



POLISH EVOLUTIONARY CONFERENCE

The 9<sup>th</sup> Polish Evolutionary Conference

18-20 September 2023

Kraków, Poland

**PROGRAM & ABSTRACT BOOK**



JAGIELLONIAN UNIVERSITY  
IN KRAKÓW



POLISH ACADEMY of SCIENCES

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- The Committee of Environmental & Evolutionary Biology of the Polish Academy of Sciences (PAN)

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- dr Agata Plesnar-Bielak, Jagiellonian University in Kraków
- prof. dr hab. Joanna Rutkowska, Jagiellonian University in Kraków (member of KBŚiE PAN)
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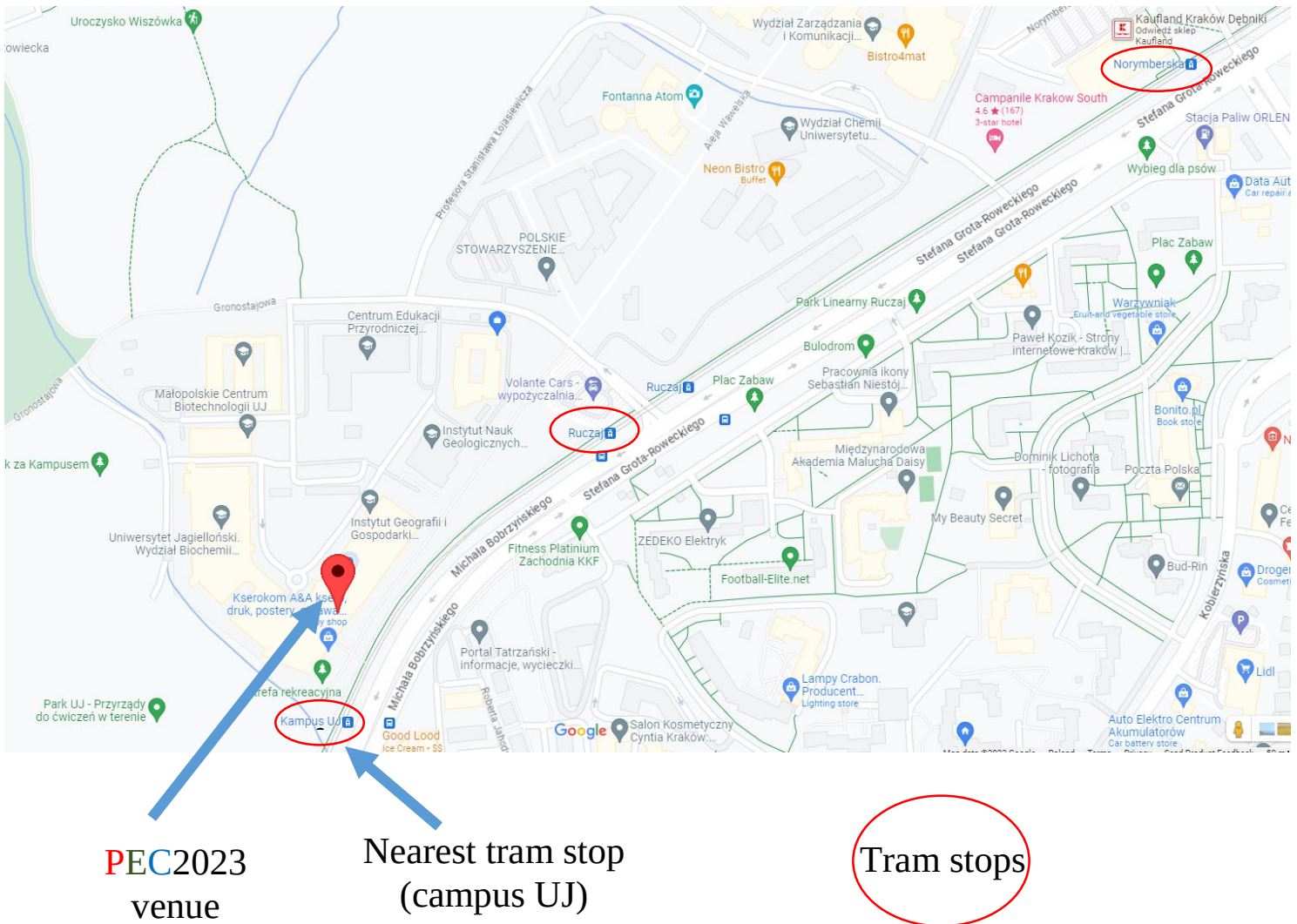
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## Conference location

Institute of Environmental Sciences  
Faculty of Biology  
Jagiellonian University  
Gronostajowa 7, 30-387 Kraków

Access map *here*



Tram numbers 11, 17, 18 and 52 will pass through Campus UJ tram stop.

From Kraków Main train Station (Kraków Główny) or the city center, any of the trams identified before with the direction “Czerwone Maki P+R” takes you to the conference venue.

# Detailed Schedule

Click on the Authors' names to go to their abstracts

| 18th September 2023 (Monday) |                                                                         |                                                                                                                                                      |
|------------------------------|-------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12:00-14:00                  | <b>Registration</b>                                                     |                                                                                                                                                      |
| 14:00-14:30                  | <b>Opening ceremony with the awarding of the Ludwik Tomiałojć Medal</b> |                                                                                                                                                      |
| <b>session:</b>              | <b>Making evolution happen</b>                                          |                                                                                                                                                      |
| <b>organizers:</b>           | <i>Ryszard Korona &amp; Paweł Koteja</i>                                |                                                                                                                                                      |
| <b>Plenary lecture 1</b>     | <i>chair: Ryszard Korona</i>                                            |                                                                                                                                                      |
| 14:30-15:30                  | <b>Richard Lenski</b>                                                   | Dynamics and Repeatability of Evolution in a Long-Term Experiment with Bacteria                                                                      |
| 15:30-16:00                  | <b>Coffee break</b>                                                     |                                                                                                                                                      |
| <b>Contributed talks</b>     | <i>chairs: Ryszard Korona &amp; Paweł Koteja</i>                        |                                                                                                                                                      |
| 16:00-16:15                  | <b>Szymon Kaczanowski</b>                                               | Adaptations in yeast short-term evolutionary experiments are mainly a result of the appearance of loss-of-function mutations (CT01)                  |
| 16:15-16:30                  | <b>Weronika Antol</b>                                                   | Experimental evolution of reproductive traits in <i>Caenorhabditis elegans</i> (CT02)                                                                |
| 16:30-16:45                  | <b>Pranav Unnikrishnan</b>                                              | Testing for the mechanisms of balancing selection maintaining 6Pgdh polymorphism in bulb mites (CT03)                                                |
| 16:45-17:00                  | <b>Neha Pandey</b>                                                      | Density-dependent selection at low food levels leads to the evolution of population stability even without a clear r-K trade-off (CT04)              |
| 17:00-17:15                  | <b>Paweł Brzęk</b>                                                      | The correlation between intraspecific variation in basal metabolic rate (BMR) and in body temperature: are mice selected for high BMR hotter? (CT05) |
| 17:15-17:30                  | <b>Paweł Koteja</b>                                                     | The molecular background of experimental evolution of physiology and behavior in the bank vole: changes in SNP allele frequencies (CT06)             |
| 17:30-19:00                  | <b>Welcome Reception</b>                                                |                                                                                                                                                      |

# Detailed Schedule

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| 19th September 2023 (Tuesday) |                                                                                   |                                                                                                                                                            |
|-------------------------------|-----------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 08:00-9:00                    | <b>Registration</b>                                                               |                                                                                                                                                            |
| <b>session:</b>               | <b>Effects of thermal and oxygen conditions on ectotherms in a changing world</b> |                                                                                                                                                            |
| <b>organizer:</b>             | <i>Marcin Czarnołęski</i>                                                         |                                                                                                                                                            |
| <b>Plenary lecture 2</b>      | <i>chair: Marcin Czarnołęski</i>                                                  |                                                                                                                                                            |
| 9:00-10:00                    | <b>Wilco Verberk</b>                                                              | The role of cell size in shaping responses to oxygen and temperature in ectotherms                                                                         |
| 10:00-10:30                   | <b>Coffee break</b>                                                               |                                                                                                                                                            |
| <b>Contributed talks</b>      | <i>chair: Adam Hermaniuk</i>                                                      |                                                                                                                                                            |
| 10:30-10:45                   | <b>Ewa Chrostek</b>                                                               | Wolbachia-Conferred Antiviral Protection Is Determined by Insect's Developmental Temperature (CT07)                                                        |
| 10:45-11:00                   | <b>Ewa Babkiewicz</b>                                                             | Uncovering the secrets of interactions between temperature, hypoxia, and competing <i>Daphnia species</i> (CT08)                                           |
| 11:00-11:15                   | <b>Piotr Dawidowicz</b>                                                           | Effects of food quality and water temperature on the fitness of species of <i>Daphnia</i> that differ in body size (CT09)                                  |
| 11:15-11:30                   | <b>Aleksandra Walczyńska</b>                                                      | Ten years of studies on the effect of temperature and oxygen on phenotypic plasticity of body size in rotifers (CT10)                                      |
| 11:30-11:45                   | <b>Piotr Maszczyk</b>                                                             | Mechanisms of increasing predation by planktivorous fish with rising temperature may explain the temperature-body size relationships in zooplankton (CT11) |
| 11:45-12:00                   | <b>Marcin Czarnołęski</b>                                                         | Cellularity of life history strategies in the face of oxygen and thermal gradients - a synthesis of concepts (CT12)                                        |
| 12:00-12:15                   | <b>BGI - sponsor talk</b>                                                         |                                                                                                                                                            |
| 12:15-13:15                   | <b>Lunch break</b>                                                                |                                                                                                                                                            |

# Detailed Schedule

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|                          |                                                                              |                                                                                                                           |
|--------------------------|------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------|
| <b>session:</b>          | <b>Poster Session</b>                                                        |                                                                                                                           |
| 13:15-13:55              | one-minute presentations of posters; chair: Ulf Bauchinger                   |                                                                                                                           |
| 13:55-14:55              | poster session 1 - odd numbers                                               |                                                                                                                           |
| 14:55-15:55              | poster session 2 - even numbers                                              |                                                                                                                           |
| 15:55-16:00              | <b>Short break</b>                                                           |                                                                                                                           |
| <b>session:</b>          | <b>Global Environmental Issues in Comparative Studies</b>                    |                                                                                                                           |
| <b>organizer:</b>        | Joanna Rutkowska                                                             |                                                                                                                           |
| <b>Plenary lecture 3</b> | chair: Joanna Rutkowska                                                      |                                                                                                                           |
| 16:00-17:00              | <b>Carlos Botero</b>                                                         | Climate change, fluctuating selection and eco-evolutionary dynamics                                                       |
| <b>Contributed talks</b> | chair: Aneta Arct                                                            |                                                                                                                           |
| 17:00-17:15              | <b>Piotr Minias</b>                                                          | Reproductive strategies in a changing environment – what drives the evolution of ground nesting in passerine birds (CT13) |
| 17:15-17:30              | <b>Szymon Drobnik</b>                                                        | Coral diseases in a warming world - meta-analysis and systematic map (CT14)                                               |
| 17:30-17:45              | <b>Tomasz Gaczorek</b>                                                       | The adaptive introgression of MHC genes in multiple vertebrate taxa (CT15)                                                |
| 17:45-18:00              | <b>Magdalena Niedziałkowska</b>                                              | Response of the European ungulate species to global environmental changes (CT16)                                          |
| 18:00-18:15              | <b>Jan Kozłowski</b>                                                         | Can life history theory save overexploited fish populations? (CT17)                                                       |
| 18:15-18:30              | <b>Piotr Łukasik</b>                                                         | Surveying microbial symbionts' roles in insect adaptation and response to the challenges of the Anthropocene (CT18)       |
| 19:00-21:00              | <b>Gala Dinner in Nature Education Center of the Jagiellonian University</b> |                                                                                                                           |

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| 20th September 2023 (Wednesday) |                                                                    |                                                                                                                                              |
|---------------------------------|--------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------|
| 08:00-9:00                      | <b>Registration</b>                                                |                                                                                                                                              |
| <b>session:</b>                 | <b>Ecology and evolution of microbes and microbial communities</b> |                                                                                                                                              |
| <b>organizer:</b>               | <i>Dominika Włoch-Salamon</i>                                      |                                                                                                                                              |
| <b>Plenary lecture 4</b>        | <i>chair: Dominika Włoch-Salamon</i>                               |                                                                                                                                              |
| 9:00-10:00                      | <b><i>Julia Pawłowska</i></b>                                      | No fungus is an island: how endohyphal bacteria may affect the fitness of their fungal hosts?                                                |
| 10:00-10:30                     | <b>Coffee break</b>                                                |                                                                                                                                              |
| <b>Contributed talks</b>        | <i>chairs: Hanna Tutaj &amp; Dominika Włoch-Salamon</i>            |                                                                                                                                              |
| 10:30-10:45                     | <b><i>Rafał Mostowy</i></b>                                        | Exploring the Coevolution of Bacteria and Phages: Insights from Studying Receptor-Binding Proteins and Polysaccharides (CT19)                |
| 10:45-11:00                     | <b><i>Bogna Smug</i></b>                                           | How phages play with LEGO: studying protein-level mosaicism in phages and its evolutionary implications (CT20)                               |
| 11:00-11:15                     | <b><i>Przemysław Gagat</i></b>                                     | Exploring the Relationship between Targeting Peptides and Antimicrobial Peptides: Insights into Evolution and Functional Implications (CT21) |
| 11:15-11:30                     | <b><i>Dawid Gmitter</i></b>                                        | Phylogeny and pan-genome of <i>Proteus mirabilis</i> : with the focus on type VI secretion system effectors diversity (CT22)                 |
| 11:30-11:45                     | <b><i>Junchen Deng</i></b>                                         | The breakdown of an ancient obligatory endosymbiont in a clade of planthoppers (CT23)                                                        |
| 11:45-12:00                     | <b><i>Filip Pietluch</i></b>                                       | New Insights into the Evolution of Complex Plastids: Unveiling the Origins and Diversification Times of Red Alga-Derived Lineages (CT24)     |
| 12:00-13:00                     | <b>Lunch break</b>                                                 |                                                                                                                                              |

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|                          |                                                                 |                                                                                                                                              |
|--------------------------|-----------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------|
| <b>session:</b>          | <b>Open: Evolution and Ecology</b>                              |                                                                                                                                              |
| <b>Organizers :</b>      | <i>Agata Plesnar-Bielak &amp; Aleksandra Walczyńska</i>         |                                                                                                                                              |
| <b>Contributed talks</b> | <i>chairs: Agata Plesnar-Bielak &amp; Aleksandra Walczyńska</i> |                                                                                                                                              |
| 13:00-13:15              | <b>Magdalena Herdegen-Radwan</b>                                | Can female guppies learn to like male colours? (CT25)                                                                                        |
| 13:15-13:30              | <b>ChuChu Lu</b>                                                | The Impact of Temperature Variability on Physiological Responses and Learning in Zebra Finches (CT26)                                        |
| 13:30-13:45              | <b>Tomasz Osiejuk</b>                                           | Response of African forest Turtur doves to conspecific and congeneric songs in sympatry and allopatry (CT27)                                 |
| 13:45-14:00              | <b>Hedvig Csapo</b>                                             | Arctic Atlantification: For how long has it been going on? A population genomic case study of the northern acorn barnacle on Svalbard (CT28) |
| 14:00-14:15              | <b>Brandon Meter</b>                                            | Development of sexual size dimorphism in lizards: The probable role of IGF1 (CT29)                                                           |
| 14:15-14:30              | <b>Julia Morales-Garcia</b>                                     | High-throughput sequencing unravels the hidden diversity of bark beetle-associated nematodes (CT30)                                          |
| 14:30-14:45              | <b>Paulina Celebias</b>                                         | How the intraspecific variation in granivores impacts seed dispersal? (CT31)                                                                 |
| 14:45-15:15              | <b>Coffee break</b>                                             |                                                                                                                                              |
| 15:15-15:30              | <b>Michael Angilletta</b>                                       | Using virtual reality to teach undergraduate students to conduct research in ecology and evolution (CT32)                                    |
| 15:30-15:45              | <b>Karol Walach</b>                                             | Where do thee come from? – Time-calibrated phylogeography of the <i>Nearctic Milnesium</i> (Tardigrada) (CT33)                               |
| 15:45-16:00              | <b>Roya Adavoudi</b>                                            | Detection of grey wolf and golden jackal hybridization with free ranging domestic dogs across Eurasia using SNP markers (CT34)               |
| 16:00-16:15              | <b>Viktor Kovalov</b>                                           | Immunity investment does not drop down if you tolerate infection and reproduce after infection (CT35)                                        |
| 16:15-16:30              | <b>Witold Wachowiak</b>                                         | Genomic insights into population history of Scots pine ( <i>P. sylvestris</i> L.) (CT36)                                                     |
| 16:30-17:00              | <b>Awards presentation and closing ceremony</b>                 |                                                                                                                                              |

# Poster Titles

*Click on the Authors' names to view their abstracts*

|     |                                      |                                                                                                                                         |                                                             |
|-----|--------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------|
| P01 | <b><i>Hanna Tutaj</i></b>            | The outstanding effect of positive epistasis on fitness in monosomic yeast strains                                                      | Open: Evolution and Ecology                                 |
| P02 | <b><i>Adrian Piróg</i></b>           | Complex genome rearrangements in the model eukaryotic organism <i>Saccharomyces cerevisiae</i>                                          | Making evolution happen                                     |
| P03 | <b><i>Monika Opalek</i></b>          | How is quiescence studied in <i>S. cerevisiae</i> ? A systematic review                                                                 | Ecology and evolution of microbes and microbial communities |
| P04 | <b><i>Konrad Miazga</i></b>          | Evolution of simulated 3D organisms                                                                                                     | Making evolution happen                                     |
| P05 | <b><i>Szymon Ptak</i></b>            | The use of computer simulations in the study of evolution                                                                               | Making evolution happen                                     |
| P06 | <b><i>Krzysztof Argasinski</i></b>   | r and K selection concept versus recruitment lotteries. Do we have laws of evolution or rather mechanisms?                              | Open: Evolution and Ecology                                 |
| P07 | <b><i>Karolina Iwińska</i></b>       | Oxidative stress correlates with immunocompetence in breeding females of wild long-living mammal - edible dormouse <i>Glis glis</i>     | Making evolution happen                                     |
| P08 | <b><i>Andrzej K Gebczynski</i></b>   | Turning up the heat: the effect of shifts in the thermoneutral zone of mice on the outcomes of translational research                   | Making evolution happen                                     |
| P09 | <b><i>Alaa Hseiky</i></b>            | Testing the thrifty and spendthrift genotype hypotheses: The experimental evolution and the “nature – nurture” experiment on bank voles | Making evolution happen                                     |
| P10 | <b><i>Alaa Hseiky</i></b>            | The effect of Western Diet on the liver metabolome: a pilot experiment based on an artificial selection experiment on bank voles        | Making evolution happen                                     |
| P11 | <b><i>Alaa Hseiky</i></b>            | Are food dyes good or bad? Studying the effects of turmeric on fruit flies' development.                                                | Open: Evolution and Ecology                                 |
| P12 | <b><i>Rouba Kiprianos</i></b>        | Food or thrill of the hunt: food preferences in bank voles selected for predatory behavior                                              | Making evolution happen                                     |
| P13 | <b><i>Małgorzata M. Lipowska</i></b> | Testing the hologenome concept: a cohabitation experiment on bank voles from a selection experiment                                     | Making evolution happen                                     |

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|     |                                 |                                                                                                                                                                    |                                                                            |
|-----|---------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------|
| P14 | <b><i>Gokul Bhaskaran</i></b>   | Correlated responses to artificial selection for predatory propensity in the bank vole: hunting skills and coping with stress                                      | Making evolution happen                                                    |
| P15 | <b><i>Anna Sanetra</i></b>      | Restricted nighttime feeding prevents the high-fat diet-evoked disruption of the hypothalamic circadian clock                                                      | Open: Evolution and Ecology                                                |
| P16 | <b><i>Joanna Palka</i></b>      | The effects of calorie restriction on microbiota of bank voles with high evolved metabolic capacity                                                                | Ecology and evolution of microbes and microbial communities                |
| P17 | <b><i>Agata Burzawa</i></b>     | How do optimal and suboptimal temperatures affect mitochondrial bioenergetics of rotifers <i>Lecane inermis</i> ?                                                  | Effects of thermal and oxygen conditions on ectotherms in a changing world |
| P18 | <b><i>Katarzyna Kilian</i></b>  | When temperature makes them panic – the effect of optimal and stressful thermal conditions on variability of life history traits in <i>Lecane inermis</i> rotifer. | Effects of thermal and oxygen conditions on ectotherms in a changing world |
| P19 | <b><i>Gulsamal Askarova</i></b> | How does evolution in a stable or fluctuating environment shape the niche breadth of a plant-feeding arthropod?                                                    | Making evolution happen                                                    |
| P20 | <b><i>Anna Spaeth</i></b>       | Temperature effect on the association between sperm production and 6Pgdh genotype in bulb mite males.                                                              | Effects of thermal and oxygen conditions on ectotherms in a changing world |
| P21 | <b><i>Tomasz Brzeziński</i></b> | Food thresholds in <i>Daphnia</i> – the effects of food quality, temperature and body size.                                                                        | Effects of thermal and oxygen conditions on ectotherms in a changing world |
| P22 | <b><i>Zhanna Buseva</i></b>     | Temperature and food quality as drivers of competition among differently sized <i>Daphnia</i> species                                                              | Global Environmental Issues in Comparative Studies                         |
| P23 | <b><i>Anna Bednarska</i></b>    | Threshold Food Concentration (TFC) as a predictor of the outcome of intraspecific competition in <i>Daphnia magna</i> , exposed to different quality diets.        | Open: Evolution and Ecology                                                |

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|     |                                  |                                                                                                                                                     |                                                                            |
|-----|----------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------|
| P24 | <b><i>Irina Feniova</i></b>      | Effects of food phosphorus contents on competitive interactions between large and small-bodied <i>Daphnia</i> species                               | Global Environmental Issues in Comparative Studies                         |
| P25 | <b><i>Zuzana Starostová</i></b>  | Metabolic scaling is unaffected by habitat aridity in geckos                                                                                        | Effects of thermal and oxygen conditions on ectotherms in a changing world |
| P26 | <b><i>Ewa Szlachcic</i></b>      | Systemic orchestration of cell size throughout the body: evolutionary and developmental responses of <i>Drosophila melanogaster</i> to environments | Effects of thermal and oxygen conditions on ectotherms in a changing world |
| P27 | <b><i>Agnieszka Gudowska</i></b> | Living with heat: Unveiling the impact of simulated heat waves of the life story on two pollinators: <i>Osmia bicornis</i> and <i>O. cornuta</i>    | Open: Evolution and Ecology                                                |
| P28 | <b><i>Guillaume Wos</i></b>      | Phenotypic and gene expression differences in coping with temperature and an invasive alien predator along a latitudinal gradient in damselflies    | Effects of thermal and oxygen conditions on ectotherms in a changing world |
| P29 | <b><i>Julita Sadowska</i></b>    | Microbial Nitrogen Recycling is Higher in Arctic Ground Squirrels Hibernating at Warmer Temperatures                                                | Open: Evolution and Ecology                                                |
| P30 | <b><i>Jan Boratyński</i></b>     | Behavioural and physiological response to strong habitat disturbance in a key wetland rodent species                                                | Open: Evolution and Ecology                                                |
| P31 | <b><i>Jan Boratyński</i></b>     | Heterothermy but not maintenance costs of homeothermy correlate with natural food availability in yellow-necked mice <i>Apodemus flavicollis</i>    | Open: Evolution and Ecology                                                |
| P32 | <b><i>Adam Hermaniuk</i></b>     | Can cell size explain different metabolic response to temperature and oxygen within the <i>Pelophylax esculentus</i> species complex?               | Effects of thermal and oxygen conditions on ectotherms in a changing world |
| P33 | <b><i>Natalia Boron</i></b>      | Variable temperature conditions and humoral immune response in zebra finches                                                                        | Open: Evolution and Ecology                                                |

