POLISH EVOLUTIONARY CONFERENCE

The 10th Polish Evolutionary Conference

11-13 September 2024

Białystok, Poland

PROGRAM & ABSTRACT BOOK

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afternoon
Posters

FACULTY
OF BIOLOGY
University
of Bialystok

PAN
POLISH ACADEMY OF SCIENCES

Organizers

- Faculty of Biology, Unversity of Białystok
- The Committee of Environmental & Evolutionary Biology, Polish Academy of Sciences

Organizing Committee

- Paweł Brzęk – chair
- Elżbieta Bonda
- Andrzej Gębczyński
- Adam Hermaniuk
- Aneta Książek
- Sebastian Maciak
- Piotr Roszkowski
- Julita Sadowska
- Jan RE Taylor

Scientific Committee

- dr hab Paweł Brzęk, prof UwB – University of Białystok
- prof dr hab Marcin Czarnołęski – Jagiellonian University, Kraków
- dr hab Andrzej Gębczyński – University of Białystok
- dr hab Katarzyna Jadwiszczak, prof UwB - University of Białystok
- dr hab Aneta Książek - University of Białystok
- dr hab Dries Kuijper, prof IBS PAN - Mammal Research Institute, Białowieża
- dr hab Krystyna Nadachowska-Brzyska - Jagiellonian University, Kraków
- dr hab Maciej Pabijan, prof UJ - Jagiellonian University, Kraków
- dr hab Małgorzata Pilot, prof UG – University of Gdańsk
- dr hab Ireneusz Ruczyński, prof. IBS PAN - Mammal Research Institute, Białowieża
- dr Julita Sadowska – University of Białystok
- dr Paulina Szafrańska – Mammal Research Institute, Białowieża
- prof dr hab Jan RE Taylor - University of Białystok

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

PEC Logo Credits

Szymon Drobniak

Volunteers

- Dariusz Basa
- Justyna Borowska
- Justyna Burzyńska
- Krzysztof Czerkas
- Ilona Kulus
- Natalia Musiuk
- Piotr Roszkowski
- Aleksandra Rozumko
- Monika Supronik
- Urszula Suprunowicz
- Jan Żeruń

The conference is supported by:

  - The Company of Biologists

Sponsors

- Silver
  - Novogene
  - Ursa Maior
- Bronze
  - Journal of Experimental Biology
  - Pyroscience

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

Conference location

Faculty of Biology
University of Białystok
Ciolkowskiego 1 J
15-245 Białystok

Link to map

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

Detailed Schedule

Click on the Authors' names to go to their abstracts

Wednesday *11 September*		*afternoon session*
12:00-18:00		*Registration*
14:00-14:30		*Opening ceremony*
14:30-15:30	**Suvi Ruuskanen**	Invisible friends: the role of the gut microbiome in adapting to environmental challenges
15:30-16:00		*Coffee break*
16:00-16:20	Maciej Kamiński	What shapes microbiome diversity in paragon urban exploiters?
16:20-16:40	Julita Sadowska	Significance of microbially-liberated urea-nitrogen in pregnant and lactating arctic ground squirrels
16:40-17:00	Veronika Andriienko	Multiple replacements shape nested symbiosis in Aphrodes leafhoppers
17:00-17:20	Monika Ostap-Chęć	No impact of microsporidian infection on honey bee carbohydrate consumption
17:20-17:40	Szymon Kaczanowski	Testing the Mitochondrial Prey Hypothesis of Apoptosis Origin
17:40-18:00	Nikhil Modak	Mitochondrial introgression affects routine metabolic rates in tadpoles
18:00-20:00		*Welcome reception*

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

Detailed Schedule

Click on the Authors' names to go to their abstracts

Thursday *12th September*	*morning session*
08:00-18:00	*Registration*
09:00-10:00 **Marta Szulkin**	Urban ecology & evolution: the new frontiers
10:00-10:30	*Coffee break*
10:30-10:50 Magdalena Fus	Cityscape symbiosis: how urbanisation shapes the gut microbiota of blue tit nestlings
10:50-11:10 Ignacy Stadnicki	Nestling period variation in the city mosaic: chicks reared in the urban environment take longer to fledge
11:10-11:30 Zuzanna Jagiełło	The plastic homes of hermit crabs in the Anthropocene
11:30-11:50 Guillaume Wos	Urbanization and latitude shape the phenotypic and physiological response to warming in the damselfly Ischnura elegans
11:50-12:10 Marcin Żebrowski	Artificial light at night bans Chaoborus from vital epilimnetic waters
12:10-12:30 Beata Bramorska	Socio-economic variables improve accuracy and change spatial predictions in species distribution models
12:30-14:00	*Lunch break*

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

Detailed Schedule

Click on the Authors' names to go to their abstracts

Thursday *12th September*		*afternoon session*
14:00-15:00	**Nicky Wybouw**	How *Wolbachia* symbionts spread within hybridizing host species
15:00-15:30		*Coffee break*
15:30-15:50	Marta Tischer	Distribution, diversity, and roles of endosymbiotic Wolbachia infections across worldwide planthopper hosts
15:50-16:10	Anastasiia Mykhailenko	Complex genomic landscape of inversion polymorphism in Europe's most destructive forest pest
16:10-16:30	Julia Morales-García	Selection inference in the complex inversion polymorphism landscape of spruce bark beetle (Ips typographus)
16:30-16:50	Mateusz Konczal	Genomic basis of adaptation to oscillating environment in a common crop pest
16:50-17:10	Rocco F Notarnicola	The Evolutionary Impact of Complement Factor H on Bank Vole Populations Across Poland
17:10-17:30	Mirosław Ratkiewicz	"It's not how you start that's important, but how well you finish" – population genetics of reintroduced Eurasian lynx in Piska forest, NE Poland
17:30-17:50		*one-minute presentation of posters*
17:50-19:00		*Poster session*

Detailed Schedule

Click on the Authors' names to go to their abstracts

Friday *13th September*	*morning session*
08:00-17:00	*Registration*
09:00-10:00 **Andreas Nord**	Keeping cool in a warming world: understanding climate-changes effects through studies of avian development
10:00-10:30	*Coffee break*
10:30-10:50 Neelam Porwal	Fighting through the heat: How sexual selection influences population demography under increasing intensity of heat shocks
10:50-11:10 Jakub Płachta	Old and cold: Age deepens rest-phase hypothermia of zebra finches (Taeniopygia guttata) in challenging conditions
11:10-11:30 Paweł Brzęk	Body temperature during gestation in females of laboratory mice with different levels of basal metabolic rate
11:30-11:50 Karolina Iwińska	Immunological rather than oxidative status prior to reproduction affects female dormice reproductive output
11:50-12:10 Katarzyna Krawczyk	On the molecular evolution of feather grasses (Stipa L., Stipeae; Poaceae) - why defining a good genetic marker for this group is such a challenge?
12:10-12:30 Ludwik Gąsiorowski	Regeneration in the absence of canonical neoblasts in an early branching flatworm
12:30-14:00	*Lunch break*

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

Detailed Schedule

Click on the Authors' names to go to their abstracts

Friday *13th September*	*afternoon session*
14:00-14:20 Piotr Minias	Nest site selection in urban blackbirds – heritability vs. Plasticity
14:20-14:40 Michał Budka	Species-specific strategies for acoustic space competition-avoidance in birds
14:40-15:00 Paweł Mirski	Movement of avian predators in farmland points to biodiversity hotspots
15:00-15:20 Gokul Bhaskaran	Investigating shared mechanisms of predatory and intermale aggression in bank voles
15:20-15:40 Tomasz Włodarczyk	Coevolutionary Interplay Between Slave-Making Ant Species and Its Host
15:40-16:00 Marcin Sielezniew	Should I stay or should I go? Selection against and for dispersal in a metapopulation of a critically endangered butterfly
16:00-17:00	*Closing ceremony*

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

Poster titles

Click on the Authors' name to go to page with the abstract

P01	Paulina Szafrańska	Positive consequences of roost sharing among male bats during spermatogenesis
P02	Gulsamal Askarova	Effect of temperature fluctuations on life history traits and strategies of phytophagous arthropods - a systematic review
P03	Andrzej Gębczynski	Size of body extremities is correlated with basal metabolism in laboratory mice
P04	Piotr Roszkowski	The effect of lactation on capacity for non-shivering thermogenesis in laboratory mice with different levels of basal metabolic rate
P05	Sylwia Buczyńska	Immunosenescence in laboratory mice divergently selected for basal metabolic rate
P06	Edyta Sadowska	The effects of short-term consumption of a Western diet on aerobic exercise performance in animals with inherently distinct metabolic rates
P07	Elżbieta Bonda-Ostaszewska	The effects of photoperiod and ambient temperature on the size of cells and lipid peroxidation in tissues of a bank vole (*Myodes glareolus*)
P08	Krzysztof Miler	Non-linear effects of dietary alcohol on life parameters in honey bees
P09	Daniel Bajorek	The lifespan of honey bees (Apis mellifera) exposed to occasional and constant dietary ethanol
P10	Katarzyna Jarosińska	Combined effects of polystyrene nanoplastics and enrofloxacin on the life histories and gut microbiota of Daphnia magna
P11	Neha Pandey	Strong sexual selection reduces population size and limits population recovery after heat stress in soil mites
P12	Justyna Borowska	Evolution of FOXP2 and ZNF362 genes in Cervidae
P13	Joanna Jakóbik	Mitonuclear coevolution and hybridization in newt species

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

Poster titles

Click on the Authors' name to go to the page with the abstract

P14	Ilona Kulus	Genetic analysis of progeny from crosses between downy birch (Betula pubescens Ehrh.) and shrub birch (Betula humilis Schrk.)
P15	Katarzyna Jadwiszczak	Climate- and soil type-depended occurrence of the Juniperus sabina varieties in Europe
P16	Amelia Chyb	Show me who you are… Expression of avian sexual ornament along the urbanization gradient
P17	Katarzyna Rutkowska	Differentiating effects of artificial light at night on the spatial composition of zooplankton communities
P18	Dawid Żegota	Urban habitat impact on skin microbiome of common toad Bufo bufo
P19	Małgorzata Lipowska	Born or raised predators? Cross-fostering experiment on bank vole selected for predatory behaviour
P20	Joanna Rutkowska	Perinatal malnutrition impairs appetitive > aversive learning
P21	Monika Sysiak	Can elevated temperature enhance task performance by improving cognitive abilities in common rudd (Scardinius erythrophthalmus)?
P22	Michał Glądalski	Great tits, aromatic plants & nest ectoparasite abundance
P23	Adam Zbyryt	Landscape of fear on a pasture land - is White Stork a scarebird for grasshoppers?
P24	Daniel Stec	Distribution of tardigrade cryptobiotic abilities across a fine-scale habitat gradient
P25	Helena Szewczyk	Diversity of coloration patterns in turtles (order Testudines)

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

Invited Speakers

Andreas Nord

Department of Biology, Lund University, Sweden

Dr Nord's research activity is focused on the question of how animals adapt to a changing world, particularly in relation to a warmer and more unstable climate. His research group addresses questions on all levels of inquiry, ranging from classical ecological studies in nature to detailed physiological assessment of heat production, thermoregulation, and cell biology in laboratory settings. This research work is carried out on both birds and insects, from small bees in southern Scandinavia to large birds in the High Arctic; all of which inhabit environments facing a variety of contemporary threats

Keeping cool in a warming world – Understanding climate change-effects through studies of avian development

There has been a recent spark of interest in how developmental temperature impacts animal form and function, necessitated by the realisation that our future will hold a warmer and more unpredictable climate, and fuelled by increased recognition of the fact that most organisms are amenable for epigenetic developmental priming of physiological and morphological traits. Previous work, mostly performed on birds, shows that higher or lower temperature during pre- or perinatal development may influence several compartments of the energy transduction chain across levels of enquiry, ranging mitochondrial function to organismal thermoregulatory performance. It is poorly understood whether such responses reflect epigenetic programming to predispose the animal for life in a particular thermal environment or if they emerge because of deviations from optimal developmental conditions. Insights into these questions require longitudinal studies of cellular and organismal respiration from birth to adulthood, which is difficult to reconcile in most available study species. In this talk, I will explore these matters across the bird phylogeny to answer questions pertaining to costs, benefits, and constraints in the context of lifelong matching between developmental and subsequent thermal environments. I will exemplify using own data from a range of experiments addressing how pre- and perinatal thermal conditions impact the ontogeny and thermal sensitivity of mitochondrial function, and how this is related to the ability to counter heat- or cold stress at organismal levels, spanning fertilisation to adulthood. I will discuss this in the context of the drivers, evolution, and plasticity of animal thermal adaptation, which is timely in our rapidly changing world.

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afternoon
Posters

Invited Speakers

Suvi Ruuskanen

Department of Biological and Environmental Science, University of Jyväskylä, Finland

Dr. Ruuskanen's research is at the intersection of environmental sciences and ecological, physiological, and molecular ecology. Dr. Ruuskanen is broadly interested in the mechanisms underlying organismal adaptation to environmental changes, including the role of transgenerational (including maternal and paternal effects) and developmental plasticity. Her research currently has a strong focus on host-microbiome interactions, to understand the causes and consequences of variation in gut microbiome, from molecular mechanisms to evolutionary patterns. These questions are being addressed in avian study systems.

Invisible friends: the role of the gut microbiome in adapting to environmental challenges

Microorganisms are everywhere, all organisms carry them, and the gut microbiome varies vastly across individuals and species. Microbiome adds a whole new layer of complexity in understanding phenotypic variation. A current key challenge is to understand if and how the microbiome may help the host respond and adapt to environmental variation. Yet, most literature is focused on laboratory model species, which do not reflect the complexity of natural conditions, life-history variation and different selection pressures. We use wild passerine bird populations as study systems to understand the role of gut microbiome in phenotypic variation and adaptations. In the talk I will focus in particular (1) What are the environmental causes of large and local scale variation in gut microbiome? How do anthropogenic disturbances affect microbiome? (2) How does microbiome play a role in host adaptations to environmental changes, with focus on thermal adaptations? (3) Does gut microbiome associate with fitness? To address these questions we use large-scale sampling, longitudinal data and various novel experimental designs. The data emphasizes the role that the microbiome plays in host responses to environmental variation and I hope to inspire new research in this young field of eco-evolutionary microbiome research.

