, Stephan Koblmüller⁴, Kacper Pyrzanowski¹, Holger Zimmermann^{1,4}

¹*University of Lodz, Łódź, Poland*

²*Czech Academy of Sciences, Czech Republic*

³*Charles University Prague, Prague, Czech Republic*

⁴*University of Graz, Graz, Austria*

*martin.reichard@biol.uni.lodz.pl

Interspecific brood parasitism has evolved repeatedly from parental care. However, many non-avian brood-parasitic lineages have ancestors lacking parental care, leaving the foundations of brood parasitism in these lineages enigmatic. We examined ecological, reproductive, and developmental data from the Lake Tanganyika radiation of *Synodontis* catfishes, where one species, the cuckoo catfish, exhibits brood parasitism of mouthbrooding cichlid fishes. Our comparative analyses, coupled with experimental parasitism, suggest that a combination of ancestral traits (large eggs and rapid embryo development) enabled the origin of brood parasitism. Evolutionary innovations then presumably enhanced the success of brood parasitism after it emerged. Novel traits comprise frequent production of small clutches to effectively utilize host availability, the evolution of egg mimicry to facilitate host egg adoption, and modifications to development to enhance the performance of catfish embryos in the host's buccal cavity. Interestingly, despite the distinct ecological and life history contexts of the origin of catfish brood parasitism, its evolutionary and developmental outcomes align with those of canonical avian brood parasites. This suggests that general patterns are repeated in the evolution of brood parasitism, despite disparate starting conditions.

P37. AldIT: AI disclosure for Improved Transparency — a Shiny app for standardised AI-use reporting

Szymon M. Drobnik^{1,2*}, Martyna Cendrowska-Pek^{1,3}, Agnieszka Gudowska⁴, Katarzyna Janas^{7,1}, Paweł Podkowa¹, Karolina Skorb^{1,8}, Monika Gronowska⁶, Wioleta Oleś¹, Faina Bikmurzina¹, Natalia Boroń¹, Magdalena Zagalska-Neubauer⁶, Shinichi Nakagawa^{2,5}, Małgorzata Lagisz^{2,5}, Aneta Arct^{1,5#}, **Joanna Rutkowska^{1#*}**

- joint senior authorship in alphabetical order

¹*Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Kraków, Poland*

²*School of Biological, Environmental & Earth Sciences, University of New South Wales, Sydney, Australia*

³*Jagiellonian University, Doctoral School of Exact and Natural Sciences, Kraków, Poland*

⁴*Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Kraków, Poland*

⁵*Department of Biological Sciences, University of Alberta, Edmonton, Canada*

⁶*Department of Behavioural Ecology, University of Wrocław, Wrocław, Poland*

⁷*Museum and Institute of Zoology, Polish Academy of Sciences, Warszawa, Poland*

⁸*Doctoral School of Natural and Agricultural Sciences, Kraków, Poland*

*joanna.rutkowska@uj.edu.pl

The rapid increase in AI use across research and education creates a need for transparent, comparable, and practical disclosure tools. This need is especially visible in academic publishing, where AI policies are emerging but often remain incomplete, inconsistent, or limited to general statements. AldIT was developed in response to an overview of AI-use policies in ecology and evolution journals, which revealed substantial gaps in current disclosure requirements. Inspired by the CRediT author contribution taxonomy, AldIT translates AI disclosure into a functional application that supports structured reporting of AI involvement across academic workflows. The app combines research-cycle stages with three main functional categories of AI use: content generation, content refinement, and content comparison. Users can report AI involvement in conceptualisation, literature review, data curation, formal analysis, methods, validation, visualisation, investigation, funding acquisition, and writing. This enables disclosure to move beyond a simple “AI used / not used” statement towards a process-level account of how AI contributed. AldIT is designed for multiple academic contexts. Students can document AI-supported assignments, teachers can define transparent rules for coursework, authors can generate structured AI-use statements for papers and proposals, and journal editors or reviewers can assess disclosures consistently. AldIT demonstrates how structured, app-based disclosure can make AI-assisted academic work more transparent, accountable, and easier to evaluate across institutional and publishing contexts.