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|     |                                        |                                                                                                                                             |                                                                            |
|-----|----------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------|
| P34 | <b><i>Joanna Rutkowska</i></b>         | Ecophysiology of cognition: The effects of ambient temperature variability on learning performance in zebra finches                         | Open: Evolution and Ecology                                                |
| P35 | <b><i>Karolina Skorb</i></b>           | Short-term consequences of ambient temperature for development in passerine birds                                                           | Open: Evolution and Ecology                                                |
| P36 | <b><i>Aneta Arct</i></b>               | A long-term study reveals a crucial role of weather conditions for avian offspring fitness                                                  | Effects of thermal and oxygen conditions on ectotherms in a changing world |
| P37 | <b><i>Rafał Martyka</i></b>            | The effect of environmental variation on age-specific reproductive patterns in a short-lived songbird                                       | Open: Evolution and Ecology                                                |
| P38 | <b><i>Michał Gładalski</i></b>         | Aromatic plants, great tits & body condition: preliminary results                                                                           | Open: Evolution and Ecology                                                |
| P39 | <b><i>Monica Sayuri Diaz Palma</i></b> | The effects of light pollution on a breeding migratory bird                                                                                 | Open: Evolution and Ecology                                                |
| P40 | <b><i>Katarzyna Janas</i></b>          | A riddle of multiple ornaments – the great tit case                                                                                         | Open: Evolution and Ecology                                                |
| P41 | <b><i>Tomasz Mazgajski</i></b>         | Great Tit females build similar nests in consecutive breeding seasons                                                                       | Open: Evolution and Ecology                                                |
| P42 | <b><i>Amelia Chyb</i></b>              | Haemoparasites in larid birds - ecological niche more important than migratory distance                                                     | Open: Evolution and Ecology                                                |
| P43 | <b><i>Amelia Chyb</i></b>              | Big city life – genetic background of urbanization processes in a common waterbird                                                          | Open: Evolution and Ecology                                                |
| P44 | <b><i>Maciej Kamiński</i></b>          | Constitutive innate immune function is associated with habitat urbanization, but not with population density in a highly-adapted urban bird | Open: Evolution and Ecology                                                |
| P45 | <b><i>Kyle Coughlan</i></b>            | Oxidative stress biology in nest box breeding birds                                                                                         | Open: Evolution and Ecology                                                |
| P46 | <b><i>Maëlle Lefevre</i></b>           | My song will tell you if I already have a partner: how breeding status affects song parameters in Zebra finches                             | Open: Evolution and Ecology                                                |

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|     |                                  |                                                                                                                                                                                  |                                                             |
|-----|----------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------|
| P47 | <b><i>Lia Zampa</i></b>          | Stand out from the crowd: breeding density affect vocal individuality in Ortolan bunting ( <i>Emberiza hortulana</i> )                                                           | Open: Evolution and Ecology                                 |
| P48 | <b><i>Pawel Podkowa</i></b>      | The Role of Ornamentation in Bird Speciation: A Study on Coloration in Divergent Populations of Painted Buntings                                                                 | Open: Evolution and Ecology                                 |
| P49 | <b><i>Martyna Cendrowska</i></b> | Prevalence of parental coordination in birds - a systematic meta-analysis                                                                                                        | Open: Evolution and Ecology                                 |
| P50 | <b><i>Adam Zbyryt</i></b>        | Sparrows are bolder with big friend behind their back                                                                                                                            | Open: Evolution and Ecology                                 |
| P51 | <b><i>Barbara Pietrzak</i></b>   | Emergence of personalities in moor frog under perceived predation risk                                                                                                           | Open: Evolution and Ecology                                 |
| P52 | <b><i>Monika Sysiak</i></b>      | The time of stress for predator can be an anti-predator window for prey                                                                                                          | Open: Evolution and Ecology                                 |
| P53 | <b><i>Nermeen Amer</i></b>       | Hatching phenology shapes the interaction between predation risk and warming in the damselfly <i>Ischnura elegans</i>                                                            | Open: Evolution and Ecology                                 |
| P54 | <b><i>Maria J. Golab</i></b>     | Looks or personality - what drives damselfly mating success in the wild?                                                                                                         | Open: Evolution and Ecology                                 |
| P55 | <b><i>Szymon Śniegula</i></b>    | Urbanization outcomes on fitness traits in the damselfly                                                                                                                         | Open: Evolution and Ecology                                 |
| P56 | <b><i>Bernardo Antunes</i></b>   | Habitat connectivity inferred from landscape genetic models at multiple spatial and temporal scales in two newt species ( <i>Lissotriton montandoni</i> and <i>L. vulgaris</i> ) | Open: Evolution and Ecology                                 |
| P57 | <b><i>Krzysztof M. Kozak</i></b> | California Conservation Genomics Project: next-generation landscape genetics helps protect Pocket Mice and other endangered life.                                                | Open: Evolution and Ecology                                 |
| P58 | <b><i>Karol Hubert Nowak</i></b> | The difficult marriage of flies and their endosymbionts                                                                                                                          | Ecology and evolution of microbes and microbial communities |

# Poster Titles

*Click on the Authors' names to view their abstracts*

|     |                                                      |                                                                                                                                                                                           |                                                             |
|-----|------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------|
| P59 | <b><i>Bartłomiej Starzyński</i></b>                  | There's always room for one more. Microbial communities in nectar of selected plant species.                                                                                              | Ecology and evolution of microbes and microbial communities |
| P60 | <b><i>Jakub Białkowski<br/>Anna Ziemiakowicz</i></b> | First insight into the evolution of the flight-control system in bark beetles                                                                                                             | Open: Evolution and Ecology                                 |
| P61 | <b><i>Kinga Larisch</i></b>                          | In search of hidden biodiversity                                                                                                                                                          | Open: Evolution and Ecology                                 |
| P62 | <b><i>Katarzyna Krawczyk</i></b>                     | The impact of wheat streak mosaic virus (WSMV) on the population growth rate wheat curl mite (WCM)                                                                                        | Global Environmental Issues in Comparative Studies          |
| P63 | <b><i>Neelam Porwal</i></b>                          | Sexually-selected male weapon and the risk of population extinction under increasing temperature                                                                                          | Open: Evolution and Ecology                                 |
| P64 | <b><i>Sebastian Chmielewski</i></b>                  | The genetic architecture of sexually-selected weapon in the bulb mite                                                                                                                     | Open: Evolution and Ecology                                 |
| P65 | <b><i>Rocco Notarnicola</i></b>                      | Genetic co-structure in the bank voles-Borrelia host-pathogen system                                                                                                                      | Open: Evolution and Ecology                                 |
| P66 | <b><i>Justyna Pogwizd</i></b>                        | The importance of integrative taxonomy: uncovering multiple species in an allegedly monotypic genus                                                                                       | Open: Evolution and Ecology                                 |
| P67 | <b><i>Tomasz Czerwiński</i></b>                      | Phylogeny of the genus Rhyzobius Coleoptera: Coccinellidae: Coccidulini) – preliminary study                                                                                              | Open: Evolution and Ecology                                 |
| P68 | <b><i>Magdalena Migalska</i></b>                     | Evolutionary trade-offs constraining the MHC gene expansion: beyond simple TCR depletion model                                                                                            | Open: Evolution and Ecology                                 |
| P69 | <b><i>Monika Gronowska</i></b>                       | Variability of evolutionarily important genes (MHC) in non-Passeriformes                                                                                                                  | Open: Evolution and Ecology                                 |
| P70 | <b><i>Emilia Grzędzicka</i></b>                      | Sosnowsky's hogweed Heracleum sosnowskyi invasion favours European honeybees Apis mellifera over other pollinators depending on its severity and traits                                   | Open: Evolution and Ecology                                 |
| P71 | <b><i>Lizaveta Vintsek</i></b>                       | Phylogeny and evolutionary history of the genus Sergia (Campanulaceae) and its response to the climate changes predicted for the Mountains of Central Asia (a world biodiversity hotspot) | Open: Evolution and Ecology                                 |

# Poster Titles

*Click on the Authors' names to view their abstracts*

|     |                                     |                                                                                                                                                                                                          |                                                    |
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| P72 | <b><i>Sebastian Szczepański</i></b> | Genetic diversity of hybrid zones of Scots pine and its close relatives                                                                                                                                  | Open: Evolution and Ecology                        |
| P73 | <b><i>Bartosz Łabiszak</i></b>      | Unravelling the evolutionary relationships and speciation patterns of European Pine taxa                                                                                                                 | Open: Evolution and Ecology                        |
| P74 | <b><i>Maryna Yarotska</i></b>       | Climate change impact on forest phytocoenoses of ukraine                                                                                                                                                 | Open: Evolution and Ecology                        |
| P75 | <b><i>Artur Górecki</i></b>         | How well can plant succession describe short climatic oscillations in the Quaternary?                                                                                                                    | Global Environmental Issues in Comparative Studies |
| P76 | <b><i>Huseyn Mammadov</i></b>       | Investigating the impact of entomopathogenic fungus <i>Beauveria bassiana</i> infection on reproduction and adult, mortality in reproductively naive tropical crickets ( <i>Gryllobates sigillatus</i> ) | Global Environmental Issues in Comparative Studies |
| P77 | <b><i>Michał Bzoma</i></b>          | Investigating sexual dimorphism of tropical house cricket ( <i>Gryllobates sigillatus</i> ) in response to infection by entomopathogenic fungus <i>Beauveria bassiana</i>                                | Open: Evolution and Ecology                        |
| P78 | <b><i>Jakub Goczał</i></b>          | Beetle elytra: evolution, modifications and biological functions                                                                                                                                         | Open: Evolution and Ecology                        |
| P79 | <b><i>Tomasz Włodarczyk</i></b>     | Coming out from the shadows: chemical strategy of a facultative slave-making ant species <i>Formica sanguinea</i>                                                                                        | Open: Evolution and Ecology                        |
| P80 | <b><i>Filip Turza</i></b>           | The mechanism of rescue actions in <i>Manica rubida</i> ants                                                                                                                                             | Open: Evolution and Ecology                        |
| P81 | <b><i>Rafał Garlacz</i></b>         | Unveiling species diversity of day active moths in the tropical Andes: the <i>Scordyliodes</i> genus (Lepidoptera, Geometridae: Larentiinae)                                                             | Open: Evolution and Ecology                        |
| P82 | <b><i>Kamila S. Zajac</i></b>       | The Slimy Bastards – uncovering the hidden diversity within taxonomically challenging genus of terrestrial slugs (Gastropoda: Agriolimacidae: Deroceras)                                                 | Open: Evolution and Ecology                        |
| P83 | <b><i>Pritam Kumar Dey</i></b>      | Convergent evolution of rare dark, UV-absorbing cuticular pigmentation in a new Afro-Oriental heterotardigrade species complex                                                                           | Open: Evolution and Ecology                        |

# Poster Titles

*Click on the Authors' names to view their abstracts*

|     |                                  |                                                                                                                                                   |                             |
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| P84 | <b>Aleksandra Sumlińska</b>      | Relevance and phylogenetic position of the genus <i>Milnesioides</i> Claxton, 1999 (Tardigrada)                                                   | Open: Evolution and Ecology |
| P85 | <b>Olga Koziol</b>               | Tardigrade Augean Stables – a challenging phylogeny and taxonomy of the family Ramazzottiidae (Eutardigrada)                                      | Open: Evolution and Ecology |
| P86 | <b>Andrzej Ostoja-Wilamowski</b> | Phylogeography and morphological evolution of the genus <i>Barbaria</i> (Heterotardigrada)                                                        | Open: Evolution and Ecology |
| P87 | <b>Alejandro López López</b>     | Patterns of evolution within Tardigrada (Ecdysozoa: Panarthropoda) unveiled by time-calibrated multilocus phylogeny                               | Open: Evolution and Ecology |
| P88 | <b>Milena Zduniak</b>            | Personality and parasites: links between open field activity, space use, and parasite loads in yellow-necked mice ( <i>Apodemus flavicollis</i> ) | Open: Evolution and Ecology |
| P89 | <b>Aleksandra Wróbel</b>         | Arolla pine ( <i>Pinus cembra</i> L.) and granivorous rodents: do they play by the numbers?                                                       | Open: Evolution and Ecology |
| P90 | <b>Sandra Ahlen Mulio</b>        | Reconstructing species distribution and intra-species diversity of Swedish Auchenorrhyncha based on Malaise trap sampling                         | Open: Evolution and Ecology |
| P91 | <b>Mateusz Konczal</b>           | Genomic consequences of artificial translocation, admixture and population replacement in the Trinidadian guppies                                 | Open: Evolution and Ecology |
| P92 | <b>Katarzyna Burda</b>           | Estimating genetic load in natural populations of guppies ( <i>Poecilia reticulata</i> )                                                          | Open: Evolution and Ecology |
| P93 | <b>Natalia Pajk</b>              | Cryptic diversity in <i>Perforatella</i> and <i>Euomphalia</i> snails                                                                             | Open: Evolution and Ecology |
| P94 | <b>Jakub Plachta</b>             | Acetamiprid – effects on life history and behavior of antlions                                                                                    | Open: Evolution and Ecology |
| P95 | <b>Karolina Doan</b>             | Origin and demographic history of the golden jackal ( <i>Canis aureus</i> )                                                                       | Open: Evolution and Ecology |
| P96 | <b>Grzegorz Jan Skórzewski</b>   | Developmental disorder and mortality caused by hybridisation and polyploidization in an asexual fish complex of <i>Cobitis</i> genera.            | Open: Evolution and Ecology |

# Plenary Speakers

## PLENARY SPEAKER 1: RICHARD EIMER LENSKI



Richard Lenski studies evolution in action. Since 1988, he and his team have watched bacteria evolve in the lab for 75,000 generations, providing insights into the dynamics of adaptation, the repeatability of evolution, and the origin of new functions. Samples from throughout the experiment are stored frozen, allowing cells from different generations to be compared and competed. Lenski is a member of the National Academy of Sciences, and a past President of the Society for the Study of Evolution. He has mentored more than 30 graduate students and postdoctoral scientists now on the faculties of universities around the world.

### **DYNAMICS AND REPEATABILITY OF EVOLUTION IN A LONG-TERM EXPERIMENT WITH BACTERIA**

#### **Richard Lenski<sup>1</sup>**

1 Microbiology and Molecular Genetics, Michigan State University, United States

Evolution has produced the wonderful diversity of life on Earth, but it is usually difficult to observe evolution while it is happening. With their rapid generations and the ability to freeze and later revive cells, microbes allow one to observe evolution in action. In my lab, we have maintained 12 populations of *Escherichia coli* in a simple environment for over 30 years and 75,000 generations. The aims of this experiment have been to characterize the tempo and mode of evolution, and to examine the repeatability and even predictability of phenotypic and genomic changes. We have quantified the dynamics of adaptation by natural selection, documented many cases of parallel evolution, observed changes in the underlying mutation rate, and seen the appearance of a new metabolic function. We have sequenced thousands of genomes to identify the mutations in longitudinal samples from the populations. These data provide insights into the dynamic coupling of phenotypic and genotypic evolution during periods of both optimization and innovation.

# Plenary Speakers

## PLENARY SPEAKER 2: WILCO C.E.P. VERBERK



Wilco Verberk is an Associate professor at the Department of Animal Ecology and Physiology, Radboud University Nijmegen, the Netherlands. He obtained his PhD in Freshwater Ecology in 2008, for his study on species traits to explain patterns in assemblages of aquatic invertebrates. Since then he has broadened his interest towards physiology and evolution and he continues to study physiological traits to better understand their ecological niche and their life-history evolution.

### THE ROLE OF CELL SIZE IN SHAPING RESPONSES TO OXYGEN AND TEMPERATURE IN ECTOTHERMS

#### Wilco Verberk<sup>1</sup>

1 Radboud University, Netherlands

Cells, the basic building blocks of life, differ in size across the tree of life. Variation in cell size across species is strongly linked to variation in the size of the nucleus and the size of the genome. The size of the cell has repercussions for the ratio between the surface area of cell membranes and the volume of the cell. As such it has repercussions for energy expenditure via maintenance of electrochemical gradients across membranes, but also for uptake of food and oxygen to generate energy. This is at the heart of the idea that there is an optimal cell size for a given life-history and body plan. Temperature may modulate costs and benefits of a given cell size, such that a small cell size is favoured in the warm to facilitate uptake of oxygen. Here I will present work addressing the question how cell size modulates responses to temperature and oxygen, focusing on growth, hypoxia tolerance and energy metabolism in ectothermic organisms.

# Plenary Speakers

## PLENARY SPEAKER 3: CARLOS A. BOTERO



Carlos A. Botero is an associate professor of Evolutionary Ecology at the University of Texas at Austin. Through the complementary use of theoretical models, comparative analyses, and laboratory experiments, his research aims to improve our understanding of how organisms cope with and adapt to frequent environmental oscillations (a phenomenon known as “fluctuating selection”). In recent years, the Botero Lab has systematically applied the lessons learned from this work to characterize organismal responses to climate change, the eco-evolutionary dynamics of the avian brain, and the evolution of human culture.

### CLIMATE CHANGE, FLUCTUATING SELECTION AND ECO-EVOLUTIONARY DYNAMICS

#### Carlos A. Botero<sup>1</sup>

1 Integrative Biology, University of Texas at Austin, United States

Long-term evolutionary studies across a wide range of organisms indicate that the direction and strength of natural selection tends to fluctuate over time. However, ecological and evolutionary theories often ignore such fluctuations, leading to an incomplete and potentially misleading understanding of natural processes. I use theoretical modeling, experimental evolution, and large-scale comparative analyses to study how organisms adapt to and cope with recurrent environmental extremes and other sources of fluctuating selection. I will begin this talk by showing that adaptive responses to fluctuating selection can be predicted and that this framework can inform our intuition about the potential consequences of climate change. I will then discuss how environmental fluctuations affect micro and macroevolutionary dynamics, including our exciting recent finding that more broadly effective, yet more difficult to reach solutions to environmental challenges are more likely to be discovered under fluctuating than constant selection. Finally, I will review my team’s comparative work on the critical role that sociality, cognition, and mate choice play in the colonization and/or occupancy of variable environments, and will highlight the challenges of distinguishing between cause and effect in the eco-evolutionary dynamics of adaptation to fluctuating conditions. Throughout the talk, I will draw upon examples from my work on a diverse set of organisms, including mammals, birds, humans, and yeast.

# Plenary Speakers

## PLENARY SPEAKER 4: JULIA PAWŁOWSKA



Julia Pawłowska is interested in the evolution of one of the most ancient groups of land fungi – Mucoromycota, and their interactions with bacteria. Her team is particularly focused on their adaptations to extreme environments (including soil-community studies from polar regions or post-industrial sites). Her research includes not only the taxonomy, ecology, and physiology of early diverged fungal lineages but also focuses on their potential biotechnological applications. A significant part of her academic activity is also focused on teaching and outreach. She teaches biodiversity, botany, mycology, and eukaryotic microbiology. Since 2012, she has been involved in the Polish

Mycological Society's development and activity.

### **NO FUNGUS IN AN ISLAND: HOW ENDOHYPHAL BACTERIA MAY AFFECT THE FITNESS OF THEIR FUNGAL HOSTS?**

**Julia Pawłowska<sup>1</sup>, Beniamin Abramczyk<sup>1</sup>, Zuzanna Blocka<sup>1</sup>, Robert Stasiuk<sup>2</sup>, Renata Matlakowska<sup>2</sup>, Alicja Okraśińska<sup>1</sup>**

1 Faculty of Biology, Institute of Evolutionary Biology, University of Warsaw, Poland

2 Faculty of Biology, Institute of Microbiology, University of Warsaw, Poland

Fungi and bacteria play an important role in soil-forming processes, as together they are responsible for the majority of decomposition. Mucoromycota fungi are one of the most ancient groups of land fungi, commonly occurring in various types of soils. Some of them can even survive in harsh, anthropogenically transformed environments, such as post-industrial soils contaminated with polycyclic aromatic hydrocarbons. At the same time, these fungi are known to harbor endohyphal bacteria (EHB). By combining different ‘omic’ techniques we aimed to understand how endohyphal bacteria may affect the enzymatic capacities of their fungal hosts in hydrocarbon-polluted environments. We confirmed that the EHB are more frequent in Mucoromycota strains isolated from soils polluted with hydrocarbons. Genomic analysis of one of the isolated fungal-bacterial pairs suggests that it is a facultative interaction, but the presence of several bacterial genes extending fungal metabolic capacities was detected. Furthermore, comparative GC-MS (gas chromatography with mass spectrometry) analysis of wildtype and cured of EHB fungal strains revealed differences in metabolite composition, indicating the significant role that these bacteria may play in the adaptation of their hosts to environmental conditions.

# *Abstract: Contributed Talks*

## **CT01: ADAPTATIONS IN YEAST SHORT-TERM EVOLUTIONARY EXPERIMENTS ARE MAINLY A RESULT OF THE APPEARANCE OF LOSS-OF-FUNCTION MUTATIONS**

**Joanna Klim<sup>1</sup>, Urszula Zielenkiewicz<sup>1</sup>, Szymon Kaczanowski<sup>2</sup>**

1 Laboratory of Environmental and Evolutionary Systems Biology, Institute of Biochemistry and Biophysics PAS, Poland

2 Bioinformatics, Institute Biochemistry and Biophysics, Poland

We noticed that during short-term experimental adaptive evolution and carcinogenesis, mutations causing gene inactivation are frequent. In the presented study, we demonstrated indications that these mutations are almost exclusively adaptive in yeasts *S. cerevisiae*. Namely, our meta-analysis of 59 published studies, based on dN/dS statistics, predicted that nonsense mutations tend to be adaptive. We experimentally confirmed this prediction. We utilized genomic data that we obtained from the short-term evolutionary experiments with yeast *S. cerevisiae* grown in continuous culture conditions and predicted that gene loss-of-function mutations in five genes (WHI2, URE2, RIM15, HOG1, PBS2) are beneficial. In these genes, mutations were recurrent and some of them were nonsense or causing frameshifts. We constructed respective knockout strains and performed a set of simple competition experiments comparing the proliferation rates of isogenic wild-type and each deletion mutant strain co-cultivated in four various experimental conditions. This experiment confirmed that the inactivation of these genes was beneficial during experimental evolution. In conclusion, the presented results confirm expectations of the classical “less is more” hypothesis that loss-of-function mutations (also named gene loss) play a basic role in rapid adaptation.