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

Marta Szulkin

Anthropocene Biology Lab, Institute of Evolutionary Biology, Faculty of Biology, University of Warsaw

Dr Szulkin is the head of the Anthropocene Biology Lab at the University of Warsaw where she focuses her research on evolution and ecology in urban ecosystems. She initiated a long-term study of great tits in a gradient of urbanization in the city of Warsaw. Recently, she has extended her research interests into a broader framework of Anthropocene biology by studying the use of artificial materials such as plastic in the context of the extended phenotype concept in birds and crustaceans.

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

Urban Ecology & Evolution: the New Frontiers

By 2050, it is projected that 70% of the global population will reside in urban areas, making urban environments a focal point of interest for people worldwide, including biologists. These urban spaces exhibit ecological and evolutionary dynamics that are markedly different from those of natural habitats. **In the first part of my talk**, I will examine the profound effects of urbanisation on wildlife, specifically – on passerine birds. I will focus on birds breeding in a Central European capital city – Warsaw, while also highlighting the importance of inferring replicated gradients of urbanisation. The magnitude of urbanisation effects on wildlife biology, and their evolutionary and conservation implications, will be highlighted by examining a broad spectrum of avian traits—encompassing phenotypic, behavioral, and fitness variation. **In the second part of my talk,** I will explore the new frontiers of Urban Ecology & Evolution research, which can also be constructively explored to improve our understanding of biology in the Anthropocene more generally. I will first focus on how religion, politics and war are overlooked drivers of variation in urban evolutionary processes. I will then highlight the need to study the interactive effects of urbanisation and climate change to improve the resilience of urban wildlife facing these dual challenges

Nicky Wybouw

TEREC, Department of Biology, Ghent University, Belgium

Dr Wybouw and his lab studies questions in the broader fields of speciation, herbivory, and symbiosis. Within these fields, dr Wybouw studies the molecular-genetic basis of key complex traits such as hybrid dysfunction and xenobiotic detoxification, integrating methods of field, population, and theoretical biology with genomics and genetics. The research of dr Wybouw's group is centered on arthropods, specifically herbivorous insects and mites. To dissect host-symbiont interactions, we mainly focus on *Wolbachia,* a common endosymbiont of arthropods that interferes with host reproduction. Finally, dr Wybouw aims to integrate our fundamental insights into translational research for durable agricultural pest control.

How Wolbachia symbionts spread within hybridizing host species

The widespread occurrence of heritable symbionts such as Wolbachia necessitates a mechanistic understanding of how these symbionts spread through natural host populations. We study the underpinning mechanisms using haplodiploid spider mites as a model system, and by integrating molecular, population, and theoretical biology. Genomic analyses show that introgression and hybridisation facilitate the acquisition of Wolbachia within spider mite genera. I will further outline our current understanding of three Wolbachia-mediated reproductive phenotypes that drive Wolbachia spread within spider mite species: cytoplasmic incompatibility, parthenogenesis, and sex allocation distortion. I will describe the causal Wolbachia genic factors and their impact on host reproductive physiology. The talk will further focus on how arthropod hosts shape the strength of Wolbachia-mediated phenotypes, affecting infection spread and persistence. Together, these and other findings underscore the importance of host genetics for symbiont-host interactions and for the development of durable Wolbachia-based pest control.

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

WHAT SHAPES MICROBIOME DIVERSITY IN PARAGON URBAN EXPLOITERS?

Maciej Kamiński[1], Sergiusz Jeziorski[2], Milena Skóra[2], Barbara Bożyk[2], Dominik Strapagiel[2], Piotr Minias[1]

[1] *University of Lodz, Faculty of Biology and Environmental Protection, Department of Biodiversity Studies and Bioeducation, Poland*
[2] *University of Lodz, Faculty of Biology and Environmental Protection, Biobank Lab, Department of Oncobiology and Epigenetics, Poland*

Microbial community of the gastrointestinal tract plays an important role in physiology of vertebrates, therefore contributing to host fitness. Diversity of gastrointestinal microbial community is shaped by multiple factors, especially environment and diet. Animal species that successfully colonized cities (urban exploiters) function in heavily transformed man-made habitats. A characteristic feature of urban exploiters is dwelling in high population density, which can facilitate horizontal transmission of microbes. Our aim was to investigate the associations of habitat urbanization and population density with the diversity of gastrointestinal microbiome in a successful urban bird – feral pigeon *Columba livia domestica.* To do so, we collected faecal samples from nearly 200 individuals across the gradients of habitat urbanization and pigeon population density in five large cities in Poland. We used meta-barcoding methods to identify microbiome taxa, relying on the high-throughput sequencing of V3 – V4 regions of the 16S rRNA gene. We found that habitat urbanization was negatively associated with microbial diversity and taxonomic richness. At the same time, we found no associations of population density with microbiome alpha diversity. Moreover, we detected conspicuous differences of microbiome composition between the cities, suggesting local environmental effects. The results improve our understanding of factors that shape diversity and composition of gastrointestinal microbiome in urban-adapted animals.

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

SIGNIFICANCE OF MICROBIALLY-LIBERATED UREA-NITROGEN IN PREGNANT AND LACTATING ARCTIC GROUND SQUIRRELS

Julita Sadowska[1], Shannon Medlock[2], Karen M. Carlson[2], C. Loren Buck[3], Khrystyne N. Duddleston[2]

[1] *Department of Evolutionary and Physiological Ecology, Faculty of Biology, University of Białystok, Poland*
[2] *Department of Biological Sciences, College of Arts and Sciences, University of Alaska Anchorage, USA*
[3] *Department of Biological Sciences, Northern Arizona University, USA*

Gut microbes may influence host energy balance via a process called Urea Nitrogen Salvage (UNS). This microbial recycling has long been proposed as a mechanism for nitrogen conservation in hibernators. The arctic ground squirrel (*Urocitellus parryii*) is an exceptional hibernator, displaying the most extreme hibernation phenotype known: hibernation lasts up to nine months with no food or water consumption, and Tb during torpor is regulated at -2.9°C, the lowest of any mammal. That leaves the animal with just a short window of activity to complete the full reproductive cycle and prepare for the next hibernation. Earlier studies suggest that demands of hibernation might have enabled the selection of the ureolytic microflora and increased relevance of UNS as a source of N. Here we tested whether high protein demands of gestation and lactation also increase incorporation of microbially-liberated urea-N into maternal tissues of active squirrels. Gestating and lactating animals were fed either a protein-deficient or protein-sufficient diet throughout the entire reproductive cycle. We measured microbial urea-N incorporation using isotopically labeled urea and assessed the bacterial diversity of gut microbiota. We found higher ureolytic bacteria activity and urea-N incorporation in the protein-deficient group. Lactating squirrels on the protein-deficient diet showed the highest incorporation of urea-N in their tissue and breath, signifying higher UNS.

MULTIPLE REPLACEMENTS SHAPE NESTED SYMBIOSIS IN *APHRODES* LEAFHOPPERS

Veronika Andriienko[1], Diego C. Franco[1], Adam Stroiński[2], Piotr Lukasik[3], Anna Michalik[1]

[1] Department of Developmental Biology and Morphology of Invertebrates, Institute of Zoology and Biomedical Research, Faculty of Biology, Jagiellonian University, Poland
[2] Museum and Institute of Zoology, Polish Academy of Sciences, Warsaw, Poland
[3] Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Poland

Auchenorrhyncha – a highly diverse group of sap-sacking hemipteran insects have engaged in complex associations with nutritional endosymbionts. The common ancestor of Auchenorrhyncha was initially colonized by two microbes: *Sulcia* and Betaproteobacterium, which are still present in many Auchenorrhyncha lineages. However, in some clades, they have been supplemented or replaced by other microorganisms. Using advanced sequencing and microscopic techniques, we analyzed symbiotic systems of three *Aphrodes* species from several European populations. Our results revealed that *Aphrodes* leafhoppers host two primary symbionts, *Sulcia* and *Nasuia*, alongside *Sodalis* symbionts. Microscopic analyses revealed a unique nested symbiosis within *Aphrodes*, where *Sulcia* and *Nasuia* reside in separate bacteriomes, while *Sodalis* is found within *Sulcia* cytoplasm. Although nested symbioses have been observed in other leafhopper species and mealybugs, our findings extend this phenomenon to *Aphrodes*, highlighting the complexity and diversity of symbiotic relationships in insects. Additionally, we have discovered previously unexplored aspects of their symbiosis through amplicon sequencing and metagenomics of *Aphrodes* populations across Europe. We found variations in *Sodalis* strains among *Aphrodes* species and populations, with multiple strains possibly coexisting within individual hosts. The observed diversity of *Sodalis* symbionts suggests their independent origins and potential functional diversification. Our study provides new insights into the complex relationship between Auchenorrhyncha insects and their bacterial symbionts, shedding light on the occurrence of nested symbioses and the genetic diversity underlying symbiont populations. Understanding these symbiotic relationships is crucial for describing the ecological roles of symbionts and unraveling the evolutionary processes of host-microbe associations in diverse insect taxa.

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

NO IMPACT OF MICROSPORIDIAN INFECTION ON HONEY BEE CARBOHYDRATE CONSUMPTION

Monika Ostap-Chęć[1,2], Daniel Bajorek[3], Krzysztof Miler[3]

[1] *Doctoral School of Exact and Natural Sciences, Jagiellonian University, Poland*
[2] *Institute of Environmental Science, Faculty of Biology, Jagiellonian University, Poland*
[3] *Institute of Systematics and Evolution of Animals, Polish Academy of Science, Kraków, Poland*

Honey bees (*Apis mellifera*) play a vital role as pollinators, essential for the functioning of both natural and agricultural environments. However, they face various challenges, with parasitic infections representing a significant threat. Among these, the microsporidian gut parasite *Nosema ceranae* stands out as particularly impactful due to its invasiveness and rapid worldwide spread. Bees have been observed to employ behavioural defence mechanisms against this parasite, such as dietary preference for food with higher antibiotic activity when infected. Given that *N. ceranae* infection primarily results in intestinal damage and substantial energetic stress, increased carbohydrate consumption by infected bees could potentially serve as a compensatory mechanism for energy loss. However, whether bees evolved the capacity to employ such a mechanism is unknown. We conducted a meta-analysis based on existing literature which explored the sugar consumption rate of healthy and infected bees. The results demonstrated that bees infected with *N. ceranae* spores do not exhibit a higher sugar consumption rate compared to healthy individuals. Our findings highlight that disrupted energy balance caused by *N. ceranae* infection is not compensated for by higher energy intake. This might be especially dangerous for honey bee foragers, which in nature face the highest infection levels and meet high energy demands during their foraging trips. These results underscore the severity of nosemosis as a threat to honey bee populations. This research was supported by the National Science Centre, Poland [grant number Preludium 2021/41/N/NZ8/02917].

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

TESTING THE MITOCHONDRIAL PREY HYPOTHESIS OF APOPTOSIS ORIGIN

Szymon Kaczanowski

Institute of Biochemistry and Biophysics, Polish Academy of Sciences, Warsaw, Poland

Based on our previous phylogenetic studies, we postulate the mitochondrial prey hypothesis of apoptosis origin. According to this hypothesis, protomitochondria used toxins to defend themselves against protoeukaryotic predators, leading to an evolutionary arms race. Later, these toxins transformed into extant apoptotic factors. This hypothesis leads to the following predictions: mitochondrial apoptotic factors are located on the mitochondrial surface, there was positive selection for gain-of-function mutations in apoptotic factors, and there was positive selection for antiapoptotic mutations in antiapoptotic factors. We tested these predictions using yeast as a model organism, which has a simplified apoptotic machinery. Using gene ontology analysis, we showed that yeast genes required for apoptosis tend to be located on the mitochondrial surface. We found indications of an ancient selection pressure favoring gain-of-function mutations in key apoptotic/antiapoptotic factors. For example, three different human Apoptotic Induction Factors (AIFs) are similar to the yeast homologs. However, human AIFs are more closely related to eubacterial orthologs than to one another. Their different parts are involved in apoptosis initiation, indicating that different initiation mechanisms evolved. Statistical analysis shows that it is unlikely to be accidental. This observation suggests putative ancestral selection pressure for evolutionary innovations leading to novel apoptotic functions. A similar analysis showed that it is unlikely that human and yeast BIR proteins acquired their different antiapoptotic functions by chance. Indeed, it is likely that the mechanism of apoptosis initiation by degradation of BIR factors by different OMI/HTRA proteases evolved due to selection pressure.

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

MITOCHONDRIAL INTROGRESSION AFFECTS ROUTINE METABOLIC RATES IN TADPOLES

Nikhil Modak[1], Adam Hermaniuk[2], Dariusz Basa[2], Monika Supronik[2], Maciej Pabijan[1]

[1] Henryk Hoyer Department of Comparative Anatomy, Institute of Zoology and Biomedical Research, Jagiellonian University, Poland
[2] Department of Evolutionary and Physiological Ecology, Faculty of Biology, University of Białystok, Poland

Mito-nuclear incompatibility in natural hybrids has garnered attention for its potential effects on fitness and life history traits including metabolism. This study investigates how metabolic rates are affected by mitochondrial introgression from *Pelophylax lessonae* (nucleotype LL) into pure *P. ridibundus* (nucleotype RR). We expected differences in metabolic rates between introgressed RR (with L mtDNA) and non-introgressed RR (with R mtDNA) individuals. Tadpoles reared at 20°C were tested at 16°C, 20°C, and 24°C, whereas individuals reared at 24°C were tested at 20°C, 24°C, and 28°C. Oxygen consumption was measured in a closed respirometry system. Linear mixed effects model was used to estimate the effect of tadpole mitotype, body mass, rearing and testing temperatures, and parental cross (as a random factor) on the metabolic rates of tested animals . Results showed that metabolic rate was affected by the interaction between test temperature and mitotype, as well as body mass and rearing temperature. Metabolic rates significantly differed between introgressed vs. non-introgressed individuals reared at 20°C (but not those reared at 24°C), with introgressed individuals having lower routine metabolic rates at lower temperatures. Our findings confirm that introgression affects metabolic rates, indicating potential biological implications.