P38. Age-related variation in summit metabolic rate in zebra finches

Edyta T. Sadowska^{1*}, Elisavet Zagkle¹, Małgorzata M. Lipowska¹, Ulf Bauchinger^{1,2}

¹*Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Kraków, Poland*

²*Nature Conservation Station Unterelbe, State Agency for Bird Conservation, Freiburg/Elbe, Germany*

*edyta.sadowska@uj.edu.pl

Age-related changes in physiological performance are central to life-history theory, which predicts trade-offs between metabolism, somatic maintenance, and ageing, potentially mediated by reactive oxygen species. However, maximal thermogenic capacity remains poorly studied in birds. We examined age-related differences in summit metabolic rate (MR_{sum}) and oxidative status in captive zebra finches (*Taeniopygia guttata*), among three adult age classes: young (1–2 years), mid-aged (3–4 years), and old (>4 years). MR_{sum} was measured using open-flow respirometry during cold exposure in a heliox atmosphere, and the resultant oxidative status was assessed in plasma based on d-ROMs (oxidative damage), OXY-adsorbent (total antioxidant capacity), and uric acid concentrations. Body mass did not vary among age classes, and MR_{sum} increased significantly with body mass ($p < 0.001$). Among age classes, MR_{sum} tended to decline ($p = 0.1$), with the highest values in young individuals (LSM $\pm$ SE: 260 ± 6 mlO₂h⁻¹), intermediate values in mid-aged birds (246 ± 9), and the lowest values in the old birds (238 ± 12), suggesting a gradual reduction in thermogenic capacity with age. In contrast, the oxidative stress markers were unaffected by either body mass or age ($p > 0.3$), indicating no detectable age-related variation in oxidative status. The maintenance of similar oxidative status despite lower MR_{sum} suggests no direct link between thermogenic capacity and oxidative balance. This pattern may reflect either compensatory regulation of antioxidant defenses or reduced physiological efficiency, whereby ageing is associated with increased ROS production per unit metabolic output or diminished capacity to mitigate oxidative damage.

P39. Effect of gut microbiome depletion in mice selected for divergent BMR

Julita Sadowska*, Andrzej K Gębczyński

Faculty of Biology, University of Białystok, Białystok, Poland

*julita.sadowska@uwb.edu.pl

Basal metabolic rate (BMR) is a benchmark metric in biology and biomedical studies. It quantifies energy metabolism in an adult endotherm at rest, within thermoneutrality, and in a post-absorptive state, and typically accounts for 50–70% of total daily energy expenditure. Since BMR varies not only between but also within species, one could expect it to have a profound impact and consequences for the individual's performance and fitness, including various trade-offs on energy allocation. In human subjects, BMR has been routinely used to diagnose thyroid dysfunctions, but a more recent resurgence of interest is related to the obesity pandemic. In today's western world, where high-calorie food is readily available and physical activity is limited, as such a huge part of the energy budget, it may mean the difference between obesity and staying lean. However, gut microbiota has also been shown to profoundly impact energy expenditure and overall metabolism of its host. Using a unique model, mice artificially selected for divergent levels of BMR, the high BMR (H-BMR) and low BMR (L-BMR) line types, we tested how gut microbiome depletion via antibiotic treatment affects some of the metabolic and physiological traits (daily energy expenditure, spontaneous physical activity, aerobic capacity, food intake and energy assimilation).

P40. A big tree of a tiny bear: first extensive multilocus phylogeny of the genus *Minibiotus* (Eutardigrada: Macrobiotidae)

Aleksandra Sumlińska^{1*}, Emilia Świechowska¹, Witold Morek^{1,2}, Piotr Gąsiorek¹, Alejandro López-López¹ & Łukasz Michalczyk¹

¹*Department of Invertebrate Evolution, Institute of Zoology and Biomedical Research, Faculty of Biology, Jagiellonian University, Kraków, Poland*

²*Tree of Life Programme, Wellcome Sanger Institute, Hinxton, Cambridge CB10 1SA, United Kingdom*