## **CT02: EXPERIMENTAL EVOLUTION OF REPRODUCTIVE TRAITS IN CAENORHABDITIS ELEGANS**

**Weronika Antol<sup>1</sup>, Joanna Palka<sup>1</sup>, Karolina Sychta<sup>2</sup>, Paulina Kosztyla<sup>1</sup>, Marta Labocha-Derkowska<sup>1</sup>, Jagoda Byszek<sup>1</sup>, Alicja Dyba<sup>3</sup>, Katarzyna Dudek<sup>1</sup>, Wiesław Babik<sup>1</sup>, Zofia Prokop<sup>1</sup>**

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

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

3 Institute of Botany, Faculty of Biology, Jagiellonian University, Poland

‘Selfing syndrome’, shared by species reproducing mostly via self-fertilization, involves diminution of traits involved in cross-fertilization. The aim of my study was to investigate whether the transition of the reproductive system from mostly selfing to obligatory outcrossing leads to the evolution towards reduction of selfing syndrome in a nematode *Caenorhabditis elegans*. I expected that change in the reproductive system would result in the evolution of higher fitness (measured as competitive fitness) and improved reproductive behaviour (males approaching females faster, longer copulation time, higher fertilization success) after 100 generations. The result was that nearly 100 generations of obligatory outcrossing did not lead to detectable evolution of the studied traits specific to outcrossing. This lack of response to the altered reproductive system could result from: strength of the selective pressure, the genetic variance available because of low genetic diversity at the onset of the study and a limited input of beneficial mutations under given population size and the experiment timespan. Moreover, we revealed that the spontaneous loss of the desired mutation can affect the maintenance of obligatorily outcrossing populations in a long-term study which points to the necessity of applying several methods to control their genotype

# Abstract: Contributed Talks

## CT03: TESTING FOR THE MECHANISMS OF BALANCING SELECTION MAINTAINING 6PGDH POLYMORPHISM IN BULB MITES

Pranav Unnikrishnan<sup>1</sup>, Anna Sapeth<sup>1</sup>, Magdalena Trojańska<sup>1</sup>, Agata Plesnar-Bielak<sup>1</sup>, Wiesław Babik<sup>1</sup>

<sup>1</sup> Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Kraków, Poland

Genetic variation is required for adaptation, but its maintenance is a major puzzle in evolutionary biology. A role in the maintenance of variation is often attributed to balancing selection. The focus of this study is environment-dependent balancing selection, where the fitness of genotypes depends on the spatio-temporal variation of the environment, maintaining genetic variation in heterogeneous environments. Specifically, we investigate Phosphoglucose dehydrogenase (6Pgdh), a sexually selected gene in the bulb mite *Rhizoglyphus robini*. The gene has two alleles (S and F), that differ by a single nonsynonymous change, where the S-bearing males achieve higher reproductive success. We use experimental evolution to test whether temperature or sexual selection intensity (manipulated by sex ratio) are the factors underlying balancing selection. A previous study has shown that these variables affected the strength of selection on 6Pgdh, but it did not find evidence of reversal of the allele fitness. Here, we test for the effect of lower temperatures (18°C vs. 12°C) and temperature by sexual selection intensity (female biased and equal sex ratio) interaction in a fully factorial crossed design. After 13 generations of selection we see an increase in F-allele frequency for the populations evolving under lower temperature (12°C) and higher sexual selection intensity (equal sex ratio). There is also a trend of decrease in F-allele frequency for both temperature treatments under relaxed selection. The results from the experimental evolution can help us understand more about the nature of environment-dependent balancing selection and also the complex relationship between conflict and ecology.

## CT04: DENSITY-DEPENDENT SELECTION AT LOW FOOD LEVELS LEADS TO THE EVOLUTION OF POPULATION STABILITY EVEN WITHOUT A CLEAR R-K TRADE-OFF

Neha Pandey<sup>1</sup>

<sup>1</sup> Evolutionary Biology Group, Adam Mickiewicz University, Poznań, Poland

Density-dependent selection, together with r-K trade-offs, has been one of the most plausible suggested mechanisms for the evolution of population stability. However, experimental support for this explanation has been both meagre and mixed. One study with *Drosophila melanogaster* yielded no evidence for populations adapted to chronic larval crowding having also evolved greater population stability. Another study, on *D. ananassae*, suggested that populations adapted to larval crowding evolved both greater constancy and persistence stability, and the data also suggested an r-K trade-off in those populations, though the evidence for the latter was not conclusive. Here, I show that *D. melanogaster* populations selected for adaptation to larval crowding at very low food amounts per vial, evolve enhanced constancy and persistence stability. The enhanced population stability in the crowding-adapted populations seems to have evolved through the increased equilibrium size (K) and reduced sensitivity of realized population growth rates to density ( $\alpha$ ). There was no clear evidence for reduced intrinsic population growth rate (r) in the more stable crowding-adapted *D. melanogaster* populations. This study adds to the growing evidence in support of the hypothesis that population stability can evolve in response to density-dependent selection through the evolution of certain life-history traits that are associated with higher K and less negative  $\alpha$ . I will discuss these findings in the light of previous work, and suggest that a model-free framework might be of great heuristic value in understanding the evolution of population stability through changes in the density-sensitivity of life-history traits.

## *Abstract: Contributed Talks*

### **CT05: THE CORRELATION BETWEEN INTRASPECIFIC VARIATION IN BASAL METABOLIC RATE (BMR) AND IN BODY TEMPERATURE: ARE MICE SELECTED FOR HIGH BMR HOTTER?**

**Paweł Brzęk<sup>1</sup>, Andrzej Gębczyński<sup>1</sup>, Aneta Książek<sup>1</sup>, Sylwia Buczyńska<sup>1</sup>, Marek Konarzewski<sup>1</sup>**

<sup>1</sup> Faculty of Biology, University of Białystok, Poland

Basal metabolic rate (BMR) and high body temperature (T<sub>b</sub>) are two most conspicuous physiological traits of mammals. BMR and T<sub>b</sub> are evolutionary coupled at interspecific level. BMR is measured in resting animal at thermoneutrality. However, mammals typically live at ambient temperatures below their thermoneutral zone. Under such conditions, intraspecific variation in BMR does not need to affect T<sub>b</sub> because it can be compensated by variation in other components of energy budget e.g. the magnitude of dedicated thermogenesis. We present results of two studies that used implanted temperature loggers to quantify T<sub>b</sub> in males and females of laboratory mice from two lines, artificially selected for either high (H-BMR) or low (L-BMR) level of BMR. These lines represent an unique model of large (>50%) intraspecific variation in BMR. Earlier studies have shown that L-BMR mice have lower BMR but higher capacity of nonshivering thermogenesis than H-BMR mice. We found that in mice acclimated to 23 °C, T<sub>b</sub> in H-BMR line was 0.3-0.5 °C higher than in L-BMR line. The magnitude of this difference was large enough to claim it represents genuine effect of divergent selection for BMR. However, it was also relatively smaller than the magnitude of between-line difference in BMR or in several physiological, behavioral, and molecular traits previously studied in H-BMR and L-BMR mice. Our results show that BMR can be genetically correlated with T<sub>b</sub> at intraspecific level but the strength of this correlation is weaker than in the case of many other traits.

### **CT06: THE MOLECULAR BACKGROUND OF EXPERIMENTAL EVOLUTION OF PHYSIOLOGY AND BEHAVIOR IN THE BANK VOLE: CHANGES IN SNP ALLELE FREQUENCIES**

**Małgorzata M. Lipowska<sup>1</sup>, Edyta T. Sadowska<sup>1</sup>, Piotr Zieliński<sup>1</sup>, Wiesław Babik<sup>1</sup>, Paweł Koteja<sup>1</sup>**

<sup>1</sup> Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Kraków, Poland

One of the main challenges in biology is to explain the evolution of complex adaptations, allowing realization of the astonishing variety of "lifestyles". Our research program is based on an the "experimental evolution", in which we attempt to mimic the process under controlled laboratory conditions. We maintain lines of the bank vole (*Myodes glareolus*) selected in three directions: the ability to achieve high aerobic exercise metabolism, tendency to predatory behavior, and the ability to cope with a low-quality, herbivorous diet. We also maintain a control, animals not subjected to any intended selection. Each of the selection categories is represented by four independent lines (populations), which allows to distinguish the effects of selection per se from those due to random processes (e.g., genetic drift). The selection was effective, and both the directly selected traits and several correlated traits have significantly changed. Here we asked what is the molecular-genetic basis of the traits evolution. We examined genetic variation at the level of DNA single nucleotide polymorphisms (SNPs) in nearly 20,000 sites in the exon parts of genome in nearly 300 individuals sampled from all the lines in generation 27-28, and from the base population. Preliminary multivariate analyses of the genetic variation showed clear genetic differences not only between the selected and control lines, but also between the control lines and the base population. It can be supposed that the latter result is a genetic evidence of domestication. In further analyses we will attempt to identify specific genes associated with the phenotypic differences.

# *Abstract: Contributed Talks*

## **CT07: WOLBACHIA-CONFERRED ANTIVIRAL PROTECTION IS DETERMINED BY INSECT'S DEVELOPMENTAL TEMPERATURE**

**Ewa Chrostek<sup>1</sup>, Nelson Martins<sup>2</sup>, Marta Marialva<sup>2</sup>, Luis Teixeira<sup>2</sup>**

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

2 Instituto Gulbenkian de Ciencia, Portugal

Wolbachia, a maternally transmitted bacterium prevalent in arthropods, provides robust antiviral protection in various species, including *Drosophila melanogaster*. Wolbachia-infected *Aedes aegypti* mosquitoes are on trials aimed at stopping the transmission of dengue and Zika viruses to humans. Nevertheless, the underlying mechanism of antiviral protection and the factors influencing it remain incompletely understood. In this study, we investigate the influence of temperature on Wolbachia-mediated protection in *Drosophila melanogaster*. The temperature in which the flies are kept post-infection directly affects the replication of *Drosophila C virus* (DCV) and modulates the level of Wolbachia-induced protection. Strikingly, the developmental temperature of the host plays a pivotal role in determining Wolbachia-conferred antiviral protection. While robust protection is observed when flies develop from eggs to adults at 25°C, this protection is significantly diminished or abolished when flies develop at 18°C. Collectively, our findings demonstrate the temperature-dependent nature of Wolbachia-conferred antiviral protection, which is contingent upon environmental conditions. This interaction is likely to influence Wolbachia-host dynamics in natural settings, impacting the frequencies of hosts and symbionts in different climatic regions. Leveraging the temperature dependence of Wolbachia-mediated pathogen blocking can aid in elucidating the underlying mechanisms and inform the deployment strategies of Wolbachia for preventing arbovirus transmission.

## **CT08: UNCOVERING THE SECRETS OF INTERACTIONS BETWEEN TEMPERATURE, HYPOXIA, AND COMPETING DAPHNIA SPECIES**

**Ewa Babkiewicz<sup>1</sup>, Karol Krajewski<sup>1</sup>, Konrad Leniowski<sup>2</sup>, Szymon Pukos<sup>1</sup>, Julia Wawrzeńczak<sup>1</sup>, Wojciech Wilczynski<sup>3</sup>, Marcin Lukasz Zebrowski<sup>1</sup>, Jae-Seong Lee<sup>4</sup>, Piotr Maszczyk<sup>1</sup>**

1 Hydrobiology, University of Warsaw, Poland

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Previous research has shown that elevated temperature and environmental hypoxia are associated with a reduced representation of larger-bodied species in ectotherms, suggesting that they are at a competitive disadvantage due to increased oxygen demand and limited oxygen availability. To investigate this, we conducted a comparative analysis of two pairs of competing zooplankton species: *Daphnia galeata* (smaller-bodied) and *D. pulex* (larger-bodied), and *D. pulex* (smaller-bodied) and *D. magna* (larger-bodied). We monitored their population dynamics at different oxygen concentrations and temperatures, and also measured haemoglobin concentrations in the latter pair. Contrary to expectations, the results showed that the larger-bodied species outcompeted the smaller-bodied species in all experimental treatments involving the first pair of species. In the second pair, elevated temperature favoured the smaller-bodied species, while environmental hypoxia had the opposite effect. The competitive advantage of *D. pulex* under elevated temperature was probably due to its ability to divert energy from somatic growth to reproduction, as indicated by the increased number of reproducing females. Conversely, the competitive advantage of *D. magna* under environmental hypoxia may be due to their ability to reallocate energy from reproduction to somatic growth, as indicated by lower reproductive effort and greater plasticity in haemoglobin production. These findings indicate that elevated temperature and hypoxia can independently and jointly influence

# Abstract: Contributed Talks

interspecific competitive abilities by impacting the pace of life. However, the numerical dominance of smaller-sized species in warm and hypoxic zooplankton communities cannot be explained by their enhanced competitive abilities resulting from a more favorable oxygen supply-demand balance.

## **CT09: EFFECTS OF FOOD QUALITY AND WATER TEMPERATURE ON THE FITNESS OF SPECIES OF DAPHNIA THAT DIFFER IN BODY SIZE**

**Piotr Dawidowicz<sup>1</sup>, Anna Bednarska<sup>1</sup>, Zhanna Buseva<sup>1</sup>, Tomasz Brzeziński<sup>1</sup>, Feneva Irina<sup>1</sup>**

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Rising temperatures in freshwater lakes caused by global warming are changing algal communities in favour of cyanobacteria, which are known to be inferior food for filter-feeding zooplankton, especially large-sized cladoceran species. Juvenile growth rate (JGR) is considered a good measure of cladoceran fitness. Using JFR as a proxy, we determined the combined effects of food quality and water temperature on fitness of a large-sized *Daphnia magna*, medium *D. pulex-pulicaria* and small-bodied *D. longispina*, each represented by 3 clones (genotypes). Daphnids were reared in a flow-through system with constant food concentration (0.54 Corg L-1) at low (18°C) and high temperature (24°C). Three food types were used, differing in terms of stoichiometry (C:P) and essential fatty acid content: (1) a suspension of the green alga *Acutodesmus obliquus* with a stoichiometric carbon to phosphorus ratio optimal for *Daphnia* (C:P  $\approx$  120), (2) a suspension of *A. obliquus* with a stoichiometric ratio of C:P  $\approx$  800 indicating severe phosphorus deficiency, and (3) a mixture of *A. obliquus* (10%) and the cyanobacterium *Synechococcus elongatus* (90%) which is deficient in sterols and unsaturated fatty acids. Temperature and food-quality regime affected the fitness of *Daphnia* in an interactive way, however no clear effect of body size on susceptibility to low quality diet was detected. We conclude that factors other than food quality are responsible for the absence of large-bodied daphnids in warm subtropical and tropical lakes.

This study was supported by a grant from the National Science Centre, Poland, project no 2019/33/B/NZ8/01567

## **CT10: TEN YEARS OF STUDIES ON THE EFFECT OF TEMPERATURE AND OXYGEN ON PHENOTYPIC PLASTICITY OF BODY SIZE IN ROTIFERS**

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Rotifers are a pleasant object for eco-evolutionary research because of their small size, short lifespan and relatively simple biological organization. In addition, they are eutelic, meaning that the cellular response to environmental changes can only be realized by manipulating cell size, not cell number. This feature is very useful for studying the plastic response to temperature-dependent oxygen conditions. During three consecutive projects, I studied the proximal and ultimate mechanisms behind this response in the rotifers *Brachionus plicatilis* cryptic species complex and *Lecane inermis*. Studies of the genetic and plastic response have been conducted under laboratory conditions, with manipulation of temperature, oxygen concentration, or both, and in the field. The results support theoretical assumptions about the role of oxygen in driving this plastic response, the cellular mechanism behind the response at the body size level, and the adaptive nature of this phenomenon. The unique contribution of these studies was to identify the conditions of the plastic response, including variability due to the different organismal 'thermal history'. All experiments consistently showed that in rotifers the reduction in body size in hot is due to a reduction in the relative availability of oxygen under such conditions, and that this response is realized only under specific, relatively mild conditions that vary even between closely related organisms. Therefore, in such studies, rotifers can be treated as a simplified model, and tests performed on organisms with more complex biology can be built on this model.

# *Abstract: Contributed Talks*

## **CT11: MECHANISMS OF INCREASING PREDATION BY PLANKTIVOROUS FISH WITH RISING TEMPERATURE MAY EXPLAIN THE TEMPERATURE-BODY SIZE RELATIONSHIPS IN ZOOPLANKTON**

**Piotr Maszczyk<sup>1</sup>, Wojciech Wilczyński<sup>2</sup>, Z. Maciej Gliwicz<sup>1</sup>, Konrad Leniowski<sup>3</sup>, Marcin Lukasz Zebrowski<sup>1</sup>, Jae-Seong Lee<sup>4</sup>, Ewa Babkiewicz<sup>1</sup>**

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The temperature-size rule has been consistently observed in numerous studies, showing that ectotherms reared at higher temperatures experience accelerated growth during the juvenile stage and ultimately reach smaller sizes and younger ages at maturity. One explanation for this response is that it occurs when the effect of temperature on mortality, including predation mortality, outweighs its effect on food intake and metabolism. While several studies have found that the latter effect is close to the expected result based on the  $Q_{10}=2$  assumption, confirmation of the hypothesis requires evidence that the effect of temperature on mortality exceeds the  $Q_{10}=2$  threshold. To test this hypothesis, we conducted experiments with two fish species: rudd and Malabar danio. We studied the capture rate, which serves as a proxy for mortality, as well as the standard metabolic rate (SMR) and several parameters characterising the mobility of the fish and their planktonic prey (*Daphnia*) at different temperatures. The results supported our hypothesis, as the capture rate increased significantly more than expected based on the  $Q_{10}=2$  assumption, especially for the danio. This significant effect cannot be attributed solely to the thermal sensitivity of the SMR, as the  $Q_{10}$  for the SMR was only around 2. The most likely explanation seems to be a much more pronounced increase in the fish's mobility and resulting reaction field volume compared to its planktonic prey at elevated temperatures. This increased mobility leads to an improved attack rate by the fish, which exceeds the prediction made by the  $Q_{10}=2$  assumption.

## **CT12: CELLULARITY OF LIFE HISTORY STRATEGIES IN THE FACE OF OXYGEN AND THERMAL GRADIENTS - A SYNTHESIS OF CONCEPTS**

**Marcin Czarnoleski<sup>1</sup>**

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Knowing what shapes the performance of organisms along environmental gradients is crucial for understanding the past, present and future of life on our planet, as well as for assessing the habitability of other parts of the universe. Along with body plans, life on Earth has evolved drastic differences in cellularity and life history, from microscopic bacteria formed from 'universal' single cells to giant metazoans composed of gigantic clusters of specialised cells. Within metazoans, the emergence of more complex and larger forms was closely linked to an increase in the diversity of cell types and the evolution of molecular mechanisms controlling the cell cycle. The evolution of body size and cellularity is conceptually studied within the framework of two 'optimality' approaches - optimal body size and optimal cell size - with little integration between the two approaches. This work synthesises existing concepts and hypotheses in these two areas, with a particular focus on adaptive changes in body size and cell size in ectotherms inhabiting environmental gradients in temperature and oxygen conditions. The ultimate goal is to formulate a coherent theoretical basis for future research

# *Abstract: Contributed Talks*

## **CT13: REPRODUCTIVE STRATEGIES IN A CHANGING ENVIRONMENT – WHAT DRIVES THE EVOLUTION OF GROUND NESTING IN PASSERINE BIRDS**

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Birds have evolved an astonishing diversity of reproductive strategies and nest location is one of their key components. Location of the nest in a three-dimensional space is expected to yield profound ecological and evolutionary consequences for birds. Sharp evolutionary transitions in nest location may also require broad co-adaptations, e.g. a transition from non-ground to ground nesting is likely to increase accessibility of nests to ground predators, which may facilitate transitions towards faster life histories and higher fecundity. Despite these specific predictions, reliable quantitative information on the evolution of avian ground nesting and its ecological consequences is still lacking. Here, we used a phylogenetically-informed comparative framework to reconstruct the evolution of ground nesting behaviour in a clade of passerine birds, quantify its biogeographical and habitat variation, and test for its associations with life history traits. Using a dataset of over 1600 passerine bird species distributed worldwide we showed: i) a scattered phylogenetic distribution and moderate phylogenetic signal in the occurrence of ground nesting; ii) high evolutionary lability of ground nesting; iii) a key role of habitat structure in the evolution of ground nesting; iv) clear latitudinal gradients in ground nesting; and v) coevolutionary associations of ground nesting with fast life histories and higher fecundity. The study lays a foundation for better understanding of mechanisms and processes that have driven macroevolution of ground nesting behaviour across changing environmental conditions.

## **CT14: CORAL DISEASES IN A WARMING WORLD - META-ANALYSIS AND SYSTEMATIC MAP**

**Szymon Drobnik<sup>1</sup>, Samantha Burke<sup>2</sup>, Patrice Pottier<sup>2</sup>, Tracy Ainsworth<sup>2</sup>, Erin Macartney<sup>3</sup>, Małgorzata Łagisz<sup>2</sup>, Shinichi Nakagawa<sup>2</sup>**

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Coral reefs are among the most biodiverse habitats on Earth, and at the same time some of the most endangered by quickly changing climatic conditions. So far, coral bleaching was the most studied cause of their systematic decline. However, warming climate affects many more aspects of their biology such as pressures experienced from invasive/displaced fish species or pathogens decimating corals. We present the first comprehensive and global account of the impacts of global warming on the pathogens-driven deterioration of coral reefs worldwide. Through a combination of novel meta-analytical methods and an extensive survey of existing review literature, we identify the drivers of disease-related declines in coral reefs' health, as well as knowledge and methodological gaps characterising this field of coral science. Our results indicate, that global warming is an important driver of the increase in coral disease prevalence, and predict catastrophic outcomes for coral reefs should the current climatic trajectories remain unchanged.

# *Abstract: Contributed Talks*

## **CT15: THE ADAPTIVE INTROGRESSION OF MHC GENES IN MULTIPLE VERTEBRATE TAXA**

**Tomasz Gaczorek<sup>1</sup>, Katarzyna Dudek<sup>1</sup>, Wiesław Babik<sup>1</sup>**

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The Major Histocompatibility Complex (MHC) is a key component of adaptive immunity and contains the most polymorphic genes in vertebrates. Its extraordinary diversity is largely driven by host-pathogen coevolution, favouring novel or rare alleles. Since novel MHC alleles can be easily acquired from related species, MHC introgression is likely to be adaptive. However, its extent and prevalence remains an open question. Here, we test for adaptive MHC introgression across major vertebrate groups by directly comparing the extent of MHC and genome-wide introgression in natural hybrid zones. In total, we examined 29 hybrid zones formed by 31 species of fish, amphibians, reptiles, birds and mammals. We used three complementary methods. First, we tested for an increased MHC similarity between species in the proximity of contact zones but beyond the reach of genome-wide introgression. Second, we used the geographic clines to test whether the width of MHC clines exceeded that of genome-wide clines. Third, we used the genomic clines to test whether the rate of transition in MHC ancestry is lower relative to genome-wide ancestry. The results of all tests were synthesised in a comparative framework. We found extensive evidence for widespread adaptive introgression of MHC genes and stronger MHC introgression towards species with lower MHC variation. Our results suggest that MHC genes are among the last genes to stop flowing between incipient species before speciation is complete. Introgression thus appears to be a general mechanism that introduces new and restores previously lost MHC variation, increasing the adaptive potential of hybridising species.

The student was funded by the project entitled "ATUT PhD Programme in Biology". The project is co-financed by the European Union under the European Social Fund – Operational Programme Knowledge Education Development.

## **CT16: RESPONSE OF THE EUROPEAN UNGULATE SPECIES TO GLOBAL ENVIRONMENTAL CHANGES**

**Magdalena Niedziałkowska<sup>1</sup>**

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In my study I focus on the impact of the global environmental changes caused by natural and anthropogenic processes on the distribution, habitat of occurrence, phylogenetic and genetic diversity patterns of several ungulate species such as red deer, moose, wild boar and roe deer. Each of the species studied responded in a slightly different way to climate oscillations, landscape change and direct human impacts. The range of all of the ungulate species was smallest during the Last Glacial Maximum (LGM), but during this time they probably survived over a much larger area than previously thought, including also more northern regions of Europe. Some of the genetic variants of red deer and moose have not survived to the present day. The populations originating from the well-known southernmost LGM refugia (Iberian, Apennine and Balkan) had a limited influence on the contemporary observed phylogenetic pattern of the studied species in the central, northern and eastern part of the continent. Several processes have shaped the distribution and genetic diversity of the ungulates in the postglacial period, such as temperature increase, admixture, hybridisation, deforestation, anthropogenic pressure, over-hunting and barriers to gene flow. Translocations and reintroductions by humans have also had some impact on the current distribution of different phylogenetic lineages of the studied species in Europe. The results of the study can help to predict the impact of the ongoing environmental changes on the ungulate populations in Europe and they provide background information for further research, e.g. on adaptive genetic variation of the studied species.