CITYSCAPE SYMBIOSIS: HOW URBANISATION SHAPES THE GUT MICROBIOTA OF BLUE TIT NESTLINGS

Magdalena Fus[1], Marta Szulkin[1], Öncü Maraci[2]

[1] *University of Warsaw*

[2] *University of Bielefeld*

Urbanisation transforms natural environments, significantly affecting not only many species of wild animals but also the microorganisms coexisting with them. Differences in microbiome composition, determined by the external environment, are likely to impact the health and survival of animals. To better understand the importance of microbiological composition and diversity in the development of birds inhabiting urban areas, we collected faecal samples from blue tit nestlings using nest boxes distributed throughout the Warsaw metropolitan area. The microbiota analysis results unveiled a pattern of reduced diversity in urbanised settings, and microbial structuring dependent on the degree of urbanisation intensity. Our discoveries complement and expand upon earlier insights from a study on great tits, a model species closely related to the blue tit.

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

NESTLING PERIOD VARIATION IN THE CITY MOSAIC: CHICKS REARED IN THE URBAN ENVIRONMENT TAKE LONGER TO FLEDGE

Ignacy Stadnicki [1,2], Michela Corsini [1,3], Eva M. Schöll [4], Marta Szulkin [1,2]

[1] Faculty of Biology, University of Warsaw, Poland
[2] Institute of Evolutionary Biology, Faculty of Biology, Biological and Chemical Research Centre, University of Warsaw, Poland
[3] Department of Biological Sciences, Boise State University, USA
[4] University of Natural Resources and Life Sciences, Vienna (BOKU), Department of Integrative Biology and Biodiversity Research, Institute of Wildlife Biology and Game Management, Austria

Urban areas are expanding worldwide. Apart from humans, cities are inhabited by much wildlife that faces both novel challenges and opportunities. Studying these organisms gives us valuable insight into eco-evolutionary dynamics in anthropogenically altered environments. Great tits (*Parus major*) occupy both urbanised and natural areas, which makes them a superb subject for such research. Previous studies have shown a significant impact of urbanisation on various aspects of avian reproduction. However, nestling period – that is the time chicks spend in the nest from hatching to fledging and a key stage in avian life history - has not been studied in cities and is generally poorly understood in a broader context. In this study, a total of c.150 broods were monitored over four breeding seasons (2021-2024) in Warsaw's city mosaic. Time spent at the nest by offspring was derived from thermologger recordings, which captured differences between nest and ambient temperatures. Preliminary results show that both biotic and abiotic factors are associated with nestling period length. In particular, a larger proportion of impervious surfaces (such as concrete or asphalt) in the nests' vicinity was associated with a prolonged nestling period. These findings raise important questions regarding developmental constraints, developmental plasticity and parental investment, all of which are set in a background of urban-driven shifts in selective pressures, response to selection, and ultimately – longer-term eco-evolutionary dynamics.

THE PLASTIC HOMES OF HERMIT CRABS IN THE ANTHROPOCENE

Zuzanna Jagiełło[1], Łukasz Dylewski[2], Marta Szulkin[1]

[1] *Institute of Evolutionary Biology, Faculty of Biology, Biological and Chemical Research Centre, University of Warsaw, Poland*
[2] *Department of Zoology, Poznań University of Life Sciences, Poland*

Plastic is the most widespread element of marine debris, posing significant threats to wildlife. Utilizing iEcology (internet Ecology, which leverages online data sources as a tool in ecological research), we present findings on a novel behavior in hermit crabs: the use of plastic or other artificial materials as protective shells. By analyzing social media images, we identified 386 hermit crabs with artificial shells, predominantly plastic caps (85%). This behavior was reported in 10 out of the world's 16 terrestrial hermit crab species, observed along all tropical coasts. The high environmental availability of plastic caps, combined with a shortage of optimal gastropod shells, likely plays a major role in this behavior. This, along with four possible non-exclusive mechanisms—sexual signaling, the lightness of artificial shells, odor cues, and camouflage in polluted environments—could explain the preference for artificial shells. Further research is essential to understand how this behavior might influence the evolutionary trajectories of hermit crabs.

URBANIZATION AND LATITUDE SHAPE THE PHENOTYPIC AND PHYSIOLOGICAL RESPONSE TO WARMING IN THE DAMSELFLY *ISCHNURA ELEGANS*

Guillaume Wos[1], Nermeen R. Amer[1,2], Andrzej Antoł[1], Robby Stoks[3], Szymon Sniegula[1]

[1] *Institute of Nature Conservation Polish Academy of Sciences, Krakow, Poland*

[2] *Department of Entomology, Faculty of Science, Cairo University, Egypt*

[3] *Laboratory of Evolutionary Stress Ecology and Ecotoxicology, KU Leuven, Belgium*

Urbanization has become a major source of disturbance for organisms and strongly impacts environmental conditions. Indeed, urban environments are generally hotter than rural areas. Consequently, we may expect differences in coping with warming between urban and rural populations. Here, we tested for differences between urban and rural populations from different latitudes in response to warming and further explored whether these effects were sex-specific. We sampled damselfly females from different urban and rural ponds located at central (southern Poland) and high latitudes (southern Sweden). We raised their larvae in growth chambers, exposed them to current (20 ºC) vs. mild warming (24 ºC) temperature and measured a set of phenotypic and physiological traits. We found that the effects of urbanization were dependent on latitude and temperature, with urban populations having lower mass than rural populations, especially at central latitudes. Rural populations grew faster than urban populations but only at 20 ºC. We also showed that urban populations from central latitude consumed more energy at 24 ºC than urban populations from high latitude. Finally, we demonstrated some sex-specific effects with urban males being lighter and having a lower growth rate than rural males. Altogether, we showed that both urban and rural populations had the potential to produce a plastic response to warming, yet the magnitude and direction of the plastic changes differed between latitudes. The latitude-specific response to urbanisation could be explained by differences in life-history strategies across latitudes.

ARTIFICIAL LIGHT AT NIGHT BANS *CHAOBORUS* FROM VITAL EPILIMNETIC WATERS

Mirosław Ślusarczyk[1,2], Anna Bednarska[1], Marcin Lukasz Zebrowski[1], Joanna Tałanda[1]

[1] Department of Hydrobiology, Institute of Functional Biology and Ecology, Faculty of Biology, Biological and Chemical Research Centre, University of Warsaw, Poland
[2] Hydrobiological Station, Faculty of Biology, University of Warsaw, Poland

Artificial light at night (ALAN) is known to affect organisms in terrestrial ecosystems and adjacent littoral habitats. In the present study, we tested the effect of ALAN on the spatial distribution of organisms in open waters, using the insect larvae of *Chaoborus flavicans* as an example. During the day *C. flavicans* typically hide from visually hunting fish in deep, dark, anoxic waters. On safer nights, they forage in rich subsurface waters. Nighttime field tests revealed that light from an HPS street lamp mounted on a boat anchored in open water attracted planktivorous fish, but deterred planktonic *Chaoborus* from rich but risky surface waters. *Chaoborus* did not descend to the safest, anoxic hypolimnion, but remained in hypoxic mid-depth metalimnion, which does not appear to be a perfect refuge. Neither light gradient nor food distribution fully explained their mid-depth residence under ALAN conditions. A further laboratory test revealed a limited tolerance of *C. flavicans* to anoxia. Half of the test larvae died after 38 h at 9 °C in anoxic conditions. The trade-off between predation risk and oxygen demand may explain why *Chaoborus* did not hide in deep anoxic waters, but remained in the riskier metalimnion with residual oxygen under ALAN conditions.

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

SOCIO-ECONOMIC VARIABLES IMPROVE ACCURACY AND CHANGE SPATIAL PREDICTIONS IN SPECIES DISTRIBUTION MODELS

Beata Bramorska, Ewa Komar, Luca Maugeri, Ireneusz Ruczyński, Michał Żmihorski

In an era marked by increasing anthropogenic pressure, understanding the relations between human activities and wildlife is crucial for understanding ecological patterns, effective conservation, and management strategies. Here, we explore the potential and usefulness of socio-economic variables in species distribution modeling (SDM), focusing on their impact on the occurrence of wild mammals in Poland. Beyond the environmental factors commonly considered in SDM, like land-use, the study tests the importance of socio economic characteristics of local human societies, such as age, income, working sector, gender, education, and village characteristics for explaining distribution of diverse mammalian groups, including carnivores, ungulates, rodents, soricids, and bats. The study revealed that incorporating socio-economic variables enhances the predictive power for *>60% of* species and overall for most groups, with the exception being carnivores. For all the species combined, among the 10 predictors with highest predictive power, 6 belong to socio economic group, while for specific species groups, socio-economic variables had similar predictive power as environmental variables. Furthermore, spatial predictions of species occurrence underwent changes when socio-economic variables were included in the model, resulting in a substantial mismatch in spatial predictions of species occurrence between environment-only models and models containing socio-economic variables. We conclude that socio-economic data has potential as useful predictors which increase prediction accuracy of wildlife occurrence and recommend its wider usage. Further, to our knowledge this is a first study on such a big scale for terrestrial mammals which evaluates performance based on presence or absence of socio-economic predictors in the model. We recognise the need for a more comprehensive approach in SDMs and that bridging the gap between human socio-economic dynamics and ecological processes may contribute to the understanding of the factors influencing biodiversity.

DISTRIBUTION, DIVERSITY, AND ROLES OF ENDOSYMBIOTIC *WOLBACHIA* INFECTIONS ACROSS WORLDWIDE PLANTHOPPER HOSTS

Marta Tischer[1], Diego Castillo Franco[1,2,3], Junchen Deng[1,4], Monika Prus-Frankowska[1], Anna Michalik[1,2], Piotr Łukasik[1]

[1] *Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Poland*
[2] *Department of Developmental Biology and Morphology of Invertebrates, Institute of Zoology and Biomedical Research, Faculty of Biology, Jagiellonian University, Poland*
[3] *Terrestrial Ecology Unit, Molecular Ecology and Evolutionary Genetics Lab, Department of Biology, Ghent University, Belgium*
[4] *Doctoral School of Exact and Natural Sciences, Jagiellonian University, Poland*

Wolbachia is a widespread intracellular endosymbiotic Alphaproteobacteria, primarily infecting arthropods and various groups of filarial and plant-parasitic nematodes. To date, at least 23 *Wolbachia* monophyletic lineages (supergroups) have been identified, exerting diverse effects on their hosts, including reproductive manipulation, vitamin supplementation, and pathogen restriction. Despite its high abundance and wide distribution, the taxonomy and diversity of *Wolbachia* within planthoppers (Hemiptera: Fulgoromorpha) remain poorly understood. In this project, we aim to detect and characterize the global diversity of *Wolbachia* within planthoppers. To elucidate the nature and molecular basis of this interaction, we screened over 170 planthopper individuals from at least 18 families distributed worldwide. Of these, at least 50 individuals were infected with *Wolbachia* and selected for genomic and further phylogenomic analysis. Furthermore, our study investigates *Wolbachia* prevalence, patterns of specificity, primary functions, and host-shift events. To observe potential host-switching patterns, we constructed phylogenies for both the host and endosymbiont and applied comparative genomic approaches. We found *Wolbachia* present in most studied planthopper families, with significant differences in prevalence among groups. Phylogenomic analyses indicate that most strains belong to the globally dominant supergroups A and B, revealing co-infection events and distinct biogeographical patterns. This research enhances our understanding of the distribution, diversity, and evolutionary dynamics of *Wolbachia* infections in planthoppers, shedding light on their ecological and evolutionary significance.

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

COMPLEX GENOMIC LANDSCAPE OF INVERSION POLYMORPHISM IN EUROPE'S MOST DESTRUCTIVE FOREST PEST

Anastasiia Mykhailenko[1,2], Piotr Zieliński[1], Krystyna Nadachowska-Brzyska[1]

[1] *Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Poland*
[2] *Doctoral School of Exact and Natural Sciences, Jagiellonian University, Poland*

In many species, polymorphic inversions underlie complex phenotypic polymorphisms and appear to facilitate local adaptation in the face of gene flow. While multiple polymorphic inversions can coexist within a genome, their prevalence, evolutionary importance, and the extent of their complexity are not well understood. In this study, we discover a complex inversions-rich genomic architecture in one of Europe's most destructive forest pests, the spruce bark beetle (*Ips typographus*). We examine the genome-wide variation, scan for polymorphic inversions, and test whether inversions are involved in key adaptations in this species. We analyzed 240 individuals from the 18 populations across the species' European range and, using a whole-genome resequencing approach, identified 27 polymorphic inversions that cover approximately 28% of the genome. The inversions are highly polymorphic across the species range, vary in size and age, and also create complex genomic patterns of structural variation by overlapping and by recombining with the homologous, collinear part of the genome. We tested various mechanisms that can maintain inversion polymorphisms in the genome, including directional selection, overdominance, and associative overdominance. Our findings suggest that a combination of evolutionary forces sustains a heterogeneous inversion landscape. We also found that inversions are enriched in odorant receptor genes, which are crucial for the recognition of host plants, mates, and symbiotic fungi. Overall, our results highlight the complex inversion landscape in the genome of the spruce bark beetle, a pest of significant social, political, and economic concern, and raise questions about the limits of complexity in genomic architecture.