*aleksandra.sumlinska@doctoral.uj.edu.pl

Tardigrade taxonomy has undergone substantial revisions over recent decades, largely driven by advances in molecular techniques. Integrative species descriptions and redescrptions have frequently led to reclassifications at higher taxonomic levels. However, phylogenetic relationships remain unresolved for many taxa, and several higher-level groups have been shown to be polyphyletic. One such case is the genus *Minibiotus* Schuster, 1980, currently comprising 56 species, whose internal relationships are unclear owing to incomplete morphological datasets and the pronounced lack of molecular data. To address these issues, we analysed a 100 populations of *Minibiotus* from across the globe, including 12 from South America, 5 from North America, 1 from Greenland, 5 from Europe, 13 from India, 1 from New Guinea, 30 from Australia, 16 from New Zealand, and 17 from South Africa. Three nuclear markers (18S rRNA, 28S rRNA, and ITS-2) and one mitochondrial marker (COI) were sequenced for selected representatives. A phylogenetic analysis based on the three nuclear markers was conducted using Bayesian inference, resulting in the first comprehensive phylogeny of the genus *Minibiotus*. In addition, a species delimitation analysis based on two markers, ITS-2 and COI, revealed extensive genetic divergence within the genus. These analyses uncovered previously unknown relationships among species and identified potential evolutionary lineages corresponding to distinct taxonomic units. Our results demonstrate that *Minibiotus* is paraphyletic, comprising two clearly distinct clades. This study highlights both the hidden and evident diversity within *Minibiotus*, providing new and significant insights into its evolutionary relationships and global genetic structure.

P41. Constant vs. seasonal photoperiod and temperature yield contrasting life-history responses to climate warming

Frank Johansson¹, Robby Stoks², Guillaume Wos³, **Szymon Sniegula^{4*}**

¹*Frank Johansson, Department of Ecology and Genetics, Animal Ecology Program, Uppsala University, Uppsala, Sweden*

²*Laboratory of Evolutionary Stress Ecology and Ecotoxicology, Leuven, Belgium*

³*Institute of Nature Conservation Polish Academy of Sciences, Kraków, Poland*

⁴*Institute of Nature Conservation Polish Academy of Sciences, Kraków, Poland*

*szymon.sniegula@gmail.com

A key goal in predictive ecology is understanding how global warming affects ectotherm growth and development. Researchers often rear organisms under constant temperature and photoperiod regimes, raising the question of whether responses under these simplified conditions reflect those in realistic, seasonally varying environments. We examined key life history traits of the damselfly *Lestes sponsa* across six combinations of constant and seasonal temperature and photoperiod regimes, simulating present-day and future climates with a projected 4°C warming. Trait responses differed qualitatively and quantitatively among treatments. Mass and development responses to warming shifted direction depending on regime. For example, the response in mass to warming was reversed between constant (decrease) and seasonal varying (increase) conditions. In addition, developmental synchrony was stronger under seasonal photoperiods, and the temperature–size rule held only under constant conditions. Our results highlight that incorporating seasonal variation is crucial for making a realistic framework for predicting species' responses to climate change.

P42. The curious case of *Minibiotus fallax* Pilato et al., 1989 (Tardigrada) from Australasia

Emilia Świechowska*, Łukasz Michalczyk, Aleksandra Sumlińska

Department of Invertebrate Evolution, Institute of Zoology and Biomedical Research, Jagiellonian University, Kraków, Poland

*emilia.helenaswiechowska@gmail.com

Despite the growing popularity of tardigrades and rapid advances in biodiversity research, the taxonomy of this group remains incomplete due to the frequent occurrence of cryptic species. Integrative studies have shown that many taxa previously regarded as cosmopolitan actually represent complexes of distinct evolutionary lineages that are difficult to distinguish based solely on morphology. One genus illustrating these difficulties is *Minibiotus*, whose taxonomy remains problematic because of the limited number of diagnostic characters and the lack of molecular data for many species. In particular, the phylogenetic position of species with two macroplacoids, including *Minibiotus fallax*, remains uncertain. The aim of this study was to conduct an integrative analysis of *M. fallax* based on material from Australia and New Zealand. Morphological observations were performed using phase-contrast microscopy (PCM) and scanning electron microscopy (SEM), and were complemented with molecular analyses based on four genetic markers (18S rRNA, 28S rRNA, ITS-2, and COI). The results indicate that the studied taxon comprises at least two geographically separated evolutionary lineages, reflected by consistent qualitative differences, including traits previously considered diagnostic. Moreover, the high degree of morphological similarity to *Macrobiotus acadianus* and *M. topali* suggests that the examined populations may belong to a subtropical complex of cryptic species, referred to here as *M. aff. topali comb. nov.* Further integrative studies with broader geographic sampling are needed to clarify their taxonomic boundaries.