# *Abstract: Contributed Talks*

## **CT17: CAN LIFE HISTORY THEORY SAVE OVEREXPLOITED FISH POPULATIONS?**

**Jan Kozłowski<sup>1</sup>**

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In fishing practice, individuals below a protective size are not harvested. This must have led to the dwarfing of the exploited species. Until recently, fishing has also been based on the false paradigm that fecundity is proportional to body weight, i.e. 10 females weighing 3 kg will lay as many eggs as one weighing 30 kg. However, comparative studies have shown that fecundity is characterised by hyperallometry (growth is faster than linear). How can fishing practices prevent fish dwarfism and overexploitation by being informed by life history theory? As I showed long ago, organisms capable of indeterminate growth should maximise fitness by allocating resources initially to growth and later between growth and reproduction, with an increasing proportion allocated to reproduction each year, leading to von Bertalanffy growth curves and hyperallometry of fecundity. In fact, age at maturity and subsequent optimal resource allocation depend on adult mortality, which varies with latitude and is dramatically increased by harvesting large individuals. Recently, I have also shown that life-history optimisation can produce interspecific patterns similar to the Beverton-Holt patterns that have been present in the fish literature since 1959 without satisfactory explanation.

My model shows that it is necessary to maintain large individuals in the population. The best solution is to create large reserves where fish reach high densities and many reach large sizes. Such reserves become source populations because the high fecundity of large and numerous females leads to an overproduction of juveniles that migrate to other fisheries, which are sink populations.

## **CT18: SURVEYING MICROBIAL SYMBIONTS' ROLES IN INSECT ADAPTATION AND RESPONSE TO THE CHALLENGES OF THE ANTHROPOCENE**

**Piotr Łukasik<sup>1</sup>, Karol Hubert Nowak<sup>1</sup>, Michał Kolasa<sup>1</sup>**

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Microbial symbionts can dramatically influence the life history traits of insects, including their nutrition, reproduction, and defense against various environmental challenges. Several known effects of symbiont infections are directly relevant to anthropogenic challenges identified as the primary drivers of insect biodiversity declines: pollution, invasive species, and climate change. However, our understanding of symbionts' diversity, distribution, transmission, and roles is limited outside model systems, and we know little about microbiome-related patterns and processes at the level of natural multi-species communities.

Here, I explain how to study microbiota across insect communities. I focus on amplicon sequencing of insect and microbial marker genes as a cost-effective tool for surveying thousands of specimens and tracking microbial symbiont transmission within and across multi-species communities. Using amplicon data for a large collection of insects from Greenland, I highlight patterns of insect community composition, as well as microbial distribution and apparent transmission across and within insect species. I explain how we can follow up on these results to reveal the importance and roles of microbial symbionts in insects' rapid response of adaptation to environmental challenges such as the rapidly warming climate.

# *Abstract: Contributed Talks*

## **CT19: EXPLORING THE COEVOLUTION OF BACTERIA AND PHAGES: INSIGHTS FROM STUDYING RECEPTOR-BINDING PROTEINS AND POLYSACCHARIDES**

**Rafal Mostowy**<sup>1</sup>

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Antimicrobial resistance is an escalating global health threat, necessitating novel therapeutic strategies. Among these, phages, or bacteria-infecting viruses, have emerged as a potential solution. However, to harness phages effectively, a profound understanding of the coevolutionary dynamics between bacteria and phages is crucial, given their extensive evolutionary battle spanning billions of years.

Our research focuses on interactions between bacterial surface sugars and phage receptor-binding proteins (RBPs) to elucidate this coevolution. In viral infection, bacterial polysaccharides are specifically recognized by phage RBPs. Simultaneously, recent advances in bacterial genomics highlight horizontal gene transfer's role in evolutionary innovation, with polysaccharide synthesis sites in bacteria emerging as hotspots.

Nevertheless, less is known about RBPs' evolutionary potential and their long-term coevolutionary dynamics with bacterial surface polysaccharides. Our findings shed light on this mystery: comparative genomics reveal that RBPs are among the most diverse and modular phage proteins, suggesting their status as evolutionary hotspots. Analysis of experimentally determined RBP structures show extensive domain modularity and sugar-specific predictive features. A study of prophages in *Klebsiella* bacteria genomes indicates presence of diversifying selection in the RBP regions in phage genomes.

In conclusion, our work points to strong co-evolutionary dynamics underlying RBP-capsule interactions and suggests that these dynamics should be considered for the design of successful phage therapeutics against bacterial infections with diverse polysaccharides.

## **CT20: HOW PHAGES PLAY WITH LEGO: STUDYING PROTEIN-LEVEL MOSAICISM IN PHAGES AND ITS EVOLUTIONARY IMPLICATIONS**

**Bogna Smug**<sup>1</sup>, **Krzysztof Szczepaniak**<sup>1</sup>, **Stanislaw Dunin-Horkawicz**<sup>2</sup>, **Eduardo P.C. Rocha**<sup>3</sup>, **Rafal Mostowy**<sup>1</sup>

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Phages exhibit remarkable genetic modularity, which allows their genomes to evolve independently and combine, resulting in astounding diversity. While genome mosaicism in phage populations has been studied, less is known about protein modularity and its impact on viral evolution. To fill this knowledge gap, here we quantified such modularity by detecting instances of protein mosaicism, defined as a homologous fragment between two otherwise unrelated proteins. We used highly sensitive homology detection to quantify protein mosaicism between pairs of 133,574 representative phage proteins and to understand its relationship with functional diversity in phage genomes. We found that diverse functional classes often shared homologous domains which was often linked to extensive protein mosaicism, particularly in receptor-binding proteins, endolysins, and DNA polymerases.

To further investigate protein mosaicism in phages, we created a database of evolutionary conserved fragments (ECFs) of phage proteins. This database contains fragments not covered by known domain databases such as PFAM or ECOD, enabling better examination of the structural architecture and mosaicism of diverse phage proteins, including receptor-binding proteins, and enhancing understanding of rare accessory proteins and underrepresented proteins due to their diversity.

Our study reveals ongoing diversification via shuffling of protein domains, indicative of co-evolutionary arms races and diversifying selection towards circumventing bacterial resistance.

# *Abstract: Contributed Talks*

## **CT21: EXPLORING THE RELATIONSHIP BETWEEN TARGETING PEPTIDES AND ANTIMICROBIAL PEPTIDES: INSIGHTS INTO EVOLUTION AND FUNCTIONAL IMPLICATIONS**

**Przemysław Gagat<sup>1</sup>, Katarzyna Sidorczuk<sup>1</sup>, Filip Pietluch<sup>1</sup>, Michał Ostrówka<sup>1</sup>, Anna Duda-Madej<sup>2</sup>, Michał Burdukiewicz<sup>3</sup>, Alicja Seniuk<sup>2</sup>, Paweł Mackiewicz<sup>1</sup>**

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Targeting peptides or presequences are N-terminal extensions of proteins that encode information about their cellular localization. They encompass signal peptides (SP), which facilitate protein targeting to the endoplasmic reticulum (ER), and transit peptides (TP) that direct proteins to organelles of endosymbiotic origin, such as chloroplasts and mitochondria. TPs are postulated to have evolved from antimicrobial peptides (AMPs), which play a vital role in host defence against various microorganisms, including bacteria, fungi, and viruses. To test this hypothesis, we investigated presequences and AMPs in terms of their amino acid composition, physicochemical properties and antimicrobial activity as well as motif composition. We identified motifs frequently occurring in each type of investigated peptide group showing specific patterns associated with their amino acid composition, and investigated their position within the peptide. Moreover, we examined motif patterns among different taxonomic groups and identified taxon-specific motifs, providing further evolutionary insights. Our results allowed us to redefine targeting peptides and indicate that TPs share many characteristics with AMPs, as well as SPs. However, it is more likely that the similarities between presequences and AMPs are a result of convergent evolution rather than common evolutionary origin. We also tested experimentally antimicrobial properties of selected targeting peptides as well as short amyloids; the latter have also been hypothesised to share evolutionary connections to AMPs. Considering the functional importance and many practical applications of targeting peptides and AMPs, we believe that our analyses will prove useful for their design, and better understanding of protein import mechanism and presequence evolution.

## **CT22: PHYLOGENY AND PAN-GENOME OF *PROTEUS MIRABILIS*: WITH THE FOCUS ON TYPE VI SECRETION SYSTEM EFFECTORS DIVERSITY**

**Dawid Gmiter<sup>1</sup>**

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Due to the increasing number of available bacterial genomes, it is possible to analyze the genetic variability of bacteria in details, e.g., through the phylogeny based on single nucleotide polymorphisms, as well as on differences in genomes arrangement. In recent years, an approach has been developed that focuses on bacterial pan-genome-based phylogeny, which allows the presentation of strains diversity based on the set of genes encoded by individual genome. *Proteus mirabilis* strains can discriminate friends from foes during swarming over agar plates. This process, known as Diene's phenomenon, reflects their genetic diversity. However, details of these dependencies, especially in terms of whole genomes relatedness, remains unclear. Therefore, this study aimed at the comparative genomic analysis of world-wide *P. mirabilis* isolates, together with the investigation of their pan-genome, in relation to kin recognition mechanisms.

The REALPHY and FastANI programs were used to study the general similarity of genomes. Next, pan-genome analysis was performed using the Roary program. The results of the pan-genome analysis were then extended by the gene-gene interaction investigation using the Coinfinder program. Finally, phylogeny based on the non-coding regions was performed using Piggy pipeline, in addition to above. Further, study focused on type VI secretion system genes diversity, as this system allows contact-dependent recognition and communication between genetically related strains. The presented studies allowed for the first time to characterize the genomic variability of *P. mirabilis* strains. Further, obtained results gave insight into the divergence of molecular basis of kin discrimination in *P. mirabilis*.

# *Abstract: Contributed Talks*

## **CT23: THE BREAKDOWN OF AN ANCIENT OBLIGATORY ENDOSYMBIONT IN A CLADE OF PLANTHOPPERS**

**Junchen Deng<sup>1</sup>, Diego Franco<sup>1</sup>, Anna Michalik<sup>2</sup>, Piotr Łukasik<sup>1</sup>**

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The highly reduced genomes of ancient mutualistic endosymbionts are often featured by the long-term stability in gene content and genome structure. However, the increasing genetic load and the changing nutritional environment may eventually push endosymbionts to degeneration, extinction, or replacement. Bacteroidetes symbiont ‘*Candidatus Sulcia muelleri*’ is known for its impressive conservation in gene order after ~300 million years of coevolution with Auchenorrhynchan hosts (planthoppers, cicadas, spittlebugs, leafhoppers, and treehoppers). Here, we show that in the planthopper genera *Stenocranus* and *Kelicia* (family Delphacidae), *Sulcia* exists in a degenerative state. The metagenomic assemblies suggest that the ancestral *Sulcia* has fragmented into ~10 lineages. A core set of seven genes (including *rpoB*) essential for genetic information processing are retained by most lineages while additional genes involved in metabolism and nutrient biosynthesis are scattered across lineages as single copies, indicating functional interdependence among them. Further screening of *rpoB* variants through species and populations indicate that the lineage splitting happened both in the ancestor of two genera and independently in each genus, and the splitting is ongoing. Overall, our findings represent a unique outcome of genome breakdown in endosymbionts. I will explain our efforts to characterize these novel symbioses through the combination of long-amplicon sequencing, single-cell genomics, and advanced microscopy.

## **CT24: NEW INSIGHTS INTO THE EVOLUTION OF COMPLEX PLASTIDS: UNVEILING THE ORIGINS AND DIVERSIFICATION TIMES OF RED ALGA-DERIVED LINEAGES**

**Filip Pietluch<sup>1</sup>, Paweł Mackiewicz<sup>1</sup>, Przemysław Gagat<sup>1</sup>**

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The double-bounded plastids represent a direct offspring of the cyanobacterial endosymbiont and therefore, they are referred to as primary plastids. Importantly, there are many plastid types with envelopes composed of more than two membranes. These plastids are known as complex plastids, and their origin required the expansion of the original version of the endosymbiotic theory. In order to explain the evolution of red complex plastids, Cavalier-Smith put forward the Chromalveolata hypotheses. The chromalveolata model postulated a single red-alga endosymbiosis for the origin of plastids in cryptophytes, haptophytes, stramenopiles, dinoflagellates and apicomplexans, and shaped our views on plastid evolution for more than a decade. Yet through the test of time, the phylogenetic analyses disproved this model, i.e. the monophyly of the Chromalveolata clade. It was next substituted for the serial plastid endosymbioses model assuming a single red-alga acquisition by cryptophytes and multiple higher order endosymbioses. In this study, we investigate the evolution of red alga-derived plastids using 96 plastid-encoded markers, 113 species and employing maximum likelihood and Bayesian approaches. Our phylogenetic analyses indicate that there must have been two independent secondary red-alga endosymbioses, which argues with all previously published models. Accordingly, we propose a new model for the origin of red alga-containing lineages and, by employing molecular clock analyses, determine the age for the lineages as well. Additionally, we investigate the influence of alignment trimming, i.e. the number of variable and parsimony informative sites on the tree topology.

# *Abstract: Contributed Talks*

## **CT25: CAN FEMALE GUPPIES LEARN TO LIKE MALE COLOURS?**

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How do female sexual preferences for male ornamental traits arise? Despite over four decades of research on sexual selection, the origin of female preferences is still an understudied area, with most explanations pointing to the role of adaptive mechanisms. One intriguing, but little-explored, alternative focuses on the role of associative learning in driving this process. According to this hypothesis, a preference learned in an ecological context can be transferred into a sexual context, resulting in changes in mating preferences as a by-product. Here, I tested this hypothesis by first training female guppies to associate either orange or black colour with food delivery; I then presented videos of males with computer-manipulated coloured spots and measured female preference towards them. I also allowed females from both treatments to mate with males differing in their ratio of orange-to-black spots and measured the males' reproductive success. After training, females from both treatments showed preference for male colouration that matched the colour they were conditioned on. In addition, orange males sired a greater proportion of offspring with females who were food-conditioned on orange compared to those conditioned on black. These results show that mating preferences can arise as a by-product of associative learning, which, via translation into variation in male fitness, can become associated with indirect genetic benefits, potentially leading to further evolution.

## **CT26: THE IMPACT OF TEMPERATURE VARIABILITY ON PHYSIOLOGICAL RESPONSES AND LEARNING IN ZEBRA FINCHES**

**ChuChu Lu<sup>1</sup>, Diego Gil<sup>2</sup>, Maëlle Lefevre<sup>1</sup>, Joanna Rutkowska<sup>1</sup>**

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The recent increase in climate variability and unpredictability poses significant challenges to the behaviour and survival of animals. Surprisingly, there is hardly any experimental study investigating the effects of temperature variability on the physiology and cognition of endothermic animals. The aim of this study is to assess the impact of temperature variability during development and adulthood on physiological responses and learning ability in zebra finches (*Taeniopygia guttata*). The birds were bred in either stable (constant daytime temperature at 21°C) or variable (daily fluctuation between 11°C and 30°C degrees with the mean of 21°C) ambient temperature conditions. We focused on testing the colour-associative learning performance of the juveniles (N = 261, 55-65 days of age) and measured the accumulated corticosterone (CORT) levels in their feathers (N = 246) at approximately 80-95 days old. We found that birds exposed to variable temperatures during development had higher CORT levels and shorter latency to choice in the learning test compared to those in stable conditions. Furthermore, increased CORT levels were associated with lower test participation rates. We conclude that ambient temperature variability has no discernible impact on associative-learning performance. However, it may indirectly affect their behavioural responses through alterations in the CORT concentration. This study emphasizes the importance of understanding the link between physiological changes and behavioural consequences of climate fluctuations in the environment.

# *Abstract: Contributed Talks*

## **CT27: RESPONSE OF AFRICAN FOREST TURTUR DOVES TO CONSPECIFIC AND CONGENERIC SONGS IN SYMPATRY AND ALLOPATRY**

**Małgorzata Niśkiewicz<sup>1</sup>, Paweł Szymański<sup>1</sup>, Michał Budka<sup>1</sup>, Tomasz Osiejuk<sup>1</sup>**

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Birds have a diverse acoustic communication system, and the ability to recognise their own species' song from a distance facilitates complex behaviours related to mate attraction and rival deterrence. However, certain species, including doves, do not learn songs and their vocal repertoires are much simpler than those of better-studied songbirds. In these so-called non-learning birds, relatively little is known about the role that bird song plays in intra- and interspecific interactions, and how such behaviours might be acquired (inherited or learned from experience). To investigate this question, we focused on two species of African wood doves whose long-range songs are used in a territorial context. We examined the responses of sympatric and allopatric populations of male blue-headed wood-doves (*Turtur brehmeri*) and tambourine doves (*Turtur tympanistria*) to playback of conspecific, congeneric, and control songs. We found that both species responded strongly to playback of their own species in both sympatric and allopatric populations. In allopatry, though, male tambourine doves misdirected their response and also approached the playback of congeneric songs. The difference in tambourine doves' response toward the song of present (sympatric) or absent (allopatric) congeners suggests that the ability to discriminate between songs of similarly singing potential competitors is acquired through earlier interactions and learning. This plasticity in response supports the misdirected aggression hypothesis, which argues that interspecific territorialism emerges as a maladaptive by-product of signal similarity. However, on an evolutionary timescale, such an ability could be considered an adaptive cognitive tool useful for resolving competing interests with congeners.

## **CT28: ARCTIC ATLANTIFICATION: FOR HOW LONG HAS IT BEEN GOING ON? A POPULATION GENOMIC CASE STUDY OF THE NORTHERN ACORN BARNACLE ON SVALBARD**

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In recent days, the Svalbard archipelago is experiencing the fastest temperature increases, and the highest sea ice loss within the High Arctic. Thus the 'Atlantification' of this area has been a focal point of present-day polar research. The alteration of the Arctic marine ecosystems towards a more temperate state and the range expansion of subarctic-boreal species at higher latitudes is a complex phenomenon, mainly induced by the warming climate conditions and potentially by human-mediated transportation. Here, we used low coverage whole genome data to study the population demography of the northern acorn barnacle, *Semibalanus balanoides* in the North Atlantic-European Arctic region. Particularly, we were interested in characterizing the Svalbard populations and their genetic connectivity to other areas within the North Atlantic. In this study 78 individuals were sampled from areas including Iceland, the Faroe Islands, the British Islands, as well as the Norwegian, Barents and White Seas and Svalbard. Svalbard populations form an independent genetic cluster, unrelated to any of the other genetic clusters inferred from our sampled populations. Summary statistics such as Tajima's D and demographic reconstruction rule out the possibility that the differentiation is the result of a recent founder event. Instead, our results point to an ancient, isolated lineage that has been living in the Arctic since the beginning of the last interglacial period.

# *Abstract: Contributed Talks*

## **CT29: DEVELOPMENT OF SEXUAL SIZE DIMORPHISM IN LIZARDS: THE PROBABLE ROLE OF IGF1**

**Brandon Meter<sup>1</sup>, Lukáš Kratochvíl<sup>2</sup>, Lukáš Kubička<sup>2</sup>, Zuzana Starostová<sup>1</sup>**

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Recent studies demonstrate that bone prolongation is stopped in many lizards by the closure of bone growth plates indicating determinate growth. Considering this, the proximate causes of sexual size dimorphism can be reevaluated. Using gecko genus *Paroedura* as a model we aimed to understand the proximate causes of sexual size dimorphism. Finding a pattern of canalized growth in male larger species *Paroedura picta* we monitored growth of this species throughout the growth curve to assess the sex specific growth and growth plate closure patterns. Activity of bone growth plates was tracked along gonad size, levels of steroids, expression of their receptors (AR, ESR1), and expression of genes from the insulin-like growth factor network (IGF1, IGF2, IGF1R, and IGF2R) in livers. More specifically, gene expression at the beginning of the growth curve or before the onset of sexual size dimorphism, after the onset and at the very end of the growth curve. This yielded results of a significant spike in the expression of IGF1 in males around the time of dimorphism development. This overexpression might be suppressed by ovarian hormones in females. This suggests a role of IGF1 in male-larger sexual size dimorphism through bone growth. Furthermore, experiments on non-dimorphic species *Paroedura vazimba*, show no biologically relevant differences in IGF1 expression among age/sex groups for this species. Monitoring of growth plates and steroid hormones for *P. vazimba* is planned to further study proximate causes of sexual size dimorphism and the possible role of ovarian hormones.

## **CT30: HIGH-THROUGHPUT SEQUENCING UNRAVELS THE HIDDEN DIVERSITY OF BARK BEETLE-ASSOCIATED NEMATODES**

**Julia Morales-Garcia<sup>1</sup>, Piotr Lukasik<sup>1</sup>, Krystyna Nadachowska-Brzyska<sup>1</sup>**

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The spruce bark beetle (*Ips typographus*) has become one of the most destructive forest pests in Europe. Under certain conditions, this species can outbreak and increase in population size by orders of magnitude, causing the death of thousands of hectares of its host, Norway spruce (*Picea abies*). These outbreaks are becoming increasingly important as they have intensified in southern and central Europe in recent years. A comprehensive description of the biotic interactions of this important species is necessary to understand these outbreaks and to manage them effectively.

The spruce bark beetle is known to be frequently parasitised by nematodes, but despite a growing number of studies on its interactions with symbiotic and parasitic species, our understanding of the diversity, distribution and biological significance of these insect-nematode associations is very limited.

Here, we use high-throughput sequencing to reveal nematode diversity in 312 specimens from 24 European spruce bark beetle populations. We found reads corresponding to seven different species of nematodes in a large percentage of beetle samples. This is the first large-scale study of nematode diversity in *Ips typographus* across the species range. In many cases, nematode DNA makes up a large proportion of the metagenomic data sets, suggesting that nematodes have a significant impact on their beetle hosts. Taken together, our data show that sequencing-based methods offer rich opportunities to unravel the diversity and distribution of interspecific interactions.

# *Abstract: Contributed Talks*

## **CT31: HOW THE INTRASPECIFIC VARIATION IN GRANIVORES IMPACTS SEED DISPERSAL?**

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The complexity of seed dispersal is intricately tied to the traits of animals, as individuals within the same species can display considerable variation. As a result, differences may arise in their performance regarding the proportion of seeds they disperse, consume, or their preferences for seeds deposition sites. Despite this complexity, few studies have thoroughly explored the effects of individual forager traits on seed dispersal. We conducted our study in Puszcza Zielonka Landscape Park near Poznań. Yellow-necked mice (*Apodemus flavicollis*) were trapped at six study sites, each with 100 traps of type “dziekanówka”, placed at 10-m spacing. We assessed sex, weight and reproductive status of each captured animal. All individuals received a unique ear tag and PIT-tag injected under mice’s skin on the back. After each trapping session we conducted a seed removal experiment using automatic pit-tag readers and camera traps, to link the individual to the removed seeds. We found that more explorative individuals tend to disperse seeds further from trees. Furthermore, larger individuals carried seeds over greater distance in two out three years of the study. However, the effect of other individual traits on seed dispersal varied among years. We concluded that the impact of individual traits of mouse on seed dispersal is strongly context –dependent and may vary depending on changes in the environment.

## **CT32: USING VIRTUAL REALITY TO TEACH UNDERGRADUATE STUDENTS TO CONDUCT RESEARCH IN ECOLOGY AND EVOLUTION**

**Michael Angilletta<sup>1</sup>, Kiara Crawford<sup>1</sup>, Madison Delaney<sup>1</sup>, Tray Geiger<sup>1</sup>, Annie Hale<sup>1</sup>, Rachel Luchmun<sup>1</sup>, Christopher Pagliarulo<sup>1</sup>, Alysha Ramirez<sup>1</sup>, Liesel Sharabi<sup>1</sup>, John Vanden Brooks<sup>1</sup>, Christian Wright<sup>1</sup>**

1 Arizona State University, United States

We present a new way of learning how to conduct research in ecology and evolution through immersive experiences in virtual reality. This new approach, called Dreamscape Learn, enables students to enter a fictional world, where an artificial intelligence has created an intergalactic wildlife sanctuary to preserve endangered ecosystems from across the galaxy. In each learning module, students become the heroes of a story—discovering, investigating, and solving novel but realistic problems. A narrative arc continues throughout experiences in VR and in the classroom, creating an immediate need to learn concepts and skills. Undergraduate students in this new curriculum were almost twice as likely to score between 90 and 100% on assignments than were students in the existing curriculum at Arizona State University. Moreover, Dreamscape Learn substantially reduced historical performance gaps between certain groups of students. Students who participated in VR more frequently also felt more engaged in the course and performed better on assignments. This research underscores the benefits of leveraging emerging technologies and narrative structure to enhance education and training in science and other fields of research.

# *Abstract: Contributed Talks*

## **CT33: WHERE DO THEE COME FROM? – TIME-CALIBRATED PHYLOGEOGRAPHY OF THE NEARCTIC MILNESIUM (TARDIGRADA)**

**Karol Walach<sup>1</sup>, Jacob Loeffelholz<sup>2</sup>, Witold Morek<sup>3</sup>, Alejandro López-López<sup>1</sup>, Jason Pienaar<sup>4</sup>, Łukasz Michalczyk<sup>1</sup>**

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2 University of Alabama, United States

3 Wellcome Sanger Institute, United Kingdom

4 Florida International University, United States

Being microscopic in size (typically ca. 0.5 mm) and exhibiting cryptobiotic abilities, tardigrades are one of the animal groups of which geographic distribution patterns should be explained by the ‘Everything is Everywhere but environment selects’ (EiE) hypothesis, which predicts quasicosmopolitan to cosmopolitan species ranges. However, recent studies, carried out under the integrative taxonomy framework, suggest that most tardigrade species have limited geographic distributions. Thus, a question what mechanisms and events have shaped tardigrade biogeography arises.

In this study, we aim to determine the origin of the Nearctic limnoterrestrial tardigrade fauna using the genus *Milnesium*, one of the few tardigrade groups for which ample distribution data are available for the Palaearctic and the Neotropics, i.e. the closest zoogeographic realms to the Nearctic. We have analysed nearly 200 *Milnesium* populations from across the world, of which over 40 were collected in the USA. We sequenced four molecular markers: 18S and 28S rRNA, ITS-2, COI and constructed a time-calibrated phylogeny.

We obtained a well-supported phylogenetic tree showing complex relationships among *Milnesium* species, with most clades limited to single zoogeographic realms. The great majority of the newly sequenced Nearctic species grouped in a single Nearctic clade and represent species new to science. Surprisingly, the Nearctic *Milnesium* fauna is more closely related to the Neotropics than the Palaearctic and is estimated to be 40 million years old. Acquired data strongly shows that *Milnesium* possess very limited dispersal abilities, further confirming that the biogeography of the genus does not conform to the EiE hypothesis.

## **CT34: DETECTION OF GREY WOLF AND GOLDEN JACKAL HYBRIDIZATION WITH FREE RANGING DOMESTIC DOGS ACROSS EURASIA USING SNP MARKERS**

**Roya Adavoudi<sup>1</sup>, Malgorzata Pilot<sup>1,2</sup>**

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2 Faculty of Biology, University of Gdansk, Poland

Hybridization between domesticated species and their wild relatives can have significant evolutionary consequences. Hybridization in the genus *Canis* is relatively frequent and typically leads to the production of fertile offspring that may back-cross into parental populations. We analyzed genome-wide SNP data to detect signatures of admixture and patterns of introgression in wolf, dog and golden jackal populations from across Eurasia. We used Bayesian clustering approach implemented in Admixture to estimate proportion of dog ancestries in wild canid populations. For identification of ancestry blocks originating from introgression in each individual, we carried out local ancestry analysis using LAMP and GHap R packages. Using global ancestry estimation, we were able to identify up to F3 generation backcrosses. The local ancestry analysis, carried out for each of the 38 autosomal chromosomes, demonstrated the presence of small blocks of dog ancestry in the genomes of wild canids. The average proportions of dog ancestry in wolves and golden jackals were estimated at 0.034 and 0.0065, respectively. Our results show that introgression of dog-derived genetic variants into gene pools of wolves was more extensive as compared

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with golden jackals. It may be explained by the fact that wolf and dog are more closely related and therefore we may expect less negative consequences for fitness in wolf-dog hybrids compared with jackal-dog hybrids. However, the rate of hybridization between dogs and golden jackals may increase as a result of the current northward range expansion of golden jackals across Eurasia, which may lead to higher introgression rates.

### **CT35: IMMUNITY INVESTMENT DOES NOT DROP DOWN IF YOU TOLERATE INFECTION AND REPRODUCE AFTER INFECTION**

**Franziska Brenninger<sup>1</sup>, Viktor Kovalov<sup>1</sup>, Hanna Kokko<sup>2</sup>**

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<sup>2</sup> Institute for Organismic and Molecular Evolution, Johannes Gutenberg University of Mainz, Germany

Originally, theoretical studies predicted the evolution of higher level of host species resistance with increase in parasitic pressure. However, greater resistance requires investments into immunity that may trade off with reproduction. Moreover, immunity investments may not pay off when the risk of infection is so high that even high investment in immunity will not be effective in preventing infection. This is why more recent theoretical and experimental work has begun exploring “resistance is futile” outcomes where individuals benefit from reduced immunity under high parasite abundance. Tolerance – the capacity of organisms to mitigate the negative effects of infections – is an alternative immunity mechanism that helps lower infection-related mortality. Thus, individuals investing into tolerance may benefit from prolonged lifespan if they can reproduce despite being infected. The effect of tolerance on immunity investments has not been investigated thoroughly, especially in combination with varying strength of sexual selection and parasite severity. Here we build a model to investigate whether optimal immunity investments differ between two scenarios, where organisms either tolerate infection or not (“resistance only” immunity). When parasites are scarce, their abundance rise initially causes immunity investments to increase in both scenarios. The difference arises at high level of parasite abundance, where individuals with tolerance keep their immunity investments constant, while “resistance only” individuals drop immunity investments, as predicted by the “resistance is futile” outcome. Our results confirm that tolerance has a potential to affect the optimal immunity investments with consequences on reproductive success and life-history traits, e.g., lifespan.

### **CT36: GENOMIC INSIGHTS INTO POPULATION HISTORY OF SCOTS PINE (P. SYLVESTRIS L.)**

**Witold Wachowiak<sup>1</sup>, Bartosz Łabiszak<sup>1</sup>**

<sup>1</sup> Faculty of Biology, Adam Mickiewicz University, Poznań, Poland

Scots pine (*Pinus sylvestris* L.) is one of the most important tree species of the temperate and boreal zones in Eurasia. Its wide distribution range and current patterns of genetic variation have been influenced by climatic changes during the Quaternary period, along with the associated demographic processes. To better understand the relationship between evolutionary history and demographic factors in this widespread species with a large genome, we used maternally inherited mitochondrial DNA markers and thousands of single nucleotide polymorphism markers (SNPs) from nuclear genome to assess patterns of genetic variation in dozens of natural populations from the wide distribution range in Eurasia. Specifically, we examined the contemporary population structure of species and analyzed the range-wide genetic diversity patterns. We identified traces of past admixture events between distinct genetic clusters. Surprisingly, these genetic signatures have persisted despite the potential for effective pollen-mediated gene flow throughout the wide range of species distribution. Through phylogenetic analyses and demographic modeling we inferred that the observed divergence between genetic lineages likely predates the last glaciation events. The study provides insights into the genetic relationships of Scots pine populations from Europe and Asia and offers a more comprehensive understanding of the species history

# *Abstract: Posters*

## **P01: THE OUTSTANDING EFFECT OF POSITIVE EPISTASIS ON FITNESS IN MONOSOMIC YEAST STRAINS**

**Hanna Tutaj<sup>1</sup>, Katarzyna Tomala<sup>1</sup>, Ryszard Korona<sup>1</sup>**

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We asked how diploid organisms can remain relatively fit despite having multiple function-canceling mutations, mostly in a heterozygous state. Initially, we studied diploid *Saccharomyces cerevisiae* yeast strains with a single heterozygous gene deletion and observed slight growth defects in many of them. When these defects were combined over entire individual chromosomes, they became burdensome enough to cause negative growth rates, that is, lethality. However, strains derived from these diploids by deleting a single copy of one of the chromosomes (monosomics) continued to proliferate despite carrying loads of such a magnitude, suggesting the presence of a very strong and positive epistasis for fitness. To explore the underlying mechanisms, we analyzed the transcriptomes of the monosomic strains. We found no widespread compensation for gene dosage or cellular stress response as potentially healing the harm caused by chromosome loss. However, genes encoding ribosomal proteins were generally upregulated, while those encoding the proteasome were downregulated. We propose that the primary obstacle to the growth of the monosomic strains was the stoichiometric imbalance of ribosomal proteins. Mutations located outside the fitness-defining module, biosynthesis, did not exert much of their predicted negative effect. Overall, it was the modular structure of the cell that effectively fragmented the overall burden of mutations resulting in the epiphenomenon of positive epistasis between the multiple and individually detrimental effects.

## **P02: COMPLEX GENOME REARRANGEMENTS IN THE MODEL EUKARYOTIC ORGANISM SACCHAROMYCES CEREVISIAE**

**Adrian Piróg<sup>1</sup>, Hanna Tutaj<sup>1</sup>, Katarzyna Tomala<sup>1</sup>, Ryszard Korona<sup>1</sup>**

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

Genome instability can be adaptative for microorganisms encountering new environments. We asked what initial genetic changes can lead to further extensive genome rearrangements. We created a collection of 400 strains of yeast *Saccharomyces cerevisiae* which were diploid and contained a homozygous deletion of a single gene presumably involved in genome stabilization. We then tested for the rate of single or complex rearrangements by scoring mutants with the loss of heterozygosity (LOH) occurring separately or simultaneously at two loci located on different chromosomes. We detected several dozen gene deletions causing a pronounced (10-100x) increase in the rate of single LOH and even higher (10-1500x) of the double LOH. Furthermore, depending on the studied gene deletion, we observed case-specific changes in ploidy, either an average reduction or increase in the amount of DNA. Subsequently, strains exhibiting the most radical deviations from diploidy were subjected to long-term evolution. We found that the initially highly aneuploid strains tended to improve their growth rate by returning to the euploid state rather than by stabilizing or extending aneuploidy. We also observed that although most aneuploids had a decreased chronological lifespan, some of them exhibited the opposite effect. In conclusion, we identified dozens of gene deletions associated with greatly increased rates of single- and multi-point gene destabilizations. Malfunctioning of these genes can enable faster adaptive evolution by providing highly altered and conditionally beneficial genomic configurations.

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## P03: HOW IS QUIESCENCE STUDIED IN *S. CEREVISIAE*? A SYSTEMATIC REVIEW

**Monika Opalek<sup>1</sup>, Hanna Tutaj<sup>1</sup>, Adrian Pirog<sup>1</sup>, Bogna Smug<sup>2</sup>, Joanna Rutkowska<sup>1</sup>, Dominika Wloch-Salamon<sup>1</sup>**

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Quiescence, the temporary and reversible arrest of cell growth, is a fundamental biological process. However, the lack of standardization in reporting experimental details of quiescent cells and populations can cause confusion and hinder the knowledge transfer. We employ the systematic review methodology to comprehensively analyse diversity of approaches to study quiescent state, focusing on all published research conducted on the budding yeast, *Saccharomyces cerevisiae*. We group research articles into those that consider all cells composing the stationary phase (SP) population as quiescent and those that recognize heterogeneity within the SP by distinguishing phenotypically distinct subpopulations. Furthermore, we investigate the chronological age of quiescent populations under study and the method used to induce quiescent state, such as gradual starvation or abrupt environmental change. We also assess whether the strains used in research were prototrophic or auxotrophic. By combining the above features, we identify 48 possible experimental setups to study quiescence, which can be misleading while drawing general conclusions. We therefore summarise our review by proposing recommendations and guidelines for information to be included in the research articles. We believe that more rigorous reporting on features of quiescent populations will facilitate knowledge transfer within and between disciplines, thereby stimulating valuable scientific discussion.

The student was funded by the project entitled "ATUT PhD Programme in Biology". The project is co-financed by the European Union under the European Social Fund – Operational Programme Knowledge Education Development.

## P04: EVOLUTION OF SIMULATED 3D ORGANISMS

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This presentation introduces Framsticks, a software environment that can simulate various biological phenomena. A simulated organism is made of a mechanical structure ("body") and a control system ("brain" – a network of artificial neurons). Such an organism (a phenotype) is encoded by a genotype.

There are many genetic encodings (genetic languages) available, each of which determines the way a genotype is transformed into a phenotype. Genetic encodings differ in the way they transform genotypes into phenotypes: some genetic representations are simple and direct, while others may involve complex developmental processes including cell differentiation or repeated interpretation of genes. Genotypes are subject to mutation and crossover.

Phenotypes can be evaluated in simulation, so their fitness can be determined. This way, the Framsticks system provides basic components (variation, selection, inheritance) sufficient to perform evolutionary processes under fully controlled conditions. In particular, Framsticks allows to model various genotype-to-phenotype mappings, pleiotropy, polygeny, artificial selection pressures and fitness criteria, fitness landscapes, evolution with exogenous and endogenous fitness, and coevolutionary dynamics. It is also possible to study the influence of mutation rates on behavioral and morphological adaptations, estimate epistasis, and build phylogenetic trees based on complete ancestral information.

The software is released for desktop and mobile devices and is available at <https://www.framsticks.com/>

# Abstract: Posters

## **P05: THE USE OF COMPUTER SIMULATIONS IN THE STUDY OF EVOLUTION**

**Szymon Ptak<sup>1</sup>**

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The study of evolution has been challenging due to its limited ability to be studied experimentally. Observational studies have been the primary method of examining the effects of evolution, with experimental studies often being restricted to model organisms with short reproductive cycles. Fortunately, recent advancements in technology have created new opportunities for research in this area, specifically through the use of computer simulations. My goal is to provide an overview of various methods based on computer simulations that can be utilized to study the diverse aspects of evolution. These include: using cellular automata to test classic evolutionary models, simple particle motion law simulations for examining the emergence of life, and artificial neural networks for designing digital animals capable of movement. The significance of such tools and studies and their potential impact on evolutionary biology, evolutionary ecology, and robotics are highlighted.

## **P06: R AND K SELECTION CONCEPT VERSUS RECRUITMENT LOTTERIES. DO WE HAVE LAWS OF EVOLUTION OR RATHER MECHANISMS?**

**Krzysztof Argasinski<sup>1</sup>**

1 Mathematics Mechanics and Informatics, Warsaw University, Poland

The idea of  $r$  and  $K$  selection is a little bit outdated; however, it still remains present in scientific debates. It has been criticized from the perspective of empirical observations and has been subsequently replaced by more sophisticated and mechanistic life history theory. Despite its historical significance, the  $r$  and  $K$  theory continues to be important for the development of theoretical ecology and evolutionary biology. It serves as a prime example of how we should NOT interpret mathematical models in biology. In this talk, we will analyze the basic assumptions underlying the  $r$  and  $K$  selection concept based on the logistic model of population growth and resulting conclusions. Subsequently, we will compare these assumptions with analogous aspects of the newer approach called recruitment lottery models. These models are based on more mechanistic growth models that explicitly take into account demographic mechanisms such as the turnover of individuals, unlike the phenomenological models mimicing trajectories. Surprisingly, the new models suggest exactly the opposite conclusions to the  $r$  and  $K$  selection concept. While  $r$  and  $K$  strategies are defined as the number of offspring at low densities versus quality at high densities, the recruitment lottery models show an opposite relationship—high number of offspring at high densities and the maintenance of a positive growth rate at low densities. This raises more general questions about the falsifiability and limits of interpretation of simplified reductionist mathematical models used in ecology and evolutionary biology.

# Abstract: Posters

## **P07: OXIDATIVE STRESS CORRELATES WITH IMMUNOCOMPETENCE IN BREEDING FEMALES OF WILD LONG-LIVING MAMMAL - EDIBLE DORMOUSE GLIS GLIS**

**Karolina Iwińska<sup>1</sup>, Jan S. Boratyński<sup>2</sup>, Joanna Błońska<sup>3</sup>, Zbigniew Borowski<sup>4</sup>, Aneta Książek<sup>3</sup>, Marek Konarzewski<sup>3</sup>**

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4 Forest Research Institute, Poland

In the last decades oxidative stress (OS) has been proposed as a mechanism mediating evolutionary trade-offs between reproduction and survival. Elevated metabolic rate during reproduction increases the risk of OS, which contributes to faster aging and shorter lifespan. Studies showed that animals use oxidative shielding - up-regulation of antioxidants to protect themselves and offspring from oxidative damage. OS is also a consequence of mounting an immune response, therefore immunosuppression during reproduction can be an adaptive reaction to shield an organism against pro-oxidants. We conducted our study on breeding (lactating and post-lactating) and non-breeding wild edible dormouse *Glis glis*, a long-living rodent, that is therefore expected to prioritize somatic maintenance. We hypothesized that in breeding females there is a direct link between oxidative and immune defence status. We expected that a proxy of immunological defence – the white blood cell (WBC) level and a marker of oxidative damage - reactive oxygen metabolites (ROM's) in plasma will be lower, while antioxidant capacity (OXY) will be higher in breeding than non-breeding females. Thus, we expected that OXY will negatively, while ROM's will positively correlate with the WBC level. There was no difference in OXY level but we found that low level of ROM's in lactating and post-lactating females was correlated with fewer WBC among reproductive groups. Our results show that females suppress cellular immunological defence to reduce the risk of OS during reproduction. This suggest that parallel changes of immunological system and oxidative stress costs during reproduction may shape evolutionary trade-off.

## **P08: TURNING UP THE HEAT: THE EFFECT OF SHIFTS IN THE THERMONEUTRAL ZONE OF MICE ON THE OUTCOMES OF TRANSLATIONAL RESEARCH**

**Andrzej K Gebczynski<sup>1</sup>, Julita Sadowska<sup>1</sup>, Marek Konarzewski<sup>1</sup>**

1 Department of Evolutionary and Physiological Ecology, Faculty of Biology, University of Białystok, Poland

Laboratory mice are commonly used for studies emulating human energetics. To render reliable results a ratio of daily (DEE) to basal (BMR) energy expenditures should mirror that of humans i.e., 1.7-1.8. Since the key factor affecting DEE/BMR ratio is ambient temperature, we demonstrate that determining the lower critical temperature (LCT) of the thermoneutral zone is not trivial and strongly dependent on the level of body mass-corrected BMR. Using mice artificially selected for high or low rates of BMR we established the range of LCTs, their DEE/BMR ratio, and pelt conductance. To further demonstrate the severity of the problem, we pooled data from the literature and calculated the range of LCTs and DEE/BMR in mouse strains commonly used in translational research to showcase along our novel data. We showed that the LCTs of mice from the high and low BMR lines differed by 9°C, and the range of variation of LCTs of mouse strains spans from 23 to 33°C. Differences between LCTs, in the selected mice and literature data, were mirrored by differences in their DEE/BMR ratio, on average increasing it at the rate of 0.164°C<sup>-1</sup> at temperatures below LCTs. We conclude that thermal housing conditions, most appropriate for translational research using mice, especially within TNZ, should be chosen based on the individual strain characteristics, because LCT, associated with BMR, does vary widely among the mouse strains.

# Abstract: Posters

## **P09: TESTING THE THRIFTY AND SPENDTHRIFT GENOTYPE HYPOTHESES: THE EXPERIMENTAL EVOLUTION AND THE “NATURE – NURTURE” EXPERIMENT ON BANK VOLES**

**Alaa Hseiky<sup>1</sup>, Natalia Strzelczyk<sup>1</sup>, Katarzyna Baliga-Klimczyk<sup>1</sup>, Małgorzata M. Lipowska<sup>1</sup>, Edyta T. Sadowska<sup>1</sup>, Paweł Koteja<sup>1</sup>**

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Obesity and co-occurring disorders have become a common problem in humans. The immediate causes are the “Western Diet” (WD), rich in fats and simple sugars, along with reduced physical activity. Many hypotheses tried to explain why we are vulnerable to such conditions. The “thrifty-genotype” hypothesis assumes that natural selection promoted efficient storage of fat reserves to endure starvation. Nowadays, however, with easy access to food, fat is continuously stored leading to various disorders. Its logical counterpart, the “spendthrift-genotype” hypothesis states that animals with evolved high metabolic capacity under unrestricted food access should be less vulnerable to the adverse effects of such an excess. Both hypotheses were simultaneously tested using lines of bank voles (*Myodes glareolus*) artificially selected in three directions: “Herbivorous” with the ability to grow on low-quality diet, “Aerobic” with high swim-induced aerobic metabolism, and “Predatory” with a propensity to hunt crickets; and unselected Control lines. The Aerobic and the Predatory lines represent the spendthrift-genotype, while the Herbivorous the thrifty-genotype. The voles were assigned to WD or standard diet groups shortly after weaning, and three months later several traits were analyzed. Surprisingly, body mass, fat content, blood glucose, and locomotor performance traits were not affected by WD. In the WD group, liver and spleen were enlarged and plasma biochemical markers indicated a compromised liver function, but most of the effects were similar in all the selection lines. These results show that the voles are highly resistant to the WD, and provided no support for either of the hypotheses.

## **P10: THE EFFECT OF WESTERN DIET ON THE LIVER METABOLOME: A PILOT EXPERIMENT BASED ON AN ARTIFICIAL SELECTION EXPERIMENT ON BANK VOLES**

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Obesity and associated disorders have become prevalent in humans, primarily attributed to the consumption of a Western Diet (WD) rich in fats and simple sugars, coupled with reduced physical activity. In a previous experiment, we investigated the effects of the WD on bank voles (*Myodes glareolus*), using lines selected for high swim-induced aerobic metabolism (Aerobic) and unselected Control lines. Surprisingly, the voles' weight, glucose concentration, and performance traits were unaffected by the WD. However, the WD did lead to enlarged liver and elevated cholesterol, and liver enzyme levels in the plasma. An important question arises how metabolome profile has changed in response to both the selection and diet factors. This pilot study was aimed to provide preliminary data concerning the question, and especially indicating specific metabolites that should be subject to a full-scale analysis. Metabolites were extracted from 20 liver samples from the previous study, and analyzed by “MS-Omics” with UP-Liquid Chromatography/mass spectrometry. With high certainty, we identified a total of 150 metabolites, including fatty acids, carnitine, key intermediates of glycolysis and the Krebs cycle. The Principal Component Analysis (PCA) revealed two distinct dietary patterns: the standard diet and the WD, explaining 40% of the PCA variance. Additional separate clouds were observed based on sex and the selection direction, which explained 34 and 31 % of the variance, respectively. Importantly, the increase in liver mass induced by the WD coincided with alterations in metabolic pathways. These findings serve as a foundation for a prospective future large-scale investigations in this field.

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## **P11: ARE FOOD DYES GOOD OR BAD? STUDYING THE EFFECTS OF TURMERIC ON FRUIT FLIES' DEVELOPMENT.**

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Food dyes have become prevalent additives in modern times, serving various purposes in the food industry. Turmeric, a popular herbal food dye known for its yellow color, is commonly used in Indian curry. This study focuses on examining the influence of turmeric on the development of fruit flies (*Drosophila melanogaster*) and its interaction with different nutrient availabilities. To achieve this, we designed diets with varying concentrations of turmeric, including 0%, 0.5%, 1%, 2% and 5%. Furthermore, we manipulated the protein-to-carbohydrate ratio to create protein-rich, balanced, and carbohydrate-rich diets. 50 eggs were placed in each of the 9 replicates of the 15 diet groups, totaling observations of 6750 eggs. Throughout the study, we closely monitored key developmental stages, including larval pupation, adult eclosion, pupal height, and pupae count. We will further count the adult flies and analyse their body composition. Our hypothesis suggests that the effects of turmeric will depend on its concentration, with higher concentrations exhibiting a more substantial influence on the flies. Additionally, we anticipate variations in these effects across the different protein-to-carbohydrate diet gradients. Although our preliminary analysis revealed that protein-rich diets were associated with shorter pupation and eclosion times, and sugar-rich diets with longer times, neither the turmeric concentrations nor their interaction with nutrient availability influenced these developmental stages. The completion of our research will provide valuable insights into the potential effects of turmeric on fruit fly development and its relationship with protein and sugar availability.

## **P12: FOOD OR THRILL OF THE HUNT: FOOD PREFERENCES IN BANK VOLES SELECTED FOR PREDATORY BEHAVIOR**

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Predatory behavior is a multifaceted adaptation that involves significant modifications across an organism's organizational structure, spanning from the molecular to the morphological and behavioral levels. Thus, understanding the factors that influence an animal's food choices is critical for elucidating the mechanisms that underlie predatory behavior. A promising model for investigating the genetic basis of predatory behavior is our evolutionary model of bank voles (*Myodes glareolus*) selected for predatory behavior towards crickets. However, it is not known if they are solely motivated to attack by living/mobile prey, or they would also prefer feeding on dead/immobile insects; is it a hunting drive/motive or an intrinsic food preference? To investigate the relative importance of these factors we conducted a food preference test on adult bank voles from the lines selected (for ca. 30 generations) for hunting propensity towards crickets and control, and randomly bred lines. After a 4-hour fast, the voles were presented simultaneously with two food items: a standard food pellet and a dead cricket. Their behaviour was videotaped (for 10 minutes) and analysed, and the mass of consumed dead cricket and pellet was measured. Our results showed that most of the "predatory" voles (i.e., those from the selected lines) ate both the dead cricket and the standard food pellet, whereas the control voles chose exclusively the food pellet. This suggests that hunting tendency plays a role in the food choices of bank voles and that the predatory voles have an increased preference for prey, even when alternative food options are available.

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## **P13: TESTING THE HOLOGENOME CONCEPT: A COHABITATION EXPERIMENT ON BANK VOLES FROM A SELECTION EXPERIMENT**

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Gut microbial community, or microbiome, plays a major role in its mammalian host performance. The microbiome structure can be determined by both the genetic (nature) and environmental factors (nurture), such as diet or bacteria transfer between individuals. However, according to the hologenome concept, the host and its microbiome (i.e., holobiome) coevolve, so that the host preferably maintains a specific microbiome. The general concept can be tested with experimental evolution approach. Here we performed an experiment on bank voles (*Myodes glareolus*) from lines selected for the ability to grow on a low-quality herbivorous diet (H lines) and unselected, control (C) lines. Juvenile animals were cohabited in pairs from different lines to allow exchange of microbiome before the feeding trials.

During the feeding trial, the H-line animals had a more positive body mass balance than the C-line ones both on standard and on low-quality diet. Apparent digestibility of either diet was not affected by selection, but the H-line animals were able to increase their food consumption of low-quality diet more than the C-line ones. The alpha-diversity metrics of caecal microbiome did not differ between animals from the two line types, but there were minor differences in bacterial phylum abundance between the line types. However, abundance of these phyla did not affect the host's performance in the feeding trial. Neither the host's performance nor its caecal microbiome were affected by the cohabitant line type. Therefore, the results indicate robustness of the host's caecal microbiome, but do not provide evidence supporting the hologenome concept.

## **P14: CORRELATED RESPONSES TO ARTIFICIAL SELECTION FOR PREDATORY PROPENSITY IN THE BANK VOLE: HUNTING SKILLS AND COPING WITH STRESS**

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Predatory behavior is a complex adaptation often associated with extensive changes at all levels of an animal's organization, from molecules to morphology and behavior. Interestingly, there is much to explore on hunting skills and it is not known whether the stress reaction plays a role in their evolution. One of the reasons of this deficiency is a limited range of suitable animal models. We have used our unique evolutionary evolution model populations (>30 generations) of bank voles (*Myodes glareolus*), selected to hunt crickets (Predatory lines), and random-bred control lines (Control lines). To study the co-evolutionary response of hunting skills and its stress hormone basis; from each of the four Predatory and Control lines, 12 males and 12 females (total 192 voles) were subjected to the study. Half of the voles from each line experienced a cricket hunting test, whereas others experienced the same test condition, but without cricket (sham hunting test). The tests were videotaped and using manual labeller conducted behavioral quantifications. We measured the latency to spot and start hunting the crickets, prey approach frequency, eating duration, eating bouts and importantly skill to attack the prey: killing bite delivery site. Furthermore, with aim to understand if coping with stress contributes to an increase in predatory behavior, blood samples were collected for corticosterone determination in plasma by the use of an immune assay. Together, I will be presenting these results that will provide insights into the stress hormonal mechanisms underlying predatory behavior and its main co-evolutionary components: motivation and skill.

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## **P15: RESTRICTED NIGHTTIME FEEDING PREVENTS THE HIGH-FAT DIET-EVOKED DISRUPTION OF THE HYPOTHALAMIC CIRCADIAN CLOCK**

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Circadian regulation of feeding behaviour is controlled by the food-entrainable oscillator, the main part of which is considered to reside in the brain structure called the Dorsomedial Hypothalamus (DMH). The DMH participates in the metabolic state-dependent control over food intake and metabolism, taking into account also the circadian timing phase. Here, we investigated whether and how the physiological circadian properties of the DMH neurons change under high-fat diet (HFD), the most commonly used rodent model for the induction of obesity. For the experiments we used rats which had been fed either control (CD) or HFD for 3-4 weeks, which precedes excessive weight gain of HFD-fed rats, therefore allowing us to study the possible causes, rather than effects of obesity. Using immunohistochemistry and electrophysiology, we discovered an impairment of the DMH circadian rhythms. Parallely we observed that HFD disrupts the feeding activity rhythm, stimulating food intake during the non-active daytime. Since the DMH is known to entrain to feeding schedule, we checked if its neuronal activity is simply a reflection of the animals' feeding behaviour, and whether it is still observed if the animals eat exclusively during nighttime. Our results clearly indicate, that the DMH clock disruption can be prevented by feeding restricted to the active phase, highlighting the importance of temporally regulated feeding behaviour on the functioning of the hypothalamic metabolic centre.

The work was supported by the programme "Excellence Initiative–Research University" at the Jagiellonian University in Kraków, Poland as well as by the Polish National Science Centre (2017/25/B/NZ4/01433).

The student was funded by the project entitled "ATUT PhD Programme in Biology". The project is co-financed by the European Union under the European Social Fund – Operational Programme Knowledge Education Development.

## **P16: THE EFFECTS OF CALORIE RESTRICTION ON MICROBIOTA OF BANK VOLES WITH HIGH EVOLVED METABOLIC CAPACITY**

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In many natural environments, energy availability varies spatially and temporally. Animals adapt to food scarcity by adjusting their metabolic processes and allocating energy towards critical functions at the cost of reduced growth, reproduction, and immunity. The gut microbiota plays a crucial role in this process, for example by aiding in extracting energy from food. Interactions between host metabolism, the microbiota, and the diet can therefore shape the co-evolution of hosts and microbiota. To examine those interactions, we performed an experiment to quantify the relative importance of diet and host metabolism on the gut microbiota. For this, we applied a 2 x 2 design, which included two kinds of diet treatment (calorie restricted or standard diet) performed on bank voles (*Myodes glareolus*) from two (selection and control) lines. Selection lines have been selectively bred for higher metabolic capacity for nearly 30 generations, and non-selected control lines have retained a lower metabolic capacity. Our results indicate that a calorie restriction

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diet can affect the microbiota composition and these effects are reversible. However, we did not detect an effect of evolution towards high metabolic capacity on microbiota. Thus, acute environmental variation influenced the microbiota more than (co-)evolved host characteristics.

### **P17: HOW DO OPTIMAL AND SUBOPTIMAL TEMPERATURES AFFECT MITOCHONDRIAL BIOENERGETICS OF ROTIFERS LECANE INERMIS?**

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Given the critical role of mitochondria in providing up to 90% of the cell's ATP, it is crucial to investigate how abiotic factors impact mitochondrial functioning under various environmental conditions. To this end, we used clones of the rotifer *Lecane inermis* with known thermal preferences and exposed them to four thermal regimes: standard temperature, optimum temperature, low suboptimal temperature, and high suboptimal temperature. The study aimed to identify how mitochondrial bioenergetic parameters vary in response to temperature shifts and whether these responses differ between clones. We evaluated the mitochondrial response, namely the maximum rate of the electron transport system (indicating the ability to synthesize ATP), the rate of proton leakage (indicating the cost of maintaining the mitochondria), ETS (indicating the activity of the electron transport chain), protein synthesis (activity of complex V), and the activity of the sodium-potassium pump (which maintains the concentration gradient between membranes). Our results show that clones with different thermal preferences vary in their respiratory chain response depending on temperature. Only a sodium-potassium pump and protein synthesis were unresponsive to different temperatures. For all studied mitochondrial traits, the interclonal differences were particularly pronounced at the suboptimal temperatures, while at standard and optimal temperatures the clones exhibited similar response. These results provide insight into the patterns of plastic organismal response to acute environmental changes at the mitochondrial level.

### **P18: WHEN TEMPERATURE MAKES THEM PANIC – THE EFFECT OF OPTIMAL AND STRESSFUL THERMAL CONDITIONS ON VARIABILITY OF LIFE HISTORY TRAITS IN LECANE INERMIS ROTIFER.**

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We investigated intraspecific variation in reproductive traits in the rotifers of *Lecane inermis* species exposed to optimal, suboptimally low and suboptimally high temperatures. Rotifers were observed at the level of individuals, and variables such as life span, mortality, and fecundity were recorded. Our results demonstrated significant variation within clonal populations of *L. inermis*, with individuals exhibiting diverse life spans, mortality rates, and fecundity. Temperature profoundly impacted these traits, with higher temperature range leading to shorter life spans, increased mortality rates, and altered fecundity patterns. These findings highlight the adaptive nature of *L. inermis*, indicating the ability to adjust its life history traits to optimal and stress-inducing temperature conditions. This research contributes to the understanding of intraspecific variation and phenotypic plasticity in ectotherms exposed to temperatures that they perceive either as optimal or as stressful.

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### **P19: HOW DOES EVOLUTION IN A STABLE OR FLUCTUATING ENVIRONMENT SHAPE THE NICHE BREADTH OF A PLANT-FEEDING ARTHROPOD?**

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Organisms are constantly exposed to environmental variability, which imposes adaptive pressure. Usually, constant environments favor specialization, whereas fluctuating environments select for generalists. Knowledge of the evolution of niche breadth plays a central role in the development of ecological and evolutionary theory. Since the niche is a multidimensional hypervolume in the ecological space that allows a population to persist, it is crucial to consider different niche dimensions when investigating the mechanisms behind the evolution of niche breadth. We studied how divergent environments shape biotic and abiotic niche dimensions, using the plant-feeding mite *Aceria tosichella*, a significant cereal pest, as a study system. We used mite populations experimentally evolved over tens of generations under constant (single host plant) or fluctuating (alternation of two plant species) conditions. We then assessed the fitness of these experimentally evolved lineages (i) on various host plant species, and (ii) over a range of temperatures. We found that the niche breadth of *A. tosichella* underwent evolutionary changes in response to environmental variability, with a tolerance to the biotic and abiotic dimensions evolving in opposite directions. Host specialization led to a broadening of thermal tolerance, whereas host generalization led to a narrowing of thermal tolerance. This suggests trade-offs between biotic and abiotic niche dimensions. Our study helps to understand how organisms respond to environmental homogeneity versus heterogeneity, which has implications for their colonization potential and range expansion. The study was supported by the National Science Centre, Poland (grant no. 2021/41/B/NZ8/01703).

### **P20: TEMPERATURE EFFECT ON THE ASSOCIATION BETWEEN SPERM PRODUCTION AND 6PGDH GENOTYPE IN BULB MITE MALES.**

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Phosphogluconate dehydrogenase (6Pgdh) is an enzyme affecting male reproductive success of bulb mite (*Rhizoglyphus robini*). Within the 6Pgdh gene, there are S and F alleles, which are codominant. Of the males with different 6Pgdh genotypes, those homozygous with the S allele achieve the highest reproductive success. In constant laboratory conditions with higher temperature (24°C), SS males have been shown to copulate more frequently and produce more sperm. Although sexual selection favours the S allele, the F allele is not displaced from natural populations, but the levels of polymorphism vary between populations. This suggests that temperature fluctuations and heterogeneity occurring in the wild might create balancing selection maintaining both variants. Here, we are looking for the mechanisms of such selection. We test if low temperature reverses S allele advantage in sperm production in favour of F allele.

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## **P21: FOOD TRESHHOLDS IN DAPHNIA – THE EFFECTS OF FOOD QUALITY, TEMPERATURE AND BODY SIZE.**

**Tomasz Brzeziński<sup>1</sup>, Anna Bednarska<sup>1</sup>, Zhanna Buseva<sup>1</sup>, Irina Fenieva<sup>1</sup>, Piotr Dawidowicz<sup>1</sup>**

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Body size determines the outcome of interspecific competition between cladoceran species. Large-bodied species outcompete small-bodied ones when food quality is good due to lower population threshold food concentration (TFC), and vice versa when food quality (in terms of stoichiometry or essential lipids) is poor. Small-bodied species are also believed to be superior in elevated temperatures, since usually with increasing temperatures food quality deteriorates. Yet, simultaneous effects of food quality and temperature on threshold food concentrations in cladocerans have not been tested.

In laboratory experiments, we determined TFCs of three species of *Daphnia* that differed with regard to body size. Daphnids were raised in two temperatures (18°C and 24°C), in gradients of food quantity that differed with regard to essential lipid content or stoichiometric ratios.

We found significant intraspecific variability in TFCs of cladocerans raised in varying food quality and temperature. We found that the temperature modifies the effect of food quality – at elevated temperature the superiority of large-bodied species, in terms of TFCs, diminished when food quality deteriorated. However, TFCs of small-bodied species were not lower than those of large-bodied ones. Thus, factors other than temperature and quality of food should be responsible for dominance of small-bodied cladocerans in elevated temperatures.

The study was supported by NCN grants: 2019/33/B/NZ8/01567 and NAWA BPN/SZN/2021/1/00023/U/00001.

## **P22: TEMPERATURE AND FOOD QUALITY AS DRIVERS OF COMPETITION AMONG DIFFERENTLY SIZED DAPHNIA SPECIES**

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Global warming leads to an increase in surface water temperature in lakes and to a decrease in the quality of algal food for herbivorous zooplankton. Small-bodied planktonic crustaceans predominate in warm-climate lakes, and a negative correlation between water temperature and mean body size within zooplankton communities is observed at the geographic scale. We tested the hypothesis that small-bodied cladoceran species are less susceptible than larger bodied daphnids to temperature increases under conditions of poor food quality (mediated by biochemical composition). The microcosms competition experiment (factorial design) was carried out with small-bodied *Daphnia longispina* and large-bodied *D. magna*, reared together at two temperatures, 18 °C and 24 °C, and fed high (green alga *Chlamydomonas klinobasis*) or poor (cyanobacterium *Synechococcus elongatus*) quality food. Contrary to our expectations, *D. magna* outcompeted *D. longispina* regardless of food quality and temperature conditions. Our results suggest that the size structure of planktonic species assemblages is determined by temperature-related factors other than food acquisition and assimilation efficiency. Thus, we suppose that large-bodied species have an advantage in surviving during cyanobacterial blooms, as long as they are not affected by interfering cyanobacterial filaments and have the ability to evolve greater tolerance to future climate warming.

The study was supported by NCN: NAWA BPN/SZN/2021/1/00023/U/00001 and OPUS 2019/33/B/NZ8/01567.

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## **P23: THRESHOLD FOOD CONCENTRATION (TFC) AS A PREDICTOR OF THE OUTCOME OF INTRASPECIFIC COMPETITION IN DAPHNIA MAGNA, EXPOSED TO DIFFERENT QUALITY DIETS.**

**Anna Bednarska<sup>1</sup>, Tomasz Brzezinski<sup>1</sup>, Zhanna Buseva<sup>1</sup>, Irina Fenieva<sup>1</sup>, Piotr Dawidowicz<sup>1</sup>**

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Food quality can be an important selection factor and can be expected to influence microevolutionary processes (changes in genotype frequencies) in *Daphnia* populations. The ability to grow when food resources are effectively exploited by competing conspecifics should be crucial for the success of individuals of a given genotype. Thus, the lower the TFC, i.e. the concentration of food at which positive growth can be achieved, the greater the competitive ability should be expected.

In the first experiment, the TFC was determined for three clones of *D. magna*, and in the second, the *Daphnia* population competed in a common garden experiment. There were three food regimes (1) a suspension of the green alga *Acutodesmus obliquus* with a stoichiometric carbon:phosphorus ratio optimal for *Daphnia* (C:P  $\approx$  120), (2) a suspension of *A. obliquus* with a stoichiometric ratio of C:P  $\approx$  800 indicating severe phosphorus deficiency, and (3) a mixture of *A. obliquus* (10%) and the cyanobacterium *Synechococcus elongatus* (90%) deficient in sterols and unsaturated fatty acids. Populations were maintained in 3L aquaria for 8 weeks.

The abundance of individuals of one of the tested clones was very low regardless of the feeding conditions and, contrary to expectation, it was the individuals of a clone with the lowest TFC. Thus, TFC alone cannot explain the outcome of the competition. However, a significant effect of food quality on the frequency of individual *Daphnia* genotypes was demonstrated, confirming that food quality can be a strong selection factor.

This study was supported by the NSC, Poland, 2019/33/B/NZ8/01567

## **P24: EFFECTS OF FOOD PHOSPHORUS CONTENTS ON COMPETITIVE INTERACTIONS BETWEEN LARGE AND SMALL-BODIED DAPHNIA SPECIES**

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The carbon:phosphorus (C:P) stoichiometry of food is known to affect the life history of consumers, including cladocerans. P limitation can slow the production of P-rich ribosomal RNA and reduce the growth potential of an organism. According to size-efficiency hypothesis large-bodied cladoceran species are competitively superior over small-sized ones, due to higher food-collection efficiency and, consequently, faster somatic growth. We hypothesize that large-bodied cladocerans would lose this superiority under low-P (i.e. high C:P) dietary conditions. To test this hypothesis, we performed competition experiments with large *D. magna* and small *D. longispina*, reared separately and in mixed cultures, fed with the green alga *Chlamydomonas klinobasis* at both low (100) and high (800) C:P ratios. The experiment lasted two months at 24°C. Contrary to our expectations, *D. magna* outcompeted the smaller-sized *D. longispina* under P-poor conditions while *D. longispina* suppressed *D. magna* under P-rich conditions. The unexpected outcome of the competition under different food quality conditions can be explained in terms of life history and threshold food concentrations of competing daphnids. We conclude that food phosphorus content can potentially alter species composition in freshwater zooplankton communities.

The study was supported by NCN grants: 2019/33/B/NZ8/01567

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## P25: METABOLIC SCALING IS UNAFFECTED BY HABITAT ARIDITY IN GECKOS

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Species from arid environments, mainly mammals and birds, often have lower metabolic rates than species from mesic environments. To test whether squamate reptiles, a group that mastered life in arid environments, follow the same trend, we compared intra- and interspecific scaling of metabolic rate in two independent lineages - the eyelid geckos, family Eublepharidae, and the geckos of the genus *Paroedura*, family Gekkonidae. Representatives of both groups live in habitats with considerable temperature and humidity gradients, ranging from deserts to tropical rainforests. Both lineages highly diversified in body size and exhibit negative relationship between habitat aridity and total evaporative water loss. Our phylogenetically informed analyses reveal that in both groups metabolic rate scales closely with body mass and the intra- and interspecific scaling in metabolic rate is nearly the same. Differences in habitat aridity and total evaporative water loss do not explain the slight departures from the conserved scaling in metabolic rate. In contrast to mammals and birds, these results rule out the possibility that changes in metabolic rate, and thus water loss via respiration, drive adaptive changes in total evaporative water loss in geckos.

## P26: SYSTEMIC ORCHESTRATION OF CELL SIZE THROUGHOUT THE BODY: EVOLUTIONARY AND DEVELOPMENTAL RESPONSES OF DROSOPHILA MELANOGASTER TO ENVIRONMENTS

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Organisms have evolved vast disparities in body size and cellularity. Although the body size of ectotherms in environmental gradients has been well studied, little is known about its cellular basis. To fill this gap, we measured body size and five cell types in two groups of *Drosophila melanogaster* flies that originated either from an evolutionary study, by evolving in three thermal environments, or from an experimental study with flies developing at two temperatures combined with two oxygen levels. In general, environmental conditions affected the phenotypic characteristics of flies. Cell size changed systemically across the body, but only to some extent, indicating a more complex nature of cell size response and some level of cell autonomy. Interestingly, despite this, females were consistently larger than males and had larger cells in their organs. We conclude that cell size should be included in studies of insect responses to climate changes and the origin of life-history traits.

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## **P27: LIVING WITH HEAT: UNVEILING THE IMPACT OF SIMULATED HEAT WAVES OF THE LIFE STORY ON TWO POLLINATORS: OSMIA BICORNIS AND O. CORNUTA**

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Extreme climatic events, especially heat waves with high-temperature peaks, are predicted to occur more often in many parts of the world due to climate change. The impact of such weather events can be particularly significant when their influence extends to organisms that play crucial roles in the functioning of the ecosystem, as well as those that hold immense value for food security and human economy. In this study, we aimed to assess the effects of heat waves on two generalist pollinators with different size and distribution ranges: *Osmia bicornis* and *O. cornuta*. Larvae of these species were exposed to varying conditions, including either average temperatures in Poland (control) or forecasted heat waves of different magnitude (36.8 °C or 39.7 °C), frequency (one or two heat waves) and duration (9.2 or 12.2 days). Throughout the experiment, we monitored food consumption, cocooning occurrence, bee emergence, and the body mass of adult bees. In both *Osmia* species, high-peak temperatures hindered feeding, and this deficit was not compensated during periods of heat stress relief. Consequently, the body mass of adult bees experienced a notable decline. Conversely, in the control conditions, almost all larvae consumed their food entirely. The success of cocoon formation varied depending on the thermal treatment applied, and differences were observed during emergence from the cocoon. The fewest bees emerged from cocoon subjected to double 12.2 days heat-waves. Our research suggest that climate-induced temperature changes may drastically alter and reduce bee communities with far-reaching consequences for ecosystems and human food production.

## **P28: PHENOTYPIC AND GENE EXPRESSION DIFFERENCES IN COPING WITH TEMPERATURE AND AN INVASIVE ALIEN PREDATOR ALONG A LATITUDINAL GRADIENT IN DAMSELFLIES**

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Understanding and predicting how organisms respond to environmental changes has become a major concern in conservation biology. Here, we tested whether a freshwater insect, the damselfly *Ischnura elegans* collected at different latitudes, central- (southern Poland) and high-latitude (southern Sweden), responded in a similar way to two factors related to human activities, warming and an invasive alien predator. For this, damselfly larvae were exposed to two experimental treatments in a crossed design. A temperature treatment: current (20 °C) and mild warming temperature (24 °C) corresponding to the average temperature increase by the end of the century according to IPCC (RCP8.5 scenario). And a predator treatment: presence or absence of an invasive alien predator cue released by the spiny-cheek crayfish *Faxonius limosus* reported in Poland but not in Sweden to date. At the end of the experiment, we measured several phenotypic traits (growth rate, development time, body size and mass) and collected samples for a gene expression analysis. Central-latitude individuals had a shorter development and a faster growth compared to high-latitude individuals when exposed to mild warming temperature and a predator cue, revealing complex relationships linking phenotype and environment. Transcriptome analysis revealed that metabolic pathways related to larval anatomy and development tended to be upregulated in response to mild warming, especially in central-latitudes. And those linked to oxidative stress tended to be downregulated in response to a predator cue, especially in central-latitude individuals. Altogether, our results provide insights into how organisms of different origins may respond to future anthropogenic changes.

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## **P29: MICROBIAL NITROGEN RECYCLING IS HIGHER IN ARCTIC GROUND SQUIRRELS HIBERNATING AT WARMER TEMPERATURES**

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Energy conservation associated with hibernation is maximized at the intersection of low body temperatures, long torpor bouts and few arousals. In the arctic ground squirrel (*Urocitellus parryi*) this is best achieved at hibernation ambient temperatures around 0°C, where Tb is ~ 2°C. Given that arctic ground squirrels occupy extreme environments and switch to mixed fuel metabolism at low ambient temperatures of hibernation, we wanted to investigate how microbial urea-nitrogen recycling, a process shown previously to contribute to the hibernating host's protein pool, is used under different hibernation thermal conditions. Injecting squirrels hibernating at two different ambient temperatures, -16°C and 2°C, as well as active euthermic squirrels with isotopically labeled urea (13C/15N) allowed us to assess the ureolytic activity of gut microbes as well as the level of liberated nitrogen tissue incorporation. Since non-lipid fuel is a limiting factor for torpor at lower ambient temperatures, we originally hypothesized we would find higher markers in animals hibernating at -16°C; however, that was not the case and we found higher markers in animals hibernating at 2°C. Since squirrels hibernating at 2 °C were characterized by overall higher Tb and longer IBAs, this most likely created more favorable conditions for the gut microbes to thrive and remain more active while simultaneously giving the host more time to absorb the microbial nitrogen metabolites during the longer IBAs.

## **P30: BEHAVIOURAL AND PHYSIOLOGICAL RESPONSE TO STRONG HABITAT DISTURBANCE IN A KEY WETLAND RODENT SPECIES**

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Disturbed habitat as post-fire environment is characterized by reduced amount of food, shelters and high predation which result in strong selection on animal behavior and physiology. The allocation model assumes that costly behaviours correlate negatively with basal metabolic rate (BMR) - the self-maintenance cost of homeothermy. However, the performance model suggests the opposite, that high metabolism promote proactive behaviours, if resources are unlimited. Thus, the context-dependent hypothesis predicts that both models can explain the link between physiology and behaviour depending on situations. In spring of 2020 a large fire (>5500 ha) burned wetlands in Biebrza National Park, (Western Poland) demolishing significant part of the habitat and the population of root vole *Microtus oeconomus*. We hypothesized that different models explain linkage between physiology and behaviour at post-fire and unburned environments. We expected negative correlation between the self-maintenance costs and the proactiveness in animals recolonizing post-fire zone and the opposite in those living in unburned area. We measured BMR and exploration (distance moved during open field test) in animals captured on burned and unburned sites. In autumn (~6 months after fire), voles from post-fire zone had slightly higher BMR and covered shorter

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distances during open field test than individuals from unburned area. There was no interaction between BMR and fire presence for distance moved, but general positive correlation between metabolism and exploration was significant. Our results suggest that the performance model is paramount in explaining the physiology-behaviour linkage while at the same time the allocation model can explain it additively.

### **P31: HETEROOTHERMY BUT NOT MAINTENANCE COSTS OF HOMEOTHERMY CORRELATE WITH NATURAL FOOD AVAILABILITY IN YELLOW-NECKED MICE *APODEMUS FLAVICOLLIS***

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The ‘food habit’ hypothesis considers food predictability, availability and quality as major factors shaping variation in basal metabolic rate (BMR) - minimum energy expenditure under homeothermy (high and stable body temperature - Tb). While interspecific studies support it at the intraspecific level, research are scant and result are ambiguous. Among others, this can be caused by ability of wild animals to mitigate costs associated with self-maintenance under homeothermy by usage of variety of energy saving mechanisms. The most effective heterothermic energy saving strategy among small endothermic animals is torpor - characterized by reduced metabolic rate (MR) and Tb. We hypothesized that as compensatory strategy, torpor use should vary among individual yellow-necked mice and correlate negatively with natural/supplementary food sources. In autumn, seeds availability (total dry mass) at 33 locations of Białowieża Forest (Poland) was repeatedly evaluated. From autumn to winter mice were supplemented with hazel nuts and sunflower seeds at 13 locations. Mice were captured in winter, transported to the laboratory, implanted with thermosensitive ID tags and BMR and Tb during short-term fasting were measured. There was no interaction between heterothermy, resources and BMR (itself did not correlate with food availability). However, unaffected by supplementary food, the length of torpor increased with decrease of natural seeds mass. Our study suggests that heterothermy among individuals varies according to ‘optimal torpor use’ hypothesis predictions - being adjusted to natural food availability as significant compensatory strategy allowing animals avoidance self-maintenance costs of homeothermy.

The study was supported by Polish National Science Center (2019/35/D/NZ8/03626).

### **P32: CAN CELL SIZE EXPLAIN DIFFERENT METABOLIC RESPONSE TO TEMPERATURE AND OXYGEN WITHIN THE *PELOPHYLLAX ESCULENTUS* SPECIES COMPLEX?**

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According to the theory of optimal cell size, the costs and benefits of cell size reflect a balance that depends on metabolic demand and supply. For example, small cells have a relatively large membrane surface area which should increase the rates of oxygen and nutrient fluxes, but at the same time carry higher costs in maintaining electrochemical gradients across membranes. For ectothermic aquatic animals metabolic demand and supply are largely shaped by oxygen and thermal conditions. Thus, in ectotherms the costs and benefits of cell size should be context dependent, differing across temperatures and oxygen regimes. In this study we capitalized on the *Pelophylax esculentus* species complex, which is comprised of lineages differing in ploidy and hence cell size. We compared metabolic performance of tadpoles reared at 20°C and then tested at different thermal (20°C and 24°C) and oxygen conditions (normoxia and hypoxia). We studied tadpoles represented by four different genotypes (LR, LLR, LRR and RR) obtained by crossing hybrids (*P. esculentus*) that originate from primary hybridization between *P. lessonae* (genotype LL) and *P. ridibundus* (RR). We observed the strongest effects of the oxygen treatment on rates of oxygen uptake in triploids with larger cells (LLR and LRR), compared to diploids with smaller cells (LR and RR). Our result may help to understand the impact of climate change on ectotherms, especially amphibians, through the lens of cell size and matching metabolic demand to oxygen supply.

### **P33: VARIABLE TEMPERATURE CONDITIONS AND HUMORAL IMMUNE RESPONSE IN ZEBRA FINCHES**

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Climate change and global warming lead to greater unpredictability and instability in daily temperatures. Coping with variable temperature rises stress hormone level, increases energy expenditure, and may in turn affect immunity in birds. This study examines the impact of ambient temperature variability on the humoral immune response of a captive population of zebra finches (*Taeniopygia guttata*).

In this experiment, zebra finches were reared in either stable or variable temperature (with the same mean). Additionally, half of the juveniles were cross-fostered between the two conditions after hatching. At adulthood, 240 of these birds were injected with sheep red blood cells. Following the injection, the birds were kept in stable temperature for 6 days. The primary immune response was measured by the hemagglutination test. No difference in humoral immune response was observed between the experimental groups. Yet, in all the groups males showed higher haematocrit and higher humoral response than females. The latter result is consistent with previous findings of other authors, but is difficult to explain.

The lack of a noticeable effect of the experimental treatments on the humoral immune response could be attributed to the birds' unrestricted access to food. This factor may have reduced the influence of temperature fluctuations. It should also be noted that birds in all groups maintained similar body mass, suggesting that the physiological burden caused by the temperature variability prior to immunisation was relatively low. It would therefore be reasonable to repeat a such study with reduced access to food.

### **P34: ECOPHYSIOLOGY OF COGNITION: THE EFFECTS OF AMBIENT TEMPERATURE VARIABILITY ON LEARNING PERFORMANCE IN ZEBRA FINCHES**

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Climate change is leading to increasingly unpredictable ambient conditions. In order to cope with highly variable environments, animals rely on effective cognition. However, environmental fluctuations may limit cognitive development because of a trade-off in the allocation of resources. These two options could be reconciled if parental effects can prepare offspring to face harsh conditions. Thus, we investigated the

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impact of ambient temperature variability during development on zebra finches' cognitive abilities, including song learning, associative learning, and social learning. We expected that parental effects would attenuate the consequences of variable temperature conditions during development; a mismatch between the pre- and post-hatching conditions should decrease the learning performance. We designed a 2×2 factorial study with two temperature conditions (stable and variable with the same mean temperature), with half of the juveniles cross-fostered at hatching. We tested the associative learning performance of 209 juveniles during their development and after independence, and we tested their social learning abilities and the song learning performance of males at adulthood. We found an impact of the temperature conditions only on song learning, males from variable pre-hatching condition learned more accurately the song of their father (or foster father) than birds from stable pre-hatching condition. We also observed a higher participation in associative learning test and song recordings when the birds developed in variable condition. Thus, variable temperature conditions may not act as a stressor as we supposed, but may be perceived as an environmental enrichment enhancing activeness in captivity.

### **P35: SHORT-TERM CONSEQUENCES OF AMBIENT TEMPERATURE FOR DEVELOPMENT IN PASSERINE BIRDS**

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To comprehend the impact of global climate change on bird reproduction, it is crucial to explore how environmental factors, specifically temperature, influence various aspects of their life-history traits. The ability of birds to adapt and modify these traits is likely to play a significant role in determining how populations respond to long-term environmental changes, including global climate change. Despite numerous studies examining the effects of climate change on birds, our understanding of the mechanisms underlying physiological responses to thermal stress in organisms remains limited. In our research we investigated the effects of temperature in the nests on offspring fitness-related traits in two bird species in a well-studied population on Gotland Island: the migratory collared flycatcher (*Ficedula albicollis*) and resident blue tit (*Cyanistes caeruleus*). For two breeding seasons, we manipulated the ambient temperature in the nest boxes of both species to investigate its impact on offspring fitness-related traits. Our study indicates that nest microclimate during both the incubation and nestling period affects offspring quality, indicating that environmental variation in nest temperature early in ontogeny can have important and long-lasting fitness consequences.

### **P36: A LONG-TERM STUDY REVEALS A CRUCIAL ROLE OF WEATHER CONDITIONS FOR AVIAN OFFSPRING FITNESS**

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Reduced fitness of individuals and declines in population size are the focus of ongoing scientific debate on the biological consequences of climate change. Typically, studies concerning these issues use measurements of local weather conditions over a specific period as parameters of climatic changes. In the case of birds, a commonly reported ecological effect of changes in these climatic parameters is a shift in phenology, particularly concerning warmer spring temperatures causing earlier timing of key events, such as the onset of breeding. However, the effects of environmental conditions experienced by birds after initial reproductive decisions remain understudied. Here, we present an exploratory analysis based on a long-term

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dataset from a nest-box population of migratory collared flycatchers (*Ficedula albicollis*). We test the effects of weather conditions during the developmental period on crucial indicators of individual fitness, including survival until fledgling and local recruitment. Our findings provide clear evidence that variation in the number of fledglings and recruits is related to climatic conditions experienced during the rearing of nestlings. Specifically, we showed that both ambient temperature and rainfall affect the number of fledglings and recruits. Due to the large heterogeneity within species in offspring production, relying on species averages might be inaccurate, which is why recent global meta-analyses fail to describe similar phenomena.

### **P37: THE EFFECT OF ENVIRONMENTAL VARIATION ON AGE-SPECIFIC REPRODUCTIVE PATTERNS IN A SHORT-LIVED SONGBIRD**

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Both individual's age and the environment are independent and important drivers of reproductive performance in animals. However, breeding responses of individuals to environmental variation may profoundly differ regarding to their age. Thus, an interaction of individual's age and the environment is expected to affect the expression of reproductive traits. Yet, the effect of this interaction on reproductive performance across the entire adult lifespan have been rarely examined. Using a 32-year dataset from a population of the collared flycatchers *Ficedula albicollis* we examine whether and how the environment interacts with age to shape female age-specific reproduction. To describe environmental variation we used the remotely sensed normalised difference vegetation index (NDVI) that estimates vegetation productivity and is used as a surrogate for habitat quality. We then analysed how the within-individual age and NDVI determine patterns in laying date, clutch size, offspring production and recruitment. We found that NDVI affected age-specific reproductive performance in case of laying date and clutch size, but no such effects were observed for offspring production and recruitment. Specifically, first-year and old females, but not middle-aged females, breeding under low NDVI values started to lay eggs later and produced smaller clutches than females in the same age but breeding under higher NDVI values. Our study demonstrate that the interaction of individual's age and environmental variation may be indeed a crucial driver that shape age-specific reproductive patterns in short-lived avian species, as it has been previously found in long-lived birds.

### **P38: AROMATIC PLANTS, GREAT TITS & BODY CONDITION: PRELIMINARY RESULTS**

**Michał Gładalski<sup>1</sup>, Adam Kaliński<sup>1</sup>, Marcin Markowski<sup>1</sup>, Joanna Skwarska<sup>1</sup>, Jarosław Wawrzyniak<sup>1</sup>, Jerzy Bańbura<sup>1</sup>**

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Blue *Cyanistes caeruleus* and great *Parus major* tits are two of a very few known hole-nesting passerine birds (among European starlings *Sturnus vulgaris* and tree swallows *Tachycineta bicolor*) that incorporate fresh aromatic plant materials into their nests during the nesting period. Those fresh green plant fragments contain ectoparasite-repellant and antimicrobial volatile compounds. In this study, we experimentally tested whether aromatic plant fragments (lavender *Lavandula angustifolia*, mint *Mentha* sp., Italian strawflower

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*Helichrysum italicum* and common yarrow *Achillea millefolium*) added into great tit nests affected condition indicators of 13-day-old nestlings. In supplemented nests the nestlings were characterised by improved condition indicators (higher hemoglobin concentration), as compared with nestlings from control nests (lower hemoglobin concentration). Present study may suggest that the behavior of adding aromatic plant materials by parents into their nests could have a positive impact on nestlings' body condition and therefore on birds fitness.

### **P39: THE EFFECTS OF LIGHT POLLUTION ON A BREEDING MIGRATORY BIRD**

**Monica Sayuri Diaz Palma<sup>1</sup>, Juliette Chapenois<sup>1</sup>, Joanna Sudyka<sup>2</sup>**

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The rapid development of cities and, consequently, the excessive use of Artificial Light at Night (ALAN) is altering the performance of many species. So far, most of studies have focused on the effects of light pollution in laboratory and captive animals, thus, very little is known about its effects in wild populations. In this talk, I will introduce my PhD research in which we are exploring whether light pollution affects the performance of a migratory bird – the collared flycatcher (*Ficedula albicollis*). Our experiment introduces light at night in nest-boxes used by these birds for breeding on Gotland, Sweden. The results gathered throughout three study seasons show that ALAN exposure is altering the behaviour of both: parents and offspring. ALAN increased the number of fledged young and the time that nestlings spent in the nest before fledging, in comparison to natural, dark control conditions. In addition, parents presented earlier daily onset and later daily cessation of feeding of ALAN broods in relation to controls. I will outline on how my PhD aims to explore underlying effects behind these results. Lastly, I will present initial results of the meta-analysis on the effects of ALAN in bird species and discuss how our study complements and develops this topic.

### **P40: A RIDDLE OF MULTIPLE ORNAMENTS – THE GREAT TIT CASE**

**Katarzyna Janas<sup>1</sup>, Tomasz Mazgajski<sup>1</sup>, Daniel Sánchez García<sup>1</sup>, Szymon Drobniak<sup>2</sup>, Anna Dubiec<sup>1</sup>**

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One of the most intriguing questions in avian evolutionary biology is why some birds express multiple sexual ornaments. According to the multiple message hypothesis, they can act as independent signals, advertising different aspects of the bird's condition. The evidence gathered so far for the great tit (*Parus major*) – a model species in avian evolutionary, ecological and behavioural studies, indicates that its conspicuous colour patches: melanin-based tie and crown, carotenoid-based breast and achromatic cheeks, might differ in their signalling meaning. However, in practice, the simultaneous expression of more than two ornaments is rarely studied. To fill this gap, we combine spectrophotometry, digital photography, and avian visual perception models to explore the colour patterns of adult birds from the nest box population of the great tit. Here, we will present initial results on the network of relationships between the expression of melanin-based crown and tie, carotenoid-based breast, and achromatic wing stripe and cheek, together with their associations with birds' condition and reproductive success. To ensure detected variation in colour traits is noticeable for great tits, we will apply the receptor-noise limited (RNL) colour discrimination model. Future research should examine within-individual repeatability in the structure of correlations between colour traits.

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## **P41: GREAT TIT FEMALES BUILD SIMILAR NESTS IN CONSECUTIVE BREEDING SEASONS**

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There is a large variation in nest sizes within the same species, and even within populations. Weather (temperature and precipitation) is considered as main factor affecting such variation, but others – like condition and experience of builders are also important. However, data presenting variation of nest sizes among individuals breeding in consecutive seasons, looking for similarities/dissimilarities of nests build by particular individuals are very scarce.

In this study nest built by females of great tits *Parus major* were studied. Birds bred in nest boxes, so the place for building of nest was similar for all individuals. Study was carried out in 2019–2021, birds were individually marked, so it was possible to assign nests to particular females. All nests were weighted and measured (nest cup diameter, nest height) in first days of incubation.

It was found that all nest parameters were highly variable within studied population: nest weight – first brood – range: 16.2–54.4 g, second brood: 10.7–44.0 g, nest height – first brood: 71–166 mm, second brood: 36–144 mm, nest cup diameter – first brood: 47–66.8 mm, second brood: 48.5–61.5 mm. However, parameters of nests built by particular individual in one season were correlated with nests built in the next season. This indicates that particular females build similar nest in consecutive years despite of high variation within population.

The study was financed by NCN grant 2017/27/B/NZ8/03118

## **P42: HAEMOPARASITES IN LARID BIRDS - ECOLOGICAL NICHE MORE IMPORTANT THAN MIGRATORY DISTANCE**

**Amelia Chyb<sup>1</sup>, Radosław Włodarczyk<sup>1</sup>, Sandra Bouwhuis<sup>2</sup>, Coraline Bichet<sup>3</sup>, Patrycja Podlaszczuk<sup>1</sup>, Piotr Indykiewicz<sup>4</sup>, Beata Dulisz<sup>5</sup>, Jacek Betleja<sup>6</sup>, Tomasz Janiszewski<sup>1</sup>, Piotr Minias<sup>1</sup>**

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Haemoparasite infections are wide-spread phenomena in birds and a growing number of study shows differences in infection rates between diverse avian taxa. However, it still remains unclear whether and how various ecological and life history traits are associated with infection rates of vector-borne parasites in birds. In this study, we aimed to assess the prevalence of the main genera of haemoparasites (*Plasmodium*, *Haemoproteus*, and *Leucocytozoon*) in two colonial bird species from the Laridae family (*Charadriiformes*), which differ in terms of habitat preferences and migration behaviour. For this purpose, we collected over 600 samples from two breeding colonies of the common terns *Sterna hirundo* and seven colonies of the black-headed gulls *Chroicocephalus ridibundus* located in Poland and Germany. Most importantly, we found significantly higher *Haemoproteus* and *Plasmodium* infection rates in black-headed

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gulls than common terns, which may probably be attributed to differences in habitat preferences (vector-rich vegetated freshwater bodies in gulls versus vector-poor coastal and sandy habitats in terns). We also revealed a negative association between colony size and haemoparasite prevalence in black-headed gulls, suggesting that they may settle in colonies in a despotic manner. Finally, we found no support for a relationship between blood parasite infection rates and migration distance in studied species. Our results suggest that ecological niche of larid species may play a leading role in parasite exposure over migratory distance.

### **P43: BIG CITY LIFE – GENETIC BACKGROUND OF URBANIZATION PROCESSES IN A COMMON WATERBIRD**

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A wide range of study shows that rapid urbanization enhances accumulation of behavioural differences between birds from urban and nonurban populations, but mechanisms generating and maintaining this divergence are poorly recognized. In this study, we investigated genetic background of behavioural adjustments to environmental conditions of human-dominated areas in a non-model bird species, the Eurasian coot *Fulica atra*. For this purpose, we sampled 160 coots from four pairs of urban and nonurban populations and searched for polymorphisms in candidate genes previously reported to be associated with avian circadian rhythms and behavioural traits that may be crucial for urban life. Most importantly, we showed conspicuous associations between the level of landscape urbanization and polymorphism of 3'UTR region of CREB1 gene involved in the development of cognitive functions and regulation of circadian rhythm. We also recorded strong differentiation among urban populations at the intronic region of CKIε gene responsible for regulation of circadian clock. This association may reflect local adaptation to particular urban sites through linkage with polymorphisms in coding regions or through gene expression regulation. While our results support the hypothesis that behavioural divergence between urban and nonurban birds may have a heritable basis, it appears that these genetic adaptations may prevail in non-coding regulatory rather than coding gene regions.

### **P44: CONSTITUTIVE INNATE IMMUNE FUNCTION IS ASSOCIATED WITH HABITAT URBANIZATION, BUT NOT WITH POPULATION DENSITY IN A HIGHLY-ADAPTED URBAN BIRD**

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Living in a large congregation of conspecifics can facilitate pathogen transmission. Therefore, birds from abundant and dense urban populations are expected to be under extensive pathogen pressure, which would require an increased investment in immunity. On the other hand, strong urbanization is likely to negatively affect immune function, but different urban habitats can differ significantly in their level of urbanization, thus producing a variable selective landscape. We aimed to test the associations of population density and habitat urbanization with the level of natural antibodies (NABs) – which are a component of the first line of innate immune defense – in an abundant urban bird, the feral pigeon *Columba livia domestica*. To do so, we collected plasma samples from 174 individuals across the gradients of both population density and urbanization in five large cities in Poland (Cracow, Warsaw, Gdańsk, Wrocław, Łódź). We used a hemagglutination assay based on serial plasma dilutions to assess the activity of NABs. We found that the

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level of NABs was negatively associated with the urbanization gradient, but not significantly related to the population density. These results indicate that heavily urbanized habitats are likely to cause immunosuppression in feral pigeons, implying that severely transformed, man-made environment may carry physiological costs for animals.

### **P45: OXIDATIVE STRESS BIOLOGY IN NEST BOX BREEDING BIRDS**

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Traditionally the model of “oxidative stress life-history” predicts a trade-off of increased metabolism i.e. during reproductive events, with accumulation of damage caused by reactive oxygen species (ROS) production, a prediction under increasing scrutiny. Using a repeat sampling procedure, we measured the oxidative stress levels of female passerines over two reproductive seasons. By sampling at two “extreme” and opposite points of the organism’s energetic state, namely out of the Rest phase while sleeping, and the Active phase while providing food to their young. Previous studies have shown the difference in energy expenditure between these two states to be between 2.5-5 times higher during Activity than Rest during the reproductive season. By repeat sampling we could compare the effects of these directly opposing metabolic states on oxidative damage markers to see if the theory holds true. Our results indicate that despite the high levels of physical activity seen during Active food provision, oxidative damage is not significantly different to levels seen during those while the animal is at Rest, and in one sub-study, these levels were actually lower. These results add to the accumulating evidence that the traditional model of oxidative stress is too simplistic in its approach and despite its attractiveness at linking physiology with ecology it may simply be incorrect.

The student was funded by the project entitled “ATUT PhD Programme in Biology”. The project is co-financed by the European Union under the European Social Fund – Operational Programme Knowledge Education Development.

### **P46: MY SONG WILL TELL YOU IF I ALREADY HAVE A PARTNER: HOW BREEDING STATUS AFFECTS SONG PARAMETERS IN ZEBRA FINCHES**

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Bird song is a crucial feature for mate choice and reproduction. Song is known to communicate information related to the quality of the mate, through song complexity, structure or finer changes in syllable characteristics. It has been shown in zebra finches that those characteristics can be affected by various factors including motivation, hormone levels or extreme temperature. However, although the literature on zebra finch song is substantial, some factors have been neglected. In this paper, we recorded male zebra finches in two social contexts (before and after pairing) and in two ambient temperature conditions (stable and variable) to see how those factors could influence song production. We found strong differences between the two social contexts: compared to their song before pairing, males that were paired had lower song rate, syllable consistency, frequency and entropy, while surprisingly the amplitude of their syllables increased. Temperature variability had an impact on the extent of these differences, but did not directly affect the song parameters that we measured. Our results describe for the first time how breeding status and temperature variability can affect zebra finch song, and give some new insights into the subtleties of the acoustic communication of this model species.

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## **P47: STAND OUT FROM THE CROWD: BREEDING DENSITY AFFECT VOCAL INDIVIDUALITY IN ORTOLAN BUNTING (EMBERIZA HORTULANA)**

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The presence of individual signatures expressed in different sensory modalities has been widely studied across many animal species. Nevertheless, the evolutionary mechanisms underpinning individual distinctiveness remain still unclear. So far, researchers look for high individuality, especially in animals living in large and complex groups, where the need to be distinct is driven by social lifestyle. However, in living in pairs and territorial animals, the correct discrimination (or recognition) between rivals may be decisive to prevent unnecessary and costly aggressions (eg. dear enemy effect). Here, we explore how different population densities, as a proxy of the number of rivals an individual may face, affect vocal identity in territorial birds. We used as a model the Ortolan bunting (*Emberiza hortulana*), a territorial song-learning species from Eurasia characterized by small song repertoire size and well recognized individual and dialect song variation. We collected acoustic, spatial, and genetic data of four populations with different size, density, and level of habitat fragmentation inhabiting Polish farmland. We found that males differ significantly from each other based on time and frequency features of both, individual and dialect, song's components. According to our prediction the level of vocal individuality was positively related to the breeding density, suggesting that when the pool of potential competitors is high, males' songs, on average, are more distinct from each other than in location with less competitors. All together our results support the hypothesis that the intra-sexual selection may act as an evolutionary driver of individuality in animal signals.

## **P48: THE ROLE OF ORNAMENTATION IN BIRD SPECIATION: A STUDY ON COLORATION IN DIVERGENT POPULATIONS OF PAINTED BUNTINGS**

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In birds, the process of speciation is closely associated with transitions in ornamentation, including plumage color and pattern, as well as song. To investigate the origins of these ornamentation shifts and their connection to genetic changes, we conducted a study on one of the most highly ornamented songbirds, the Painted Bunting (*Passerina ciris*).

Male Painted Buntings exhibit a stunning array of colors, such as red chests, blue heads, green backs, green coverts, and pink rumps. To evaluate how these colorful plumage patches appear to birds with their tetrachromatic visual system, we performed spectral analysis on six colored patches. We found that these colorations would be even more striking to a bird's eye than to a human's, as birds can perceive a broader range of colors due to their advanced retinal cone discrimination, including sensitivity to UV light.

Using non-invasive spectrophotometry techniques, we obtained measurements from 88 male specimens in definitive plumage collected from multiple museums. To understand if ornamentation evolved in conjunction with genotype changes, we assessed coloration differences in three genetically distinct Painted Bunting populations. Surprisingly, despite significant genetic divergence, we found no consistent differences in plumage coloration.

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These results suggest that ornamentation shifts do not occur in conjunction with initial population divergence but are likely to serve as reinforcing factors for post-zygotic isolating mechanisms that emerge after populations have become reproductively isolated. This study contributes to a deeper understanding of the intricate relationship between ornamentation, genetics, and the speciation process in birds. 0 Support: National Science Centre doctoral scholarship (no. 2019/32/T/NZ8/00256).

### **P49: PREVALENCE OF PARENTAL COORDINATION IN BIRDS - A SYSTEMATIC META-ANALYSIS**

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In birds with biparental care, it is believed that behavioral coordination over offspring provisioning between breeding partners - if present - increases both the parents' and offspring fitness. Therefore, pairs that coordinate better, should have higher reproductive success. Coordination between breeding partners can possibly reduce sexual conflict. Alternating (i.e., visits of one individual followed by a visit of its mate) and synchronous (i.e., visits of both parents occurring within a short time interval) feeding can occur randomly, but can be also induced by environmental conditions, or as a consequence of parental coordination. Thus, the occurrence of one of the above patterns more frequent than expected under chance can be seen as an indication of parental coordination. Here, using a meta-analytical approach, we want to investigate what is the prevalence of parental coordination in birds and how, if present, it affects the resolution of sexual conflicts within a breeding pair. Furthermore, we want to analyze how coordination affects fitness of both parents and offspring, and how this phenomenon distributes across bird orders.

### **P50: SPARROWS ARE BOLDER WITH BIG FRIEND BEHIND THEIR BACK**

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The White stork is hypothesized to play the role of protective 'umbrella species' for small passerines breeding in stork's nests (e.g. sparrows and starlings). Predatory birds avoid white stork's nests what can reduce predation risk for small birds. As a result, small passerines can be expected to be more bold in the presence of white storks. However, the only previous study that has found evidence that the vicinity of White storks reduce fear of smaller birds are observations of alien invasive Monk parakeet (*Myiopsitta monachus*) inhabiting stork nests in Spain. Our aim was to test experimentally whether the presence of White storks increases the feeling of security of small passerines. We compared reaction of House sparrows and Tree sparrows breeding in occupied and abandoned nests of White storks in Biebrza valley (NE Poland) to a drone circling the stork's nest at a distance of 10 m. The initial number of sparrows observed near both types of stork's nest did not differ. However, sparrows breeding in abandoned White stork's nests were more likely to flee in the presence of drone than birds inhabiting occupied nests (Fisher exact test,  $P=0.001$ ). Our results confirm that small birds feel more safe in the presence of White stork, and suggest that the antipredatory defence provided by storks can be beneficial for smaller species. Our study also shows that the behavior of potential prey can be modulated by the perceived level of the predation risk ('landscape of fear').

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## **P51: EMERGENCE OF PERSONALITIES IN MOOR FROG UNDER PERCEIVED PREDATION RISK**

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Animal behavioural individuality, i.e. personality, results from an ongoing cumulative process rather than merely current performance. It is thus shaped during the whole life of an individual and the emergence of consistent behavioural differences between individuals has been shown to be context dependent in many species. General patterns have not been found yet, though. In the present study, we hypothesised that (H1) consistent between-individual differences in behaviour arise (i) under challenge and ii) via state-behaviour feedback. We also tested the hypothesis that (H2) where development is indirect, adult behavioural type is related to state upon entering metamorphosis rather than to larval behavioural phenotype. We tested these in an anuran, moor frog *Rana arvalis*, in a longitudinal experiment spanning over tadpole and juvenile frog stages. According to expectations (i), we found activity (but not boldness) of the tadpoles, and boldness of juvenile frogs exposed to predator cues to be more repeatable than those of control individuals. Contrary to the expected (ii), tadpole behaviour was not linked to their body size. While, in accordance with the second hypothesis, juvenile frog behaviour was better explained by their body size than by their behaviour as tadpoles. We briefly discuss the insights into how perceived risks shape behavioural phenotypes.

## **P52: THE TIME OF STRESS FOR PREDATOR CAN BE AN ANTI-PREDATOR WINDOW FOR PREY**

**Monika Sysiak<sup>1</sup>, Matylda Kubiak<sup>1</sup>, Barbara Pietrzak<sup>1</sup>, Anna Bednarska<sup>1</sup>, Andrzej Mikulski<sup>1</sup>**

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Chemical communication is crucial for organisms to obtain information about their environment. Prey detect signals like kairomones released by predators involuntarily, which inform them of the predator's presence. Prey adaptive response to such signals is associated with changes in their behavior, life history or morphology. The cost of defense is high, so controlling its activation is critical.

We hypothesize that some chemical cues, such as disturbance cues, alarm signals or high predator kairomone concentrations from populations where cannibalism is common, could inform prey about predator stress. Prey sensing predator stress should be favored by natural selection to avoid unnecessary defense costs - the anti-predator window.

We analyzed the behavioral response cannibalistic predator of damselfly larvae *Ischnura elegans* to two kairomone concentrations and tested the physiological response of *Daphnia magna* (prey of *I. elegans*) to two *I. elegans* kairomone concentrations mixed with alarm signals or disturbance cues. *I. elegans* exposed to higher kairomone concentrations showed decreased hunting activity. *Daphnia* response to high kairomone concentrations and chemical signals indicative of predator stress was weaker, suggesting that *Daphnia* perceives a stressed predator as less dangerous. Our study provides insights into the role of chemical communication in predator-prey interactions and mechanisms by which prey adjust anti-predator defenses in response to predator stress.

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## **P53: HATCHING PHENOLOGY SHAPES THE INTERACTION BETWEEN PREDATION RISK AND WARMING IN THE DAMSELFLY ISCHNURA ELEGANS**

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It has been reported that global warming and non-consumptive predator effects (NCPE) affect fitness traits in prey. However, it is still unclear whether warming and seasonal time constraints modify NCPE in ectotherms. In laboratory conditions, we investigated the effects of NCPE (presence and absence of predator cues from either native noble or invasive spiny-cheek crayfish), temperature (current and warming), and time constraints (early and late hatching date) on life history (survival, mass, and growth rate), behavioral (boldness and the number of prey eaten), and physiological traits (immune function measured as phenoloxidase activity, PO) in a damselfly *Ischnura elegans*. Exposure to predator cues started when larvae entered the final instar (F-0) and lasted another five days. Under both temperatures, early hatchers expressed higher survival up to the entrance into F-0 than late hatchers. Unlike noble crayfish cues, spiny-cheek crayfish cues caused lower larval mass and growth rate, but only in early hatchers and under the current temperature. Spiny-cheek crayfish cues decreased the number of preys eaten, but only in early hatchers, whereas noble crayfish cues decreased the number of preys eaten, but only in late hatchers. Predator cues from both crayfish species decreased boldness in early and late hatchers. There was a trend for increased PO activity in early and late hatchers under both crayfish cue treatments. These results indicate that hatching phenology should be considered when predicting the direct and interacting effects of warming and invasive predators on native ectotherms.

## **P54: LOOKS OR PERSONALITY - WHAT DRIVES DAMSELFLY MATING SUCCESS IN THE WILD?**

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Understanding the link between personality and fitness is vital in behavioral and evolutionary ecology. While most knowledge comes from lab studies, studying natural populations yields ecologically relevant insights into behavioral variation and mating success. In this study, we examined *Calopteryx splendens* mating success in a central-core population, representing an optimal environment. We assessed courtship and boldness-aggression as behavioral axes and measured wing patch area and body size as traits important in sexual selection.

Among the measured traits, courtship positively influenced mating success, highlighting the role of personality. Smaller wing patch size correlated with greater male mating success, while thorax size emerged as a better predictor of success than personality or plasticity in boldness and activity.

This research is the first to demonstrate the connection between personality and mating success in a territorial insect, specifically in a wild setting.

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## P55: URBANIZATION OUTCOMES ON FITNESS TRAITS IN THE DAMSELFLY

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Adaptation to urbanization may require ecological and evolutionary changes in response to anthropogenic factors such as urbanization and invasive species. Moreover, a seasonal time limitation, which increases with latitude, may further mediate the effects of the anthropogenic factors. Here, we studied single and combined effects of increased temperatures and invasive alien predator on the phenotypic response of replicated urban and rural populations (i.e., different urbanization types) of the damselfly *Ischnura elegans* and contrasted these between central and high latitude populations. *I. elegans* larvae were exposed to current (20°C), mild warming (24°C), and heat wave (28°C; for high latitude only) temperature treatments crossed with the presence or absence of the invasive alien spiny-cheek crayfish *Faxonius limosus*. We measured larval development time, mass, and growth rate. Urbanization type affected all damselfly traits, still, these responses depended on latitude, temperature, and sex. Mild warming decreased mass in rural and increased growth rate in urban populations. The urbanization effect on mass was more pronounced in central-latitude populations. Urbanization effects were sex-specific with urban males being lighter and growing slower than rural males. At the current and mild warming temperature, spiny-cheek cues reduced the growth rate, independently of urbanization and latitude. Remarkably, predator effect reversed under a heat wave in high-latitude damselflies. The results underline the context-dependency of fitness traits responses to urbanisation, and indicate that responses to cities at a local scale should not be generalized.

## P56: HABITAT CONNECTIVITY INFERRED FROM LANDSCAPE GENETIC MODELS AT MULTIPLE SPATIAL AND TEMPORAL SCALES IN TWO NEWT SPECIES (*LISSOTRITON MONTANDONI* AND *L. VULGARIS*)

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The movement of organisms across landscapes is influenced by multiple environmental variables that are experienced at spatial and temporal scales determined by species ecology. Landscape genetic studies are therefore advised to directly incorporate such processes by analyzing the contribution of multiple variables at different scales. Here, we investigate how the analyses of multiple variables at multiple scales improves our understanding of population and habitat connectivity in the closely related but ecologically distinct Carpathian newt (*Lissotriton montandoni*) and smooth newt (*L. vulgaris*). Our results show the importance of forested habitats for maintaining population connectivity in both species, and further support the requirement of open forest for *L. vulgaris* found in previous studies. The negative effect of cropland and urban areas was clear for *L. montandoni*, but almost undetectable for *L. vulgaris*. For both species, models built using land-cover available within distances of ~1 to 2 km predicted population genetic differentiation better than models based on other land-cover scales. This suggests that the amount of suitable habitat available at distances close to the species' maximum per-generation dispersal range is a key determinant of connectivity. Analyses of historical forest data showed that recent (post-1970) forest cover following a major reforestation event was a better predictor of current genetic differentiation. This suggests that deep time lags greater than 40 years (approximately 10 newt generations), are unlikely. Overall, we find that considering multiple spatial and temporal scales has improved our understanding of population and habitat connectivity.

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The student was funded by the project entitled "ATUT PhD Programme in Biology". The project is co-financed by the European Union under the European Social Fund – Operational Programme Knowledge Education Development.

## **P57: CALIFORNIA CONSERVATION GENOMICS PROJECT: NEXT-GENERATION LANDSCAPE GENETICS HELPS PROTECT POCKET MICE AND OTHER ENDANGERED LIFE.**

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The rapidly changing conditions of the Anthropocene necessitate conservation plans informed by all available lines of evidence. The California Conservation Genomics Project is a public consortium aiming to rapidly produce, distribute, and compare reference genomes and landscape genetic data for 235 iconic, keystone, and endangered species across the State. I present the goals and challenges of this pioneering effort, using as an example the comparative evolutionary studies of the pocket mice (*Perognathus*).

Pocket mice are an exquisite model of coping with arid conditions, with adaptations ranging from torpor to enhanced osmoregulation: their ability to survive without water made them suitable for the Apollo 17 lunar mission. We present a new, highly contiguous (N50 = 73.2Mbp) reference genome of the widespread *P. longimembris longimembris*, revealing a dynamic landscape of transposable elements. A comparison with the critically endangered *P. l. pacificus* shows structural variation, and substantial divergence at the sex chromosome X. Next, several hypotheses about the evolution of the genus are addressed based on whole genome resequencing of 155 individuals sampled across the range of six *Perognathus* species. Autosomal, X-linked, and mitochondrial markers reveal gene flow across the genome. A major phylogeographic break along the Teháchapi mountains is identified in the Little Pocket Mouse, but admixture between populations persists in the Mojave Desert. Spatial patterns of genetic diversity imply that *P. l. brevinasus* may be used for genetic rescue of the captive population of the nearly extinct *P. l. pacificus*. These results will soon inform conservation policy and actions.

## **P58: THE DIFFICULT MARRIAGE OF FLIES AND THEIR ENDOSYMBIONTS**

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Alphaproteobacteria from the genus *Wolbachia* are among the most prevalent insect symbionts, infecting approximately half of all insect species. They can substantially impact host evolution through mechanisms such as nutritional provision, viral protection, horizontal gene transfer, or a wide range of reproductive manipulation strategies. An example of which could be *Wolbachia*-induced cytoplasmic incompatibility, capable of stimulating host speciation. To assess the evolutionary history, current drivers, and possible future trajectories of insect species and populations, it is crucial to consider diversity and distribution patterns of their symbiotic component.

In this study, we analysed amplicon sequencing data of a section of the cytochrome oxidase I gene (COI) for over 1,500 individual insects representing more than 100 species of scuttle flies (family Phoridae) from several locations in northern Sweden, and of their *Wolbachia* symbiont. Our objective was to unravel the patterns of *Wolbachia* infections and shed light on the dynamics of these critical insect symbionts in the scuttle fly community.

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Our findings indicate that, on average, *Wolbachia* exhibited a twofold higher infection rate in females, although the ratio varied across insect species. At the host genotype level, we observed a strong host specificity of *Wolbachia*, with certain bacterial variants infecting multiple species. Notably, in one of the fly genotypes with a 100% infection rate, we identified a strong pattern of double *Wolbachia* infection in females. The results contribute to our understanding of insect symbiont dynamics and provide insight into the underlying evolutionary forces and their potential impacts on insect populations and ecosystems.

### **P59: THERE'S ALWAYS ROOM FOR ONE MORE. MICROBIAL COMMUNITIES IN NECTAR OF SELECTED PLANT SPECIES.**

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Pollination is one of the most important ecological interactions, without it many plant populations would decline and eventually disappear. To protect biodiversity, human well-being and the economy we need a robust assessment of factors influencing pollination, and one of them are nectar microbial communities. The presence of microorganisms in nectar is a common and important phenomenon. Moreover, every living organism, including pollinators, has its microbiota. Current research on microorganisms in nectar shows their great role in pollination efficiency, plant and pollinator fitness. Surprisingly, many of the fundamental views concerning microorganisms in nectar are untested hypotheses. Our project addresses crucial gaps concerning the role of floral traits and pollinators in shaping nectar microbiome. We collected nectar from 10 species of flowering plants with different flower features, where we examined nectar properties and nectar microbiome. We also recorded plant-pollinator interaction. We hypothesize that plant species visited by the same types of pollinators may support pollinator-linked specific nectar microorganisms communities. Our results indicate the important role of pollinators with a smaller influence of flower traits and nectar properties.

### **P60: FIRST INSIGHT INTO THE EVOLUTION OF THE FLIGHT-CONTROL SYSTEM IN BARK BEETLES**

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Gaining the ability to fly actively was a ground-breaking moment in insect evolution. Active flight influences several key aspects, including the ability to escape predators, overcome migration barriers, exploit novel resources, and find a mate. Nevertheless, powered flight in a complex landscape requires an advanced flight-control system that provides fast and reliable feedback. A growing body of evidence now points to the role of mechanosensation as a crucial modality required for effective course control during aerial maneuvers of insects. Specialized mechanosensors located within a flight apparatus transduce local strain fluctuations and airflow pressure into neural signals, providing extremely fast feedback regarding airflow and aeroelastic deformations of the wings surface. Among insects, bark beetles (Curculionidae:

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Scolytidae) constitutes an ideal group to study flight-related morphology, as it is known that their dispersal abilities in this group vary greatly even within closely related taxa. Some bark beetle species can fly over dozens of kilometers, while their congeners disperse over only dozens of meters. We have analyzed the number, types, and distribution of mechanosensors on wing and elytra in 27 species of bark beetles using SEM and advanced optical microscopy, together with the analysis of phylogenetic background. The main goal was to answer the question of whether the higher resource investment in the development of flight wings will result in a larger number of mechanosensors. We found that flight investment does select for an increased number of single mechanosensors and an increased size of sensing fields on flight apparatus in bark beetles.

## **P61: IN SEARCH OF HIDDEN BIODIVERSITY**

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Explaining the mechanisms of biodiversity maintenance is one of the central goals of evolutionary ecology. It is important to learn about all biotic and abiotic factors that guarantee species persistence, that is, about species' ecological niche. Such knowledge can help to understand how organisms respond to environmental changes as well as those resulting from human activity. Biological diversity, however, can be underestimated due to the existence of cryptic species complexes. Recently, as DNA-based techniques for the detection of genetic diversity have become popular, more and more new species are being discovered. It is becoming more frequent that organisms, which have long been treated as a single taxon, are, in fact, complexes consisting of numerous cryptic species, differing in their ecological requirements. My goal is to present the importance of identifying cryptic species complexes in many fields, from crop protection to forensic entomology. I review various methods of and approaches to identifying the species complexes, including molecular, acoustic, and morphologic, using the examples of Troschel's tree frog (*Hypsiboas calcaratus*), a trematode of the genus *Echinostoma*, and the wheat curl mite (*Aceria tosichella*). Such studies are crucial for recognizing the complexity of ecological and evolutionary relationships and understanding the extent of biodiversity.

## **P62: THE IMPACT OF WHEAT STREAK MOSAIC VIRUS (WSMV) ON THE POPULATION GROWTH RATE WHEAT CURL MITE (WCM)**

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Wheat streak mosaic virus (WSMV) (Potyviridae, Triticumovirus) is worldwide distributed virus that affects cereals, mainly wheat. The only vector for WSMV is *Aceria tosichella* (wheat curl mite, WCM), which belongs to the Eriophyidae family, highly specialized obligate phytophagous mites. According to vector manipulation hypothesis, plant viruses can affect its' arthropod vectors to facilitate their spread. It was suggested WSMV manipulates WCM to increase the number of dispersible viruliferous mites. The aim of the study was to determine the population growth rate of the WCM population in 7, 14, 21, and 28 days after colonisation of the mites on WSMV-positive and -negative *Triticum aestivum* L. In addition, the number of leaves was counted, and their leaf area was assessed to determine mite densities. The results showed that the WSMV infection had a positive effect on mite population density. The mite populations

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feeding on plants without WSMV on average reached a faster growth rate than the mite population feeding on the WSMV-infected plants. However, WSMV infection had a positive effect on mite population density, which is probably a cue for mite windborne dispersal, along with host plant condition. This is the first insight into the virus-vector manipulation phenomenon in mites transmitting plant viruses, because the viral manipulation strategy had previously been demonstrated for their insect vectors.

The study is a part of research project No. 2021/43/D/NZ8/01130 financed by the National Science Center (Poland)

### **P63: SEXUALLY-SELECTED MALE WEAPON AND THE RISK OF POPULATION EXTINCTION UNDER INCREASING TEMPERATURE**

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Exaggerated sexually selected traits, occurring more commonly in males, help individuals to increase reproductive success, but are costly to produce and maintain. These costs, on the one hand, may improve population fitness by intensifying selection against maladapted males, but on the other hand may increase the risk of extinction under environmental challenge. However, the impact of sexually selected traits on extinction risk has not been investigated experimentally