SELECTION INFERENCE IN THE COMPLEX INVERSION POLYMORPHISM LANDSCAPE OF SPRUCE BARK BEETLE (*IPS TYPOGRAPHUS*)

Julia Morales-García[1,2], Wiesław Babik[1], Piotr Zieliński[1], Krystyna Nadachowska-Brzyska[1]

[1] *Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Poland*
[2] *Doctoral School of Exact and Natural Sciences, Jagiellonian University, Poland*

Understanding the genetic basis of adaptation is a fundamental goal in evolutionary biology. Recent advancements in genomic selection scans have facilitated the exploration of adaptation signatures, yet challenges persist in distinguishing true selection signals from false positives, particularly in regions of reduced recombination, such as polymorphic inversions. These chromosomal mutations which suppress recombination between inverted and non-inverted arrangements, are becoming apparent as important drivers of adaptation. The emerging prevalence of inversion-rich genomes poses intriguing questions about the role of selection in maintaining inversion polymorphisms and the potential identification of adaptive loci within inversions. This study investigates genome-wide selection signatures in the eighth-toothed spruce bark beetle (*Ips typographus*), the most destructive forest pest in Europe, that also has one of the most complex inversion-related recombination landscapes. By analysing 312 individuals from 23 populations across the species' European range and employing diverse selection scan methods on whole genome resequencing data, we elucidate the impact of inverted genomic regions on selection inference and identify candidate loci under selection within and outside inversion regions. We performed analysis with nSL and Λ selection scans that revealed numerous selection signals within inversion regions, which were consistent across different datasets and methods, highlighting the significant role of inversions in local adaptation. Our findings underscore the contribution of inversions to species adaptation while emphasising the significance of understanding species-specific genomic architecture in interpreting selection scan results.

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

GENOMIC BASIS OF ADAPTATION TO OSCILLATING ENVIRONMENT IN A COMMON CROP PEST

Mateusz Konczal[1], Alicja Laska[2], Anna Skoracka[2]

[1] *Evolutionary Biology Group, Adam Mickiewicz University in Poznan, Poland*
[2] *Population Ecology Lab, Adam Mickiewicz University in Poznan, Poland*

In seasonal environments, certain resources become temporally unavailable, creating strong evolutionary pressure for species that rely on them. Nevertheless, many species occur in such environments, which necessitates an understanding of the mechanisms that allow their persistence. Here, we performed Evolved and Resequence experiments, on herbivorous mite, *Aceria tosichella*, a widespread wheat pest, to understand how seasonality affects its evolution. Wheat-bred mite population were subjected to replicated experimental evolution in a constant single-host environment (wheat [cT] or barley [cH]) or in an alternation between these two hosts every three generations (aTH populations). After 45 generations cT populations evolved increased fitness on wheat, while cH and aTH populations evolved increased fitness on barley. All three treatments differentiated its performance on a different host, namely smooth brome, which allows populations to persist (albeit with negative growth rate) when the source habitat is gone in nature. We identified a single genomic region, showing strong and consistent response to selection in cT populations. The only two SNPs that significantly differentiated between all three treatments are localized within the same region, and its allele frequency changes mimic phenotypic response observed on brome. Differentiated SNPs are localized next to Allostatin C receptor 2, a gene playing critical role in response to nutrient stress. Several other genes within the region are also associated with starvation resistance. Thus, this genomic region might allow persistence in suboptimal conditions bringing some costs on the main host plant. Oscillating selection pressure might maintain genetic variation in this locus.

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

THE EVOLUTIONARY IMPACT OF COMPLEMENT FACTOR H ON BANK VOLE POPULATIONS ACROSS POLAND

Notarnicola Rocco F., Herdegen-Radwan Magdalena, Różańska-Wróbel Joanna, Radwan Jacek

Adam Mickiewicz University, Poznan, Poland

Complement Factor H (CFH) is a crucial regulator of the innate immune response in vertebrates, protecting self-cells by inhibiting the constitutively expressed, alternative complement pathway. CFH engages in co-evolutionary interactions with bacterial pathogens, which can hijack this immune inhibitor to evade clearance. These co-evolutionary dynamics may involve balancing selection, causing enhanced flow of immunity genes among populations, or in local adaptation, restricting the flow. However, population-genetic structure of CFH relative to genomic average remains underexplored. This study aims to test whether population differentiation differs in CFH compared to the genomic background. To address this, we performed RAD sequencing on 16 bank vole populations across Poland, analyzing CFH sequences alongside hundreds of random genomic markers generated via RADseq. To analyse population differentiation and gene flow, we conducted Fst outlier (BayPass) and cline analyses. Preliminary results reveal high polymorphism in CFH within Poland (seven variants) and positive selection in codons involved in pathogen interactions, indicating co-evolution. We also found differentiation in CFH variants between western (Carpathian) and north-eastern bank vole populations in Poland. These findings underscore the importance of CFH and other immune genes in the evolution of natural infections, with implications for species conservation and possibly human epidemiology.

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

"IT'S NOT HOW YOU START THAT'S IMPORTANT, BUT HOW WELL YOU FINISH" – POPULATION GENETICS OF REINTRODUCED EURASIAN LYNX IN PISKA FOREST, NE POLAND

Mirosław Ratkiewicz[1], Maciej Matosiuk[1], Stefan Jakimiuk2[1], Jose Godoy[3], Enrico Bazzicalupo[3] and Krzysztof Schmidt[4]

[1] *Faculty of Biology, University of Białystok, Poland*
[2] *WWF Poland*
[3] *Department of Integrative Ecology, Estación Biológica de Doñana (CSIC), Seville, Spain*
[4] *Mammal Research Institute, Polish Academy of Sciences, Białowieża, Poland*

Reintroductions of large mammalian predators lower the risk of their extinction and can assure better ecosystem functioning. Such initiatives, often called "rewilding" could work as sound wildlife restoration programs, however they may also act like "Pandora box". We evaluated population genetic structure of reintroduced Eurasian lynx population in Piska forest, NE Poland that has been reestablished ca. 20 years ago as an effect of two independent (wild-to-wild and captive "Born to be free") programs. Despite lack of knowledge about genetic identity of first three pairs of captive-born founders prior to their release, the contemporary *Lynx lynx* population fully corresponds to so-called 'lowland' (or Baltic) populations of the species and exhibits increased genetic polymorphism when compared to founders. These facts positively contrast with other reintroductions of lynx in Europe and may suggest that among others, immigration from natural neighboring populations is essential for sustainability of reintroduced populations of this apex predator.

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

FIGHTING THROUGH THE HEAT: HOW SEXUAL SELECTION INFLUENCES POPULATION DEMOGRAPHY UNDER INCREASING INTENSITY OF HEAT SHOCKS

Neelam Porwal[1], Neha Pandey[1], Agnieszka Szubert-Kruszyńska[1], Jonathan Parrett[1], Tom Cameron[2], Rob Knell[3], Jacek Radwan[1]

[1] Department of Evolutionary Biology, Adam Mickiewicz University, Poland
[2] School of Life Sciences, University of Essex, United Kingdom
[3] School of Natural Sciences, University of Hull, United Kingdom

Sexual selection has been shown to have detrimental, beneficial and neutral effects under environmental change. Even though these costly traits may increase the fitness of the individuals they may also increase inbreeding in a population. This existing literature is contradictory and lacking evidences with respect to the risks of sexual selection on population survival. To assess these risks with a condition dependent sexually selected trait we used male-dimorphic soil mites *Sancassania berlesei*. The expression of the trait is density dependent, and the prevalence of the sexually selected males (fighters) can be suppressed using pheromones from a high-density population. We ran a multi- generation experiment with discrete generation cycles for nine generations with a rise in the temperature of heat shocks every two generations. The populations were shocked at the adult stages and the sexes and morphs were recorded before and after to calculate survival rates every generation. We also compared female productivity at the end of the experiment. Three non-sexually selected populations went extinct over time. We expect fighter populations to maintain lower population sizes over generations due to the combat mortality and mortality related to male harm over females.

OLD AND COLD: AGE DEEPENS REST-PHASE HYPOTHERMIA OF ZEBRA FINCHES (*TAENIOPYGIA GUTTATA*) IN CHALLENGING CONDITIONS

Jakub P. Płachta[1,2], Małgorzata M. Lipowska[1], Edyta T. Sadowska[1], Ulf Bauchinger[1]

[1] *Faculty of Biology, Institute of Environmental Sciences, Jagiellonian University, Poland*
[2] *Doctoral School of Exact and Natural Sciences, Jagiellonian University, Poland*

Evolution of endothermy was a milestone for the success of birds and mammals. However, most endotherms are in fact heterotherms and modulate their body temperature to some extent. While mammals reach very low temperatures during hibernation, in birds the drop in body temperatures is less pronounced but may occur much more frequently. Avian rest-phase hypothermia allows to conserve energy and becomes especially relevant when energy resources are limited and/or environmental conditions are unfavorable. While we know thermoregulation is impaired with increasing age, the effects of senescence on rest-phase hypothermia are still poorly understood. To study the effect of environmental conditions in conjunction with age on facultative rest-phase hypothermia, we exposed zebra finches (*Taeniopygia guttata*) of different ages (1-8 y/o) to a food deprivation period for the last 4 hours before the night in two ambient temperatures (15 and 25˚C). We measured body mass loss and, using a custom-designed experimental setup involving subcutaneous temperature sensing transponders (PIT tags), continuously tracked the birds' body temperature. Both lower ambient temperature and fasting deepened rest-phase hypothermia, and both effects were more pronounced in lighter compared to heavier animals. Older individuals reached lower mean body temperatures at night when fasted, particularly at low ambient temperature. The difference in depth of rest-phase hypothermia between old and young birds manifested only during fasting in 15 ˚C. In conjunction with the body mass effect our data suggests that old birds are more susceptible to resource scarcity when thermal conditions become unfavorable.

BODY TEMPERATURE DURING GESTATION IN FEMALES OF LABORATORY MICE WITH DIFFERENT LEVELS OF BASAL METABOLIC RATE

Paweł Brzęk, Aneta Książek, Sylwia Buczyńska, Marek Konarzewski

Faculy of Biology, University of Białystok, Poland

In mammals, gestation period represents an unique challenge for thermal biology of females. Pregnant females increase the rate of their energy expenditure but at the same time their body temperature must meet demands not only females but also developing fetuses. As a result, body temperature of females can show complex pattern of changes during gestation. In females of laboratory mice, body temperature typically initially increases during pregnancy but then decreases before parturition and is also less variable than in non-pregnant females. However, little is known about the inter-individual variation in body temperature during pregnancy. Here, we studied body temperature of pregnant females of laboratory mice from two lines, selected divergently for either high (H-BMR) or low (L-BMR) level of basal metabolic rate (BMR). Earlier studies revealed that H-BMR females have both higher rate of energy turnover and higher level of parental investment. Initial mean body temperature measured by means of implanted loggers was 0.5 °C higher in H-BMR mice. This difference decreased to ca. 0.3 °C during pregnancy but was still significant. Initial variation of body temperature did not differ between both lines but for most of gestation period body temperature of H-BMR mice was less variable than L-BMR mice. Thus, thermal conditions of developing fetuses vary between individuals with high and low BMR. We discuss potential importance of this difference for the origin of maternal effects and the evolution of endothermy.

IMMUNOLOGICAL RATHER THAN OXIDATIVE STATUS PRIOR TO REPRODUCTION AFFECTS FEMALE DORMICE REPRODUCTIVE OUTPUT

Karolina Iwińska[1], Hanna Kletkiewicz[2], Joanna Błońska[1], Jan S. Boratyński[3]

[1] Doctoral School in Exact and Natural Sciences, University of Białystok, Poland
[2] Faculty of Biological and Veterinary Sciences, Nicolaus Copernicus University in Toruń, Poland
[3] Mammal Research Institute, Polish Academy of Sciences, Białowieża, Poland

Oxidative stress (OS) is not only a direct cost of reproduction, but it can also constrain breeding investments. Studies show equivocal results - OS before reproduction correlates negatively or positively with maternal investments, suggesting that other physiological functions might co-vary with OS and shape female reproductive investments. Here, we tested whether immunology, OS parameters, and markers of aging change during reproduction and whether they determine female reproductive output. Our animal model - edible dormouse spends most of the year hibernating, thus experiencing variation of OS as an effect of rapid increases in metabolism during periodic rewarming. We prevented part of the dormice from torpor use during winter to separate the effects of hibernation and following reproduction. We measured total oxidant and antioxidant status, neutrophil to lymphocyte ratio (N/L), white blood cell level and relative telomere length (RTL) in the blood of female dormice before and after breeding, and lipid peroxidation marker, enzymatic antioxidants, RTL in liver and parasite load *post mortem*. We found increased antioxidant defense and lowered lipid damage in breeders, with no effect of hibernation. However, hibernating females entered reproduction with a lower N/L ratio that did not differ after reproduction. We also found higher parasite loads as a delayed effect of hibernation but not as an effect of reproduction. The N/L before breeding was the only parameter negatively correlated with litter size, suggesting that investments into immune status rather than OS shape life-history traits in this species.

The study was supported by Polish National Science Center (2019/35/O/NZ8/03545).

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

ON THE MOLECULAR EVOLUTION OF FEATHER GRASSES (*STIPA* L., STIPEAE; POACEAE) - WHY DEFINING A GOOD GENETIC MARKER FOR THIS GROUP IS SUCH A CHALLENGE?

Katarzyna Krawczyk

Department of Botany and Nature Protection, University of Warmia and Mazury in Olsztyn, Poland

In studies on the evolutionary history of closely related plant species, the analysis of plastid genome sequence variability is most often used. This is dictated by their abundance in the cell, uniparental inheritance, high level of substitution variability, and conservative structure. However, an in-depth comparative analysis of plastid genomes in *Stipa* L. (Stipeae, Poaceae) showed that the observed level of plastome variability in this genus is very low compared to other Poales and does not allow for a comprehensive picture of the phylogenetic relationships or effective species discrimination, even when whole plastomes are used for this purpose.

Here, we report the advances of our studies to summarize the series of research on the utility of plastid, mitochondrial, and nuclear sequences in reconstructing the phylogeny of feather grasses, as well as in the molecular identification of species and lower taxa from this genus. We characterize mutational hotspots in organellar genomes, report on evolutionary lines with accelerated evolution, evidence of adaptive pressure, the phenomenon of horizontal gene transfer between the plastid and mitochondrial genomes, and the rapid evolution of the nucleolar organizing region. We also discuss the effectiveness of super-barcoding in this closely related group of grasses compared to other representatives of the Poales order. Our studies allowed us to gain a better understanding of the evolutionary processes taking place in feather grasses and therefore propose molecular markers suitable for research on *Stipa* and other representatives of the tribe Stipeae.

REGENERATION IN THE ABSENCE OF CANONICAL NEOBLASTS IN AN EARLY BRANCHING FLATWORM

Ludwik Gąsiorowski[1,2], Chew Chai[3], Andrei Rozanski[1], Gargi Purandare[1], Fruzsina Ficze[1], Athanasia Mizi[4], Bo Wang[3], Jochen C. Rink[1]

[1] *Department of Tissue Dynamics and Regeneration, Max Planck Institute for Multidisciplinary Sciences, Germany*
[2] *Institute of Evolutionary Biology, Faculty of Biology, University of Warsaw, Poland*
[3] *Department of Bioengineering, Stanford University, USA*
[4] *Institute of Pathology, University Medical Centre Göttingen, Germany*

The remarkable regenerative abilities of flatworms are related to the neoblast – a population of ever-dividing adult pluripotent stem cells that show functional and molecular conservation across platyhelminths. Full-body regeneration based on the neoblast-like cells has also been reported in other animals, e.g. acoels and cnidarians, giving reason to believe that these features may represent the ancestral metazoan conditions. Here we show that catenulids, the phylogenetically earliest-branching flatworms, which are capable of full-body regeneration and asexual reproduction, lack the cell type that could be classified as the conventional neoblast. We use a combination of stem cell ablations, bulk, and single-nuclei transcriptomics, and gene expression at the cellular level to uncover the stem cell system of a catenulid *Stenostomum brevipharyngium*. We find out that the cell divisions are not restricted to a single cell type, and some of the differentiated somatic cell types remain division-competent. Moreover, the canonical molecular markers of the neoblast are not expressed in the dividing cells and we experimentally probe that they are not necessary for regeneration. Altogether our results challenge the idea that the canonical neoblast is necessary for regeneration in all flatworms and open the possibility that the neoblast-like cells evolved many times independently in animals regardless of their regenerative abilities.

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

NEST SITE SELECTION IN URBAN BLACKBIRDS – HERITABILITY VS. PLASTICITY

Piotr Minias[1], Marta Cholewa[2], Dariusz Wysocki[3]

- University of Lodz, Faculty of Biology and Environmental Protection, Department of Biodiversity Studies and Bioeducation, Banacha 1/3, 90-237 Lodz, Poland
[2] *University of Wrocław, Faculty of Biological Science, Laboratory of Forest Biology, 50-335 Wrocław, Poland*
[3] *University of Szczecin, Institute of Marine and Environmental Sciences, Szczecin, Poland; University of Szczecin, Molecular Biology and Biotechnology Centre, Szczecin, Poland*

In this study, we explored long-term data on nest site selection by urban European blackbirds *Turdus merula* to decompose phenotypic variation in nest site characteristics into genetic and environmental sources. The analyses revealed negligible additive genetic component in nest site selection traits (location, height, and concealment) and provided no support for maternal effects or natal induction of nest site selection. In contrast, we found evidence for considerable phenotypic variation in nest site selection that was likely driven by extraordinary plasticity of urban blackbirds. We found clear support for plastic modulation of nest site selection patterns with respect to phenology, age, and previous reproductive experience. We also revealed important fitness consequences of nest site selection in urban blackbirds, however these associations were highly complex, reflecting interactive effects of different nest site characteristics on breeding performance. The results indicate that phenotypic plasticity in nest site selection may be constitute a key mechanism responsible for successful persistence of blackbirds in an urban environment.

SPECIES-SPECIFIC STRATEGIES FOR ACOUSTIC SPACE COMPETITION-AVOIDANCE IN BIRDS

Michał Budka, Agata Staniewicz, Emilia Sokolowska, Adrianna Muszyńska

Department of Behavioural Ecology, Faculty of Biology, Adam Mickiewicz University in Poznań, Poland

To communicate effectively, acoustic signals should reach receiver in relatively undisturbed condition. In natural environments, many species and individuals vocalize simultaneously, creating apparent cacophony. In fact, animals use complex strategies to avoid masking and degradation of acoustic signals, which are not fully known and understood.In our study, we experimentally examined how different bird species inhabiting boreal, temperate and tropical forests respond to artificial, unfamiliar acoustic competitors representing various levels of song similarity to their vocalizations. We found various strategies to avoid competition for acoustic space. Some species fell silent during broadcasting sounds overlapping their song frequency and vocalize more intensively in the silent gaps. Other species decreased their singing activity only when broadcasting signals covered their frequency range of vocalization, ignoring other frequency-band noise. We also found the opposite strategy in some species, which consists of increasing singing rate during the playback of acoustic competitors, which is consistent with the signal redundancy hypothesis. Our results suggest that novel sounds can modify birds' singing behaviour, and its effects depend on the similarity of acoustic sound to species vocalization. We also demonstrate that birds have multiple different species-specific strategies for song masking avoidance, including temporal, spectral, or mixed acoustic partitioning.

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

MOVEMENT OF AVIAN PREDATORS IN FARMLAND POINTS TO BIODIVERSITY HOTSPOTS

Paweł Mirski [1,2], Ülo Väli [1,2]

[1] Institute of Agricultural and Environmental Sciences, Estonian University of Life Sciences, Estonia
[2] Faculty of Biology, University of Białystok, Poland

Agricultural landscapes have undergone rapid transformations in the last few decades, leading to a degradation in their quality and a decrease in biodiversity. To preserve farmland biodiversity and support agricultural management that promotes it, we need to better identify biodiversity hotspots and the factors affecting them. Between 2019 and 2021, we GPS-tracked over sixty individuals of four avian predator species inhabiting the agricultural landscape of Estonia. We divided the study area into a 50x50 m grid and counted the number of different individuals and species we followed in each square. This allowed us to identify hotspots of raptor activity and assume that these sites were characterized by high prey abundance and diversity, making them hotspots of general biodiversity. To confirm this assumption, we conducted surveys of birds, small mammals, amphibians, and vascular plants in those hotspots and control sites (within a 500 m radius from hotspots). We found that hotspots of raptor activity were characterized by significantly higher abundance and diversity of all studied prey groups, as well as a more diverse flora. Therefore, the movement of avian predators proved to be a reliable indicator of farmland biodiversity hotspots on a fine scale. Moreover, we confirmed that the same hotspots were still significantly more often visited by the tracked individuals in the next season (but not in two seasons) after they were identified as hotspots. In conclusion, multispecies GPS telemetry of avian predators emerges as an objective, reliable, and spatially accurate biodiversity indicator.

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

INVESTIGATING SHARED MECHANISMS OF PREDATORY AND INTERMALE AGGRESSION IN BANK VOLES

Gokul Bhaskaran[1, 2], Paweł Koteja[1], Edyta T. Sadowska[1]

[1] *Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Poland*
[2] *Doctoral School of Exact and Natural Sciences, Jagiellonian University, Poland*

The question of whether predatory and intermale aggression share control mechanisms is debated and offers insights into the mechanisms of aberrant human aggression. To explore this, we used a unique experimental evolution model consisting of lines of bank voles (*Myodes glareolus*) selected to hunt crickets (Predatory lines) and random-bred lines (Control lines). From each of the four Predatory and four Control lines, 10 males (total 80 males) were sampled across two generations – 36 and 38 (5 males per line in each generation). The focal males underwent multiple cricket hunting tests at various experimental stages (before and after mating) to compare their hunting behaviour. The males were then mated with females, and on the 12th and 14th days after mating, the focal male and a naïve intruder male (from Control lines) were placed together to interact for 20 minutes. Their interaction was videotaped and analysed for the duration and frequency of aggressive behaviours such as boxing, wrestling, chasing, escaping, and other activities. Preliminary results indicate that voles from the Predatory lines had higher prey capture success in all hunting tests and were more aggressive towards intruder males in the intermale tests than those from Control lines. The Predatory voles attacked the intruder more frequently and for longer durations, while Control voles exhibited higher vigilance, spending more time observing the intruder. Therefore, selection for predatory behaviour also elevated intermale aggression suggesting a common genetic basis and the possibility of shared hormonal and neural mechanisms in these two types of aggressive behaviours.

COEVOLUTIONARY INTERPLAY BETWEEN SLAVE-MAKING ANT SPECIES AND ITS HOS

Tomasz Włodarczyk[1], Thomas Schmitt[2]

[1] *Faculty of Biology, University of Białystok, Poland*
[2] *Department of Animal Ecology and Tropical Biology, University of Würzburg, Germany*

Slave-making ant species secure their workforce by stealing developing individuals from host colonies and integrating them into their parasitic society. Some species represent an earlier evolutionary stage in slavery, where the colony can survive without slaves. We studied one such species, *Formica sanguinea*, along with its common host, *Formica fusca*. Our research shows that free-living host ants can recognize parasitic workers and often attempt to eliminate them before their nest is pillaged. This inherited ability poses a potential threat to *F. sanguinea's* use of *F. fusca* ants as slaves, as they might sabotage the parasitic colony. The seemingly seamless coexistence of both species within a single colony implies an efficient mechanism for slave manipulation. We found that *F. sanguinea* ants significantly alter the slaves' recognition odor to resemble their own. This modified odor serves as a signal for nestmate recognition, overriding the host's inherent tendency to perceive ***parasitic workers*** as enemies. Additionally, *F. sanguinea* can employ the alternative strategy of chemical mimicry when their numbers within a colony are too small to exert control over the colony's recognition odor.

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

SHOULD I STAY OR SHOULD I GO? SELECTION AGAINST AND FOR DISPERSAL IN A METAPOPULATION OF A CRITICALLY ENDANGERED BUTTERFLY

Marcin Sielezniew[1,2], Tomasz Jaworski[3], Izabela Sielezniew[2], Krzysztof Deoniziak[1], Cezary Bystrowski[3], Jacek Hilszczański[3] and Piotr Nowicki[4]

[1] *Faculty of Biology, University of Bialystok, Poland*
[2] *Association for Butterfly Conservation, Warsaw, Poland*
[3] *Forest Research Institute, Sękocin Stary, Poland*
[4] *Institute of Environmental Sciences, Jagiellonian University, Poland*

The Danube Clouded Yellow *Colias myrmidone* butterfly has suffered a dramatic decline in Europe, and one of the last metapopulations in the European Union has survived in the eastern part of the Knyszyn Forest (NE Poland), where it is now completely dependent on forestry. We have found that all currently known habitats are forest clear-cuts located mainly on former agricultural land, i.e. mostly on extensively used pastures that were afforested in the 20th century. *Chamaecytisus ruthenicus*, the only local larval food plant of *C. myrmidone*, occurs almost exclusively in first -generation forests. Logging allows the host plants to thrive and the clear-cuts are colonized by the butterfly. In 2017 the total occupied area was only about 10 ha. Mark-release-recapture studies showed that dispersal occurred mostly between neighbouring patches, and isolation of patches contributed to the high mortality of emigrants (ca. 50%). The most distant local population was clearly isolated from the others. In the following years number of available habitat patches increased and the local species range expanded. Subsequent studies conducted in 2022 and 2023 showed that the improved connectivity between habitat patches resulted in a very high proportion of dispersing individuals successfully reaching other patches. At the same time, we found a significant decline in numbers between two years of research, which, however did not affect the species mobility. To our knowledge, this is the first study to document a reversal of selection against dispersal and it demonstrates that such changes can occur relatively quickly, i.e. within a few generations.

Abstracts - Posters

P01. POSITIVE CONSEQUENCES OF ROOST SHARING AMONG MALE BATS DURING SPERMATOGENESIS

Paulina A Szafrańska[1], Ewa Komar[1,2], Dina KN Dechmann[3,4,5], Lara Keicher[3,4], Dominika Koprowska[1], J Ryan Shipley[6], Ireneusz Ruczyński[1].

1 Mammal Research Institute, Polish Academy of Sciences, Poland
2 Faculty of Biology, University of Warsaw, Poland
3 Max Planck Institute of Animal Behavior, Germany
4 Department of Biology, University of Konstanz, Germany
5 Centre for the Advanced Study of Collective Behaviour, University of Konstanz, Germany
6 Swiss Federal Institute for Forest, Snow, and Landscape Research WSL, Switzerland

Energy can be limiting, especially for small animals with high metabolism. They have to develop strategies to compensate for periods of low food availability and/or high energy costs, particularly if they rely on ephemeral resources. Energy-saving strategies involving a lowered metabolism, such as torpor, can impair physiological processes and decrease future reproductive success. Alternatively, group living can reduce energetic costs through social thermoregulation. This may allow individuals to maintain their metabolism high as well as processes such as gamete production. Although this group living is commonly observed, its energetic consequences for heterothermic animals remain unknown, especially during periods of greatly increased expenditure, such as spermatogenesis in male bats. We remotely quantified the daily energy expenditures of individual parti-coloured bats (*Vespertilio murinus*) kept single and in groups during spermatogenesis, using high-resolution heart rate monitoring. Data showed that the energetic benefits of group living are complex. In the group, total individual daily energy expenditures were more than 50% lower. Sociality enabled decreasing intensity but not duration of torpor use. Group living enables bats to buffer unfavorable environmental conditions. Energy saved this way can then be invested into fitness-relevant processes potentially making this a driver of the evolution of male sociality.

P02. EFFECT OF TEMPERATURE FLUCTUATIONS ON LIFE HISTORY TRAITS AND STRATEGIES OF PHYTOPHAGOUS ARTHROPODS - A SYSTEMATIC REVIEW

Gulsamal Askarova[1], Ewa Puchalska[2], Lechosław Kuczyński[1], Anna Skoracka[1]

1 Faculty of Biology, Adam Mickiewicz University, Poland
2 Department of Plant Protection, Warsaw University of Life Sciences, Poland

The effect of temperature on arthropod biology is well understood under constant conditions, but much less so under fluctuating conditions. In the wild, however, arthropods are constantly exposed to daily and seasonal temperature variations. As climate change continues to increase environmental variability, it is crucial to understand how temperature fluctuations affect life history traits, strategies and, consequently population dynamics.

This systematic review aims to explain how temperature fluctuations affect the life history traits and strategies of plant-feeding arthropods. The fitness of these ectotherms depends directly on the ambient temperature, but can also be affected indirectly by temperature changing the quality of their host plants. We conducted a comprehensive literature review by searching Scopus and Web of Science databases. From articles that met our search criteria we extracted information on the aim, subject, and design of the study. We then critically analysed the approaches used to assess the effects of temperature on arthropod traits and strategies, with particular attention to temperature fluctuations.

Our review showed that current knowledge of the effects of temperature fluctuations on phytophagous arthropods is highly limited. We also identified challenges with the approaches and methods used in existing studies. Knowledge of how temperature fluctuations affect the life history traits and strategies of phytophagous arthropods is crucial for understanding their distributions, predicting their outbreaks, and developing effective management strategies needed to maintain ecosystems' functions, especially in the face of global environmental change.

The study was supported by National Science Centre, grant no. 2021/41/B/NZ8/01703.

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

P03. SIZE OF BODY EXTREMITIES IS CORRELATED WITH BASAL METABOLISM IN LABORATORY MICE

Andrzej K. Gębczyński, Julita Sadowska

Faculty of Biology, University of Białystok, Poland

In the face of global warming and climate change, endothermic animals face new challenges, some of which might be associated with their genetically determined metabolic traits (e.g. Basal Metabolic Rate – BMR). BMR, the minimal cost of maintenance of endothermic animals, plays a thermoregulatory role and affects the range of the so-called thermoneutral zone (TNZ).

Results from a unique animal model, mice divergently selected for high (H-BMR) and low (L-BMR) BMR, show that there is a significant shift of TNZ between the two selected line types, however the lack of difference in pelt thermal conductance, and very low differences in body temperature in 23°C are indicative of H-BMR individuals having additional mechanism easing excess heat dissipation. Often greater heat loss can be achieved by increasing body surface including body extremities like the tail, paws (feet), and ears. Morphometric measurements and analyses of RTG images of animals from the selected line types showed that body mass corrected length of the body, tails, ear conchas, and feet were significantly higher in H-BMR. Moreover, the bodies and tails were longer in females, probably due to their high heat dissipation during reproduction. We conclude that a higher level of BMR, which, on the one hand, would enable more effective reproduction, on the other hand, may be biased by difficulties with surplus heat dissipation caused by climate warming if it is not accompanied by more effective cooling mechanisms.

P04. THE EFFECT OF LACTATION ON CAPACITY FOR NON-SHIVERING THERMOGENESIS IN LABORATORY MICE WITH DIFFERENT LEVELS OF BASAL METABOLIC RATE

Piotr Roszkowski, Paweł Brzęk, Aneta Książek, Sylwia Buczyńska, Sebastian Maciak, Marek Konarzewski

Faculty of Biology, University of Białystok, Poland

Lactating females of mammals have high level of energy turnover that results in elevated rate of heat production. As a result, lactating females can downregulate their capacity for dedicated thermogenesis. In rodents, the key role in thermogenesis is played by non-shivering thermogenesis (NST) that relies on UCP1 protein and occurs in brown adipose tissue (BAT). The object of our study were laboratory mice from two lines, selected divergently for either high (H-BMR) or low (L-BMR) level of basal metabolic rate (BMR). L-BMR mice may be expected to possess higher need for dedicated thermogenesis because of lower heat production by BMR. We compared the total amount of UCP1 protein in BAT (an index of capacity for NST) in non-lactating females acclimated to 23 ℃ and in females at the peak of lactation (14 day postparturition), acclimated to either 23 ℃ or 30 ℃. The total UCP1 content was significantly reduced in lactating females but did not depend on ambient temperature during lactation. As predicted, L-BMR females possessed higher total UCP1 content. Interestingly, this effect was independent on lactation, as indicated by non-significant interaction between effects of selection and lactation at both ambient temperatures. Thus, total UCP1 content is significantly affected by divergent selection for BMR also at thermoneutral zone, when thermogenic needs are absent even without lactation. We conclude that our results reveal the key role of variation in BMR in thermal physiology, that sometimes is still significant even when thermogenic needs are removed.

P05. IMMUNOSENESCENCE IN LABORATORY MICE DIVERGENTLY SELECTED FOR BASAL METABOLIC RATE

Sylwia Buczyńska, Aneta Książek, Elżbieta Bonda-Ostaszewska, Sebastian Maciak, Marek Konarzewski

Faculty of Biology, University of Białystok, Poland

According to the rate of living and free-radical hypotheses, a higher metabolic rate is associated with a shorter lifespan. However, it has been documented that aging is also related to the decline of an adaptive immune response, leading to increased susceptibility to infections and shorter life expectancy. This process, called an ‘immunosenescence’, is related to thymus involution, the organ responsible for T-cells maturation. We tested the association between metabolic rate and aging, drawing attention to the loss of thymus function related to the immunosenescence process. As an experimental model, we used males of laboratory mice selected for high or low basal metabolic rate (H-BMR and L-BMR line type, respectively). We assessed immunosenescence rate (expressed as thymus mass changes, thymic T-cell number and immune response) every 2 months in mice between the 18th and 58th weeks of age. In agreement with our predictions, thymus mass decreased with age within both line types but remained higher in the L-BMR males. Histological examinations revealed a progressive reduction in the thymic cortex, diffusely irregular degeneration of the medulla, and accumulation of fatty tissue in the thymuses of aged individuals, similar in both line types. However, maturation of T-cells in thymic tissue was more effective in the aging H-BMR individuals. To detect the ability to develop an adaptive immune response, males were immunized with the KLH (keyhole limpet hemocyanin) antigen. We observed that the H-BMR produced more anti-KLH IgM antibodies than their counterparts. Our results suggest that despite faster thymic atrophy, the H-BMR males maintain a higher pool of naïve T-cells, better insuring them against unknown antigens than the L-BMR individuals.

P06. THE EFFECTS OF SHORT-TERM CONSUMPTION OF A WESTERN DIET ON AEROBIC EXERCISE PERFORMANCE IN ANIMALS WITH INHERENTLY DISTINCT METABOLIC RATES

Alaa Hseiky [1,2], Edyta T. Sadowska[1], Paweł Koteja[1]

1 Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Poland
2 Doctoral School of Exact and Natural Sciences, Jagiellonian University, Poland

Purpose: Several studies have examined the effects of high-sugar or high-fat diets on endurance performance, but the potential benefits of short-term supplementation with Western diet (WD), high in both fat and sugar, have been little studied. We asked whether WD supplementation can improve the performance of animals with inherently distinct aerobic exercise capacity.
Methods: We used bank voles from lines selected for high swim-induced aerobic metabolism (A) and unselected control lines (C). In a cross-over design, we measured endurance running distance, aerobic capacity (VO_2max), peak treadmill speed (Vmax), and respiratory exchange ratio at VO_2max (RER) in 98 animals fed WD or standard diet (SD) two days before the trials.
Results: VO_2max, Vmax, and endurance distance were 38%, 30%, and 70% (respectively) higher in A-lines than in C-lines. In A-lines, endurance distance was correlated with Vmax but not with VO_2max, whereas in C-lines it was more correlated with VO_2max than with Vmax. WD consumption did not affect VO_2max, but tended to decrease Vmax (Least Squares Means ± Confidence Intervals, WD vs. SD: 3.4±0.4km/h vs. 3.7±0.4km/h), endurance distance (1452±303m vs. 1593±303m), mass loss during the trials (1.55±0.1g vs. 1.72±0.1g), and, in A-lines only, RER (0.92±0.02 vs. 0.96±0.02).
Conclusions: This experiment provides a model of genetically distinct aerobically athletic (A-lines) and non-athletic (C-lines) individuals, with different mechanisms limiting performance. Regardless of the genetic background, short-term supplementation does not improve endurance in multi-hour challenges. It may be beneficial in multi-day challenges but reduces the effectiveness of exercise in combating obesity.

P07. THE EFFECTS OF PHOTOPERIOD AND AMBIENT TEMPERATURE ON THE SIZE OF CELLS AND LIPID PEROXIDATION IN TISSUES OF A BANK VOLE (*MYODES GLAREOLUS*)

Bonda-Ostaszewska Elżbieta, Piotrowska-Niczyporuk Alicja

Faculty of Biology, University of Białystok, Poland

The bank vole is a species that undergoes winter body mass reduction. This phenomenon, known as Dehnel's effect, is thought to be a mechanism to offset winter increased energy demands. Our previous research showed that reductions of body and organ mass of bank vole's were the effect of reducing in size of cells under short photoperiod. Because smaller cells are characterized by higher maintenance costs and higher metabolism, in this study we tested dependence between cell size and lipid peroxidation, as an indicator of the intensity of metabolic processes. As the effect of temperature on winter organ mass reduction still remains unknown, we performed analysis under long (LP) and short (SP) photoperiod and ambient temperature 20°C or 5°C (respectively LP-20, SP-20, SP-5, LP-5 groups). The highest body and organs mass loss was observed in SP-20 animals. The research confirmed, that organ mass reduction is the effect of cells size reduction and remains both photoperiod and temperature control. The smallest hepatocytes and nephrocytes were observed in bank vole organs in SP-5 group. The reduction in cells size was accompanied by decrease in lipid peroxidation in both organs. These observations indicate, that decrease in cells size in autumn-winter conditions might to reduce their metabolic activity and, as a result, lead to energy savings at the tissue and organ level. However, elucidation, whether this mechanism could be responsible for energy saving during winter at the individual level requires additional research.

P08. NON-LINEAR EFFECTS OF DIETARY ALCOHOL ON LIFE PARAMETERS IN HONEY BEES

Monika Ostap-Chęć[1,2], Daniel Bajorek[3], Weronika Antoł[3], Daniel Stec[3], Krzysztof Miler[3]

1 Doctoral School of Exact and Natural Sciences, Jagiellonian University, Poland
2 Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Poland
3 Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Poland

Hormesis is a relationship in which a low level of a factor induces the opposite effect of its higher level. For example, many substances are beneficial at certain concentrations but detrimental at higher levels due to organisms' adaptation to typical environmental encounters. Our research investigates whether such a response occurs in honey bees exposed to dietary alcohol. These pollinators are likely adapted to low levels of fermentation products, such as ethanol, in their diet, but suffer negative effects from ethanol overconsumption. We examine bees' body condition and flight parameters under different dietary ethanol regimes and present novel findings on hormesis in bees. This research was supported by the National Science Centre, Poland [grant number: UMO-2021/43/D/NZ8/01044].

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

P09. THE LIFESPAN OF HONEY BEES (*APIS MELLIFERA*) EXPOSED TO OCCASIONAL AND CONSTANT DIETARY ETHANOL

Monika Ostap-Chęć[1,2], Daniel Bajorek[3], Weronika Antoł[3], Daniel Stec[3], Krzysztof Miler[3]

1 Doctoral School of Exact and Natural Sciences, Jagiellonian University, Poland
2 Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Poland
3 Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Poland

Flower nectar and juices of overripe fruits contain ample sugars and low levels of ethanol due to fermentation by yeasts. Thus, within a certain range of concentrations, ethanol is likely a diet component for insect pollinators, such as honey bees. Yet, the effects of repeated intake of low levels of ethanol on bees' survival and physiology remain poorly understood. We aimed to investigate the impacts of occasional and constant consumption of food spiked with low ethanol concentration (1%) on honey bee mortality and the activity of ethanol-degrading enzymes (alcohol dehydrogenase, ADH). To this end, we conducted an experiment in which bees were exposed to three types of long-term diets: constant sugar solution (control group), sugar solution spiked with ethanol every third day (occasional exposure) and daily ethanol consumption (constant exposure). The results revealed that ethanol consumption did not impact the level of ADH in bees, but that its constant and occasional intake leads to increased mortality of bees. However, it takes several days for the toxic ethanol effects to appear. In nature, bees likely die for other reasons before the negative impact of ethanol exposure in their food appears, particularly when this exposure is only occasional. Together with other research, this suggests adaptations to ethanol consumption in bees. Further research in this area is needed to find ecologically relevant levels and frequencies of ethanol exposure in bees as well as their responses to this dietary component. This research was supported by the National Science Centre, Poland [grant number Sonata UMO-2021/43/D/NZ8/01044].

P10. COMBINED EFFECTS OF POLYSTYRENE NANOPLASTICS AND ENROFLOXACIN ON THE LIFE HISTORIES AND GUT MICROBIOTA OF *DAPHNIA MAGNA*

Katarzyna Jarosińska[1], Bartosz Kiersztyn[1], Sebastiano Gozzo[2], Grzegorz Kowalczyk[1], Javier Jimenez-Lamana[2], Joanna Szpunar[2], Joanna Pijanowska[1], Cristina Jines-Muñoz[1], Marcin Lukasz Zebrowski[1], Ewa Babkiewicz[1], Piotr Maszczyk[1]

1 Department of Hydrobiology, Institute of Functional Biology and Ecology, Faculty of Biology, University of Warsaw, Poland
2 IPREM, UMR 5254, E2S UPPA, CNRS, Universite de Pau et des Pays, France

The effects of nanoplastics (NPs) have been shown to interact with contaminants, including antibiotics. However, little is known about the combined effects of NPs and contaminants on freshwater organisms. In this study, we aimed to test the hypothesis that both NPs and antibiotics affect the life history traits of freshwater planktonic *Daphnia magna*, a model organism in ecotoxicological research, as well as the metabolic and taxonomic fingerprint of their gut microbiota, and whether there is an interaction between the effects of the two stressors. To assess this, we experimented with different concentrations of spherical polystyrene nanoplastics and the antibiotic enrofloxacin, measuring (i) Daphnia body size and selected reproductive parameters (clutch size, egg volume and total reproductive investment), (ii) the metabolomic diversity of the gut microbiota (respiration rate and relative use of different carbon sources), and (iii) the microbial taxonomic diversity in the Daphnia gut. Our results supported the hypothesis, as each stressor alone significantly affected most of the measured parameters, and there was a significant interaction between the effects of both stressors on all measured parameters. Therefore, the results suggest an interactive negative effect of the stressors and a possible link between the observed effects at different levels of biological organisation.

P11. STRONG SEXUAL SELECTION REDUCES POPULATION SIZE AND LIMITS POPULATION RECOVERY AFTER HEAT STRESS IN SOIL MITES

Neha Pandey[1], Neelam Porwal[1], Jonathan M. Parrett[1], Robert J. Knell[2], Jacek Radwan[1] and Tom C. Cameron[3]

1 Evolutionary Biology Group, Faculty of Biology, Adam Mickiewicz University, Poznań, Poland.
2 Faculty of science and Engineering, School of Natural Sciences, University of Hull, Hull, United Kingdom.
3 School of Life Sciences, University of Essex, Colchester, United Kingdom.

How populations recover from declines induced by environmental stressors is crucial to conservation biology under global warming. It is possible that this recovery is different in populations facing different levels of sexual selection. The earlier studies which explored the effects of sexual selection on population dynamics have shown both a positive and negative effect. We revisited this effect of sexual selection and its interaction with environmental stress in the soil mite experimental system Sancassania berlesei, which has dimorphic males in the form of fighters, that have exaggerated limbs as weapons, and scramblers that do not have such weaponry. We manipulated the levels of sexual selection concerning intra-male competition shaped by the presence of weaponry, by establishing populations having males of only the fighter type, and thus facing such sexual selection treatment, or only the scrambler type (without such sexual selection treatment). We specifically asked (i) if such sexual selection affects the population size and dynamics before and after a heat spike, (ii) whether such sexual selection has different effects on the dynamics of populations of different sizes, and (iii) if such sexual selection affects growth rate and recovery of populations after a heat spike. We performed a multigenerational experiment on small- and medium-sized populations in the two treatments. When these populations approached equilibrium, we gave them a heat spike to examine their post-stress recovery. We found that the populations containing fighter males (i.e., those facing such sexual selection treatment) maintained an overall lower overall population size than those with scrambler males. The medium-sized scrambler populations were least affected by heat spike, in comparison to others. The fighter treatment showed a lower growth rate under small population size, but had higher growth rate under medium population size after heat stress, as compared to the respective scrambler populations. However, the recovery for fighter populations was slow in both small and medium populations as compared to scrambler populations. Our study shows that sexual selection concerning the presence of male weaponry 1) can reduce population size and growth rates, and that 2) this effect continues after perturbations, slowing the recovery of populations following environmental stress.

P12. EVOLUTION OF FOXP2 AND ZNF362 GENES IN *CERVIDAE*

Justyna Borowska, Maciej Matosiuk, Anetta Borkowska,

Faculty of Biology, University of Bialystok, Poland

The work focuses on understanding evolutionary processes within the cervid family (*Cervidae*), concentrating on two genes encoding transcription factors: FOXP2 and ZNF362. The main objectives of the study were to investigate genetic changes in the sequences of these genes, determining their evolutionary rates and phylogenetic relationships within the cervid family based on analysis of their combined sequences. During the study, parameters for individual exons were checked, such as haplotype (h) and nucleotide (π) diversity, the number of synonymous (M_S) and non-synonymous (M_{NS}) mutations, as well as transitions (T_I) and transversions (T_V). The results obtained indicate significant genetic variability within the FOXP2 gene, especially in exon 5. Despite reports of possible positive selection in the FOXP2 gene in some cervid lines, the performed analysis did not show its effect. The variation study of the ZNF362 gene indicated high conservativity in exon 1. Analysis of the structure of the FOXP2 and ZNF362 genes using InterProScan and ScanProsite tools confirmed the presence of all important domains. In the FOXP2 gene, a significant expansion of the glutamine region was discovered, and in the case of the ZNF362 gene, the position of the C2H2 zinc finger type domains and the location of the KRAB domain were confirmed. Phylogenetic analysis showed a clear division into two subfamilies, *Cervinae* and *Capreolinae*, reflecting evolutionary relationships in the deer family. The obtained nucleotide network shows a topology similar to the phylogenetic tree, but the protein network shows a different arrangement, illustrating the complex evolutionary dynamics of the *Cervidae* species.

P13. MITONUCLEAR COEVOLUTION AND HYBRIDIZATION IN NEWT SPECIES

Joanna Jakóbik[1], Maciej Matosiuk[2], Zuzanna Bujak[1], Maciej Pabijan[1]

1 Institute of Zoology and Biomedical Research, Jagiellonian University, Poland
2 Faculty of Biology, University of Bialystok, Poland

The co-evolution of nuclear (nDNA) and mitochondrial (mtDNA) genomes is crucial and mito-nuclear mismatches may cause serious disruption. Amphibians can be used for testing the influence of co-adaptation on reproductive isolation due to widespread hybridization and mtDNA introgression. We investigated 14 pairs of hybridizing newt species from 3 genera: Ichthyosaura, Lissotriton, and Triturus. For each pair, we analyzed transcriptome-derived sequences to assess sequence divergence (d_{xy}), the ratio of substitution rates at non-synonymous and synonymous sites (dN/dS) and the number of radical amino acid substitutions in 12-13 mitochondrial genes (mt), 119-140 nuclear genes interacting with mtDNA (Nmt) and 161-186 nuclear genes non-interacting with mtDNA (N, control). Expectedly, we found that divergence values in mt genes were highest. Among Nmt genes (5 groups) only nuclear encoded mitochondrial ribosome proteins demonstrated high divergence compared to control. For all other comparisons including genes encoding OXPHOS complexes, we found lower or equal levels of divergence in Nmt and N groups. However, closer investigation of I. a. alpestris - I. a. reiseri with highly diverged mtDNA, T. macedonicus - T. ivanbureshi with partial introgression of mtDNA and L. vulgaris-L. montandoni with complete introgression of mtDNA revealed radical substitutions between many genes in all species pairs. Our results indicate amino acid sequence conservation and strong purifying selection in mt and Nmt genes across species pairs, limiting potential post-hybridization mitonuclear mismatches. On the other hand, we speculate that a few substitutions of large effect in Nmt genes may compensate for high mitochondrial divergence and limit mitochondrial introgression.

P14. GENETIC ANALYSIS OF PROGENY FROM CROSSES BETWEEN DOWNY BIRCH (*BETULA PUBESCENS EHRH.*) AND SHRUB BIRCH (*BETULA HUMILIS SCHRK.*)

Ilona Kulus, Katarzyna Jadwiszczak, Agnieszka Bona

Faculty of Biology, University of Białystok, Poland

Climate change leads to the deterioration of environmental conditions, which increases the likelihood of hybridization between closely related species. When hybrids show higher adaptation compared to the parental taxa, they can displace populations of pure species. One of the endangered plant species in Poland is the shrub birch (*Betula humilis Schrk.*), which is being displaced from its stands by the common tree birches. Artificial pollination of shrub birch with downy birch pollen in the Szuszalewo population (Biebrza National Park) provided 33 individuals from two parental pairs. From 740 seeds, 83 seedlings were received, of which only 33 survived until the genetic material was collected. Genotypes of individuals were determined on the basis of eight nuclear microsatellite DNA loci. Among the progeny, four tetraploid, six triploid and 23 diploid individuals were found. Principal Coordinate Analysis (PCoA) analysis confirmed that most of the progeny are genetically similar to the diploid maternal individuals. The hybrid index analysis conducted using Genodive software revealed that four individuals from the first parental pair had a value below 0.9, while 14 individuals from the second parental pair had a value in the range from 0.238 to 0.899. The low percentage of tri- and tetraploid individuals may be due to the lack of specific alleles in the parental species or pollination with extraneous pollen coming from uknown specimens. The experiment shows that there is no complete reproductive isolation between shrub and downy birch.

P15. CLIMATE- AND SOIL TYPE-DEPENDED OCCURRENCE OF THE *JUNIPERUS SABINA* VARIETIES IN EUROPE

Katarzyna Jadwiszczak[1], Małgorzata Mazur[2], Katarzyna Marcysiak[2], Agnieszka Bona[1], Adam Boratyński[3]

1 Faculty of Biology, University of Białystok, Poland
2 Faculty of Biological Sciences, Kazimierz Wielki University, Poland
3 Institute of Dendrology, Polish Academy of Sciences, Poland

Climate changes occurring on Earth can lead to the fragmentation or disappearance of habitats, ultimately resulting in the extinction of populations and species. Conversely, the shift in species ranges enforced by climate change can lead to hybridisation and the formation of new taxa. One example is *Juniperus sabina L*., a plant whose diversification was impacted by the Tertiary climate drying. In Europe, the species is represented by two varieties: the allotetraploid J. sabina var. balkanensis, of hybrid origin, and its maternal parent *J. sabina var. sabina*. Currently, both varieties of juniper are almost completely geographically isolated.

We analysed the mean annual values of eight climatic parameters (dew/frost point temperature, maximum and minimum air temperatures, surface and profile soil moistures, precipitation, cloudiness, photosynthetically active radiation) from 1983 to 2021, as well as four soil parameters (extractable phosphorus and potassium contents, carbonates content, pH) to examine the factors responsible for the geographic disjunction of the var. sabina and var. balkanensis ranges in Europe. We found that var. balkanensis occurred in habitats with higher temperatures, lower cloud cover, and less precipitation compared to var. sabina. Moreover, the tetraploid variety inhabited soils with significantly higher potassium content than var. sabina. As potassium has been shown to mitigate the harmful effects of water deficit on plants, we hypothesise that the substantially higher potassium concentrations in the var. balkanensis localities help this juniper cope with drought stress. Thus, the balkanensis variety may be resilient, at least to some extent, to the ongoing climate warming.

P16. SHOW ME WHO YOU ARE… EXPRESSION OF AVIAN SEXUAL ORNAMENT ALONG THE URBANIZATION GRADIENT

Amelia Chyb[1], Radosław Włodarczyk[1], Joanna Drzewińska-Chańko[1], Jan Jedlikowski[2], Piotr Minias[1]

1 Faculty of Biology and Environmental Protection, University of Lodz, Poland
2 Faculty of Biology, Biological and Chemical Research Centre, University of Warsaw, Poland

Urbanization may remarkably affect phenotypic characteristics of wild-living animals, including body size and condition. However, there is little information on whether and how urban environment affects visual components of sexual signalling in birds, including non-feather ornaments. Here, we assessed the association between the level of landscape urbanization and the expression of a putative sexual ornament (i.e. frontal shield) in a common waterbird, the Eurasian coot Fulica atra. For this purpose, we measured the shield size of nearly 500 coots from four urban and four nonurban populations across Poland. Most importantly, we found the association between the size of the ornament and urbanization, as urban coots had bigger shields than nonurban individuals. We also found the relationship between the shield size and haemoglobin concentration, which is considered a robust indicator of body condition in birds. Despite the condition-dependent expression of frontal shield, landscape variation in its size could not be entirely attributed to differences in coot condition between urban and nonurban environment. In conclusion, our study provides one of the first evidence for enhanced expression of an avian sexual ornament in an urban landscape.

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

P17. DIFFERENTIATING EFFECTS OF ARTIFICIAL LIGHT AT NIGHT ON THE SPATIAL COMPOSITION OF ZOOPLANKTON COMMUNITIES

Katarzyna Rutkowska, Ewa Babkiewicz, Piotr Maszczyk, Mirosław Ślusarczyk,
Marcin Lukasz Zebrowski, Joanna Tałanda

Faculty of Biology, University of Warsaw, Poland

Several studies have shown that artificial light at night (ALAN) can affect the mutual distribution of different animal taxa in both terrestrial and aquatic communities. However, it remains unclear whether ALAN differentiates the spatial community composition of zooplankton. To fill this gap, we compared the vertical and horizontal distribution of zooplankton in Lake Roś (Masurian Lake District, Poland) at midnight, with and without light from a high-pressure sodium (HPS) lamp mounted on the boat mast, and at midday by collecting stratified samples at different distances from the boat (5, 15 and 30 m). An echosounder was also used to assess the distribution of fish. We found that all zooplankton taxa showed a significant shift towards deeper water layers during the day. However, ALAN affected these taxa in different ways. Some species (such as *Bosmina longirostris*, *Daphnia longispina* and *Chaoborus flavicans*) showed a strong negative response to ALAN even at 30 metres from the boat. Others (such as *D. cucullata*) showed a weaker response, while ALAN had negligible effects on taxa such as *Leptodora kindtii*, *B. coregoni* and copepods even at close range from the boat (5 metres). Whereas in the absence of ALAN the distribution of fish remained uniform during both day and night, the presence of ALAN caused fish to concentrate where light intensity was highest, potentially increasing predation on zooplankton. Therefore, the discrepancy between the effect of daylight and ALAN on the mutual distribution of different zooplankton taxa suggests that ALAN may affect zooplankton community composition.

Research funded by Grant Preludium NSC (No. 2016/21/N/NZ8/00914).

P18. URBAN HABITAT IMPACT ON SKIN MICROBIOME OF COMMON TOAD *BUFO BUFO*

Dawid Żegota, Grzegorz Zięba

Faculty of Biology and Environmental Protection, University of Lodz, Poland

The condition of animals depends on the diversity of their microbiome. Given the undeniable impact of habitat quality on the microbiota, understanding the extent of habitat transformation is crucial for biodiversity conservation. The common toad (*Bufo bufo*), a widespread amphibian species that uses water bodies exclusively for mating, is seen as relatively resilient to habitat deterioration and can therefore serve as a model organism for assessing impact of aquatic habitat transformation on its inhabitants.

Studying the skin microbiome (the layer of the body directly exposed to the external environment and responsible for chemical sensing and cutaneous respiration in amphibians) will allow us to assess the impact of anthropogenic habitat transformation on the protective barrier that is the common toad's microbiome. This, in turn, can serve as a method to assess the status of urban amphibian populations.

The study included several water bodies in the city of Łódź, Poland, ranging from a retention reservoir to recreational ponds and sites of ecological interests, from which skin swabs of mating toads were taken. We assume that as the degree of reservoir transformation increases, the diversity of organisms associated with the skin of toads will decrease.

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

P19. BORN OR RAISED PREDATORS? CROSS-FOSTERING EXPERIMENT ON BANK VOLE SELECTED FOR PREDATORY BEHAVIOUR

Rouba Kiprianos[1], Gokul Bhaskaran[1, 2], Małgorzata M. Lipowska[1], Paweł Koteja[1]
and Edyta T. Sadowska[1]

1 Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Poland
2 Doctoral School of Exact and Natural Sciences, Jagiellonian University, Poland

Predatory behaviour is important not only from ecological and evolutionary, but also from biomedical perspective, due to its plausible relevance to pathological aggression in humans. While the contribution of genotype versus social environment to aggression has been intensively studied in humans, surprisingly little is known about “nature versus nurture” aspects of predatory aggression. One reason for this gap is the limited range of suitable animal models. Here, we combined our unique model of experimental evolution on the bank vole (*Myodes = Clethrionomys glareolus*), including Predatory lines selected for propensity to hunt crickets and random-bred Control lines, with cross-fostering in a “nature versus nurture” scheme to determine the relative contribution of genetic and maternal postnatal environment to predatory behaviour. New-borns were reared by mothers from the same or the other linetypes, and the predatory behaviour of the adult offspring was measured. We asked whether rearing by a Predatory mother enhances the predatory propensity, irrespective of the genetic background of the focal individual. None of the Control voles reared by Control mothers (N=119) caught crickets and only 3% (i.e. 3 of 120 individuals) Control voles reared by Predatory mother caught crickets. Among the Predatory voles reared by either Control or Predatory mothers (N=122 each), about 65% animals caught crickets (73 and 83 individuals, respectively; difference not statistically significant). The foster mother’s linetype did not affect the time to catch cricket, either. Our results suggest that genetic factors are the primary determinants of predatory behaviour, with limited impact from the early maternal environment.

P20. PERINATAL MALNUTRITION IMPAIRS APPETITIVE > AVERSIVE LEARNING

Malgorzata Lagisz[1], Yefeng Yang[1], Joanna Rutkowska[2], Katie Hector[3], Michael Colombo[4], Shinichi Nakagawa[1]

1 Evolution & Ecology Research Centre, School of Biological and Environmental Sciences, University of New South Wales, Australia
2 Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Poland
3 Department of Zoology, Otago University, New Zealand
4 Department of Psychology, Otago University, New Zealand

Sub-optimal maternal nutrition during perinatal development of her offspring can affect brain development and cognitive functions in later life in mammals. However, we understand very little about the causes of variation among experimental studies which investigated the effects of maternal dietary restriction on offspring learning abilities. To address this gap, we investigated behavioral measures of cognition following inadequate nutrition during gestation and/or lactation in rats. Via meta-analysis on the rodent literature using data from 88 papers (455 effect sizes), we tested an evolutionary hypothesis that when resources are restricted, learning abilities crucial for offspring survival should be less impacted than those of lesser importance. In line with this hypothesis, we show that maternal dietary restriction (caloric restriction and protein restriction) indeed negatively affected offspring cognition, but less so than physical size. Furthermore, by analyzing the different types of behavioral tests used to measure cognition, we found that appetitive learning was more severely impaired than aversive learning. Our meta-analysis not only clarifies the inconsistency among the relevant experiments, but also clearly supports the evolutionary hypothesis that has previously been neglected. Further, our finding supports the claim that aversive and appetitive learning paradigms have different mechanisms and also suggests that different evolutionary selection pressure has shaped these two types of learning.

P21. CAN ELEVATED TEMPERATURE ENHANCE TASK PERFORMANCE BY IMPROVING COGNITIVE ABILITIES IN COMMON RUDD (*SCARDINIUS ERYTHROPHTHALMUS*)?

Monika Sysiak, Ewa Babkiewicz, Marcin Lukasz Zebrowski, Katarzyna
Rutkowska, Piotr Maszczyk

Institute of Functional Biology and Ecology, Faculty of Biology, University of Warsaw, Poland

The effect of a given factor on an animal's task performance results from its combined effects on cognitive ability and mobility. Although several studies have examined the effect of temperature on task performance in ectotherms, it remains unclear how much of this effect is due to changes in mobility versus cognitive ability. It is also unclear whether the relationship between thermal sensitivity of mobility and cognitive ability changes with individual experience and task difficulty. We addressed these questions through experiments with groups of fish (*Scardinius erythrophthalmus*) foraging for a food reward at one of two temperatures (16°C and 23°C) in consecutive daily sessions under six scenarios of varying task difficulty, a combination of three different distances to the food reward, and the presence or absence of experienced individuals familiar with the reward location. The results showed that task performance was 3-4 times higher at the high temperature in the first session, increased further between sessions 2 and 4, and then declined sharply to a level 2 times higher than at the low temperature in the remaining sessions. The thermal sensitivity of task performance was greater when the task was more difficult. In contrast, the average speed of the fish only doubled at the higher temperature, and this relationship remained constant over subsequent sessions, regardless of task difficulty. The difference in thermal sensitivity between task performance and swimming speed suggests that improved task performance at elevated temperatures is not solely due to increased speed, but also to enhanced cognitive abilities.

P22. GREAT TITS, AROMATIC PLANTS & NEST ECTOPARASITE ABUNDANCE

Michał Glądalski, Maciej Bartos, Adam Kaliński, Marcin Markowski,
Joanna Skwarska, Jarosław Wawrzyniak, Iwona Demeško, Jerzy Bańbura

Faculty of Biology and Environmental Protection, University of Lodz, Poland

Blue tits *Cyanistes caeruleus* and great tits *Parus major* are two of a very few known passerine bird species that incorporate aromatic plant fragments into their nests during the breeding period. The ‘nest protection hypothesis’ assumes that some birds may add aromatic plants into their nests to repel or kill ectoparasites. In the present study, we experimentally tested whether aromatic plant fragments (lavender *Lavandula angustifolia*, mint *Mentha sp.*, Italian strawflower *Helichrysum italicum* and common yarrow *Achillea millefolium*) added into great tit nests affected the abundance of arthropod ectoparasites. The numbers of ectoparasites were high in both, treated and control nests. Only ticks (*Ixodidae*) were affected by the treatment and occurred less frequently in the nests with aromatic plant fragments added. Present study may suggest that the behavior of adding aromatic plant materials by parents into their nests could have a positive impact on birds fitness.

P23. LANDSCAPE OF FEAR ON A PASTURE LAND - IS WHITE STORK A SCAREBIRD FOR GRASSHOPPERS?

Adam Zbyryt[1], Paweł Brzęk[2], Łukasz Jankowiak[3]

1 Doctoral School of Exact and Natural Sciences, University of Bialystok, Poland
2 Faculty of Biology, University of Białystok, Poland
3 University of Szczecin, Poland

Studies of interactions between predators and their prey provide a valuable insight into the processes that shape the population dynamics, structure of ecosystems, or distribution of animals. The concept of the 'landscape of fear' proposes that the perceived risk of predation can affect behaviour and spatial distribution of prey. It has been showed that the presence of invertebrate predators like spiders can affect behaviour of grasshoppers. However, sometimes the difference in size between predator and prey can be more dramatic: for example, White Stork (*Ciconia ciconia*) is an important predator of invertebrates including grasshoppers in different open habitats. We checked if grasshoppers can recognize the presence of White Stork as a potential threat. Our experiment was carried out in northeastern Poland. On 66 pastures, we compared the number of grasshoppers caught using a sweep net near a stuffed white stork, near a displayed pine branch of the size comparable to the stork, near grazing cow, or at a random point. The number of grasshoppers caught near stuffed White Stork was significantly lower than at any other site type. We conclude that grasshoppers can recognize the silhouette of a White Stork as a threat and adjust their behaviour accordingly whereas they are not afraid of neutral novel objects like tree branch.

P24. DISTRIBUTION OF TARDIGRADE CRYPTOBIOTIC ABILITIES ACROSS A FINE-SCALE HABITAT GRADIENT

Daniel Stec[1], Matteo Vecchi[1], Krystian Budzik[1], Yelyzaveta Matsko[1,2],
Krzysztof Miler[1]

1 Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Poland
2 Institute of Biology, Biotechnology and Environmental Protection, Faculty of Natural Sciences, University of Silesia, Poland

Cryptobiotic organisms, capable of surviving extreme arid and cold environments, also thrive in less extreme habitats subjected to varying frequencies of desiccation and freezing. Here, we examine the distribution of desiccation and freezing tolerance in tardigrade communities across a fine-scale habitat gradient in a forest (from the forest edge with a desert to the forest centre). Our study demonstrates no correlation between anhydrobiotic and cryobiotic abilities in tardigrades at the community level. Our results also show a higher cryptobiotic performance in tardigrade communities inhabiting the forest centre. The observed distribution pattern of cryptobiotic abilities cannot be explained by different community compositions or differences in body sizes, as both these variables are uniform across the studied habitat gradient. However, tardigrades from the forest centre are characterised by better conditions expressed as slower mortality rates during fasting. This suggests that tardigrade communities at the forest edge have lower energy reserves, possibly due to their higher exposure to cryptobiotic events that deplete their resources. Overall, our study sheds light on the functional characteristics underlying the distribution of tardigrades and highlights the significance of environmental factors in shaping cryptobiotic responses in meiofauna communities. This research was supported by the National Science Centre, Poland [grant number Sonatina 2022/44/C/NZ8/00050].

P25. DIVERSITY OF COLORATION PATTERNS IN TURTLES (ORDER *TESTUDINES*)

Helena Szewczyk, Alejandro Ibáñez

Faculty of Biology and Environmental Protection, University of Lodz, Poland

Turtles (order *Testudines*) are a group of reptiles with a well-developed visual system. As other animals do, turtles display a wide variety of markings and colors all over their bodies. Their coloration has a very important role in survival through camouflage, which allows them to stay hidden from the eyes of predators. However, turtles can also display striking and bright markings made up of pigments such as carotenoids. Due to the costs of maintaining vivid coloration, markings serve as honest signals of the animal's health, success in finding proper nutrients and, in some cases, their sex. In order to further analyze the importance of markings and coloration, we gathered over 700 verified photos of 292 species of turtles from websites such as INaturalist.org and ReptileDatabase.com. Through categorizing the markings based on their locations (head and shell) and their color, it was possible to pinpoint the most common markings displayed by turtles. Thanks to the data provided by other publicized research, it was possible to additionally gather data on sexual size dimorphism (SSD) for a subset of the species. Statistical tests revealed a connection between striped head markings and the SSD. Species with stripes had female-biased SSD (e.g. males were smaller than females) suggesting an important role of head coloration in turtle sexual selection processes. A potential explanation is that species with relatively small males use colorful marks during nuptial courtship instead of engaging on aggressive behaviors or forced inseminations.

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

|Our conference is supported by:

The Company of Biologists

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

Sponsors

Silver

Novogene

BIESZCZADZKA WYTWÓRNIA PIWA
URSA MAIOR

Bronze

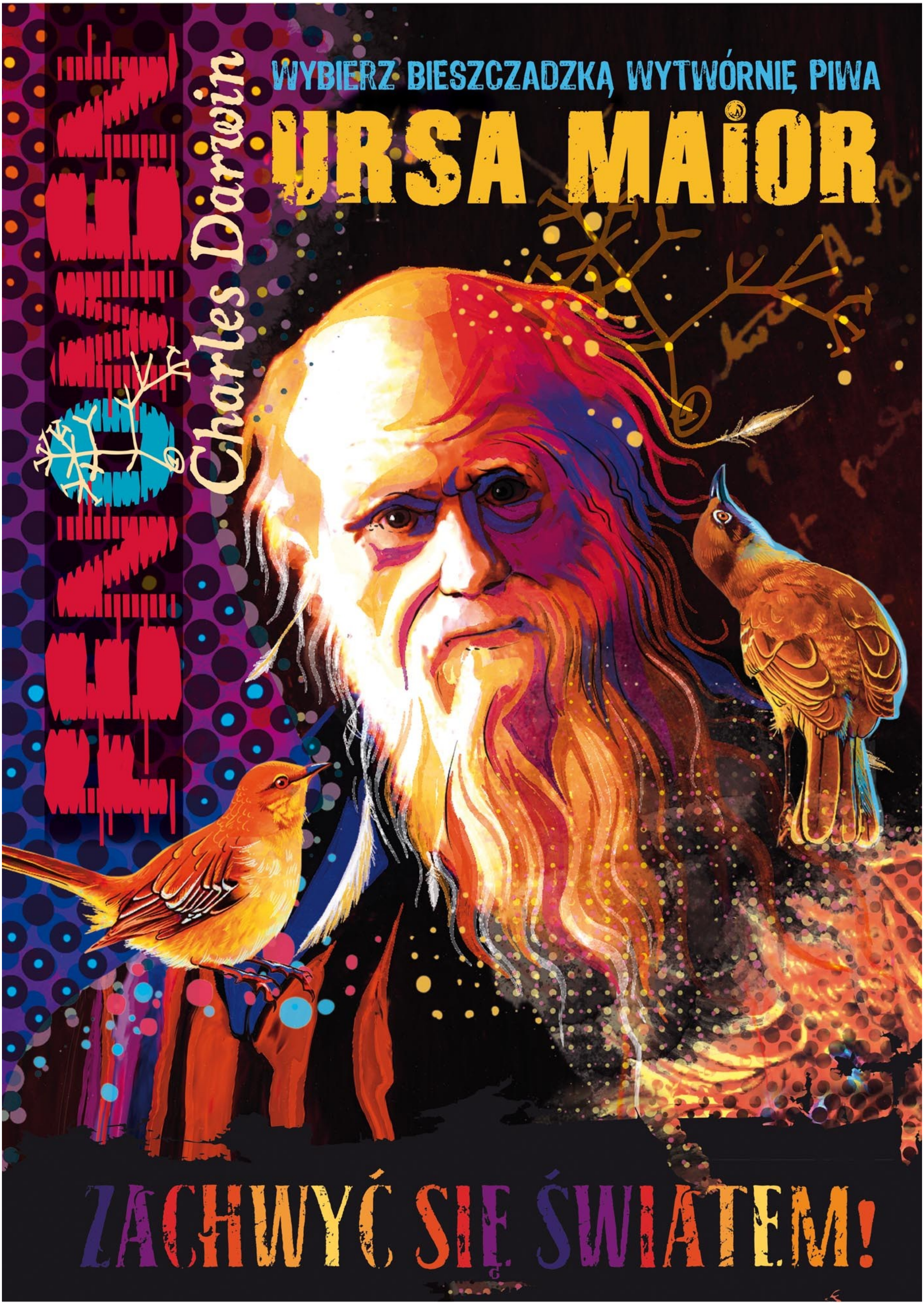
pyroscience
sensor technology

Journal of
Experimental Biology

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afternoon
Posters

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afternoon
Posters



Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters

Wednesday
Thursday Morning
Thursday Afternoon
Friday Morning
Friday Afernoon
Posters