P43. Tc1-Mariner domestication in the Ponto-Caspian polychaete *Hypania invalida* (Grube, 1860)

Shrikant Vichare^{1,2*}, Tomasz Mamos², Serena Mucciolo², Tomasz Rewicz², Andrea Desiderato²

¹*Bio-Med-Chem Doctoral School, University of Lodz and Lodz Institutes of the Polish Academy of Sciences, Łódź, Poland*

²*Department of Invertebrate Zoology and Hydrobiology, University of Lodz, Łódź, Poland*

*shrikant.vichare@edu.uni.lodz.pl

Transposable elements (TEs) are ubiquitous components of eukaryotic genomes, increasingly recognised for driving evolution via host co-option and domestication. In this study, we investigate a novel TE domestication event in the Ponto-Caspian polychaete *Hypania invalida* (Grube, 1860) by integrating a draft genome and a de novo transcriptome assembly. Using a pipeline of automated repeat annotations, domain searches and reciprocal best hits, we generated a consensus TE library. Splice-aware alignments identified a host transcript with a complete, intact open reading frame derived from a standalone Tc1-Mariner transposase. Phylogenetic reconstruction within a broad metazoan baseline resolved the co-opted *H. invalida* protein within a well-supported Bilateria-only clade. Only *Sedentarian annelids* were found clustering together with a few molluscan, cnidarian and arthropod lineages in this clade. From more than 120 Annelida genomes in the database, only a few Sedentarian taxa had sequence homology to the *H. invalida* protein query, suggesting a complex evolutionary history likely driven by horizontal gene transfer events across multiple phyla rather than a uniform vertical inheritance model. Within our focal group, this domesticated sequence formed a tightly conserved orthogroup shared among *H. invalida*, *C. teleta*, *L. polybranchiata* and *P. palmiformis*, establishing a shared evolutionary history. Primary sequence and 3D structural analyses confirmed that this domesticated protein is systematically disarmed. Eliminating the catalytic DDE motifs while preserving the N-terminal Helix-Turn-Helix DNA binding domain, the host genome effectively neutralises transposon toxicity while exploiting its DNA binding function, suggesting potential utility in transcriptional regulation. This integrated approach validated TE domestication and predicted its potential role in the *H. invalida* functional toolkit, providing new insights into the mechanisms of TE domestication in annelids.

P44. Ungulates limit seedling survival but do not consistently generate density dependence in either native or invasive tree species

Martyna Wirowska^{1*}, Sarah Serafini¹, Urszula Eichert², Michał Bogdziewicz², Marcin K. Dyderski³, Rafał Zwolak¹

¹*Department of Systematic Zoology, Adam Mickiewicz University in Poznan, Poznań, Poland*

²*Forest Biology Center, Adam Mickiewicz University in Poznan, Poznań, Poland*

³*Department of Systematic and Environmental Botany, Adam Mickiewicz University in Poznan, Poznań, Poland*

*martyna.wirowska@amu.edu.pl

Large generalist herbivores can strongly influence tree recruitment, but it remains unclear whether their foraging generates density-dependent mortality and whether such effects differ between native and invasive species. Filling this gap is important for understanding how herbivores shape forest communities and biodiversity. We experimentally tested these questions in a temperate forest in Central Europe, manipulating seedling density of four native and four invasive tree species in paired control and ungulate exclusion plots. We expected that ungulates reduce survival, that their effects increase with seedling density, and that both effects are stronger in native than in non-native species. Ungulate exclusion increased seedling survival across species and sites, particularly during early establishment. In contrast, seedling density usually did not predict survival. Density-dependent responses were often weak, inconsistent in direction, and varied among species. Importantly, ungulate effects did not translate into density-dependent regulation: responses to density were similar in control and exclusion plots. Thus, herbivory affected overall survival but did not mediate density dependence. Invasion status did not predict responses to herbivory or density, and no consistent advantage of invasive over native species was detected. Overall, our results show that while ungulates are a strong constraint on seedling survival, they do not consistently generate density-dependent mortality, and their effects are better understood at the species level rather than broad ecological categories such as invasive vs. native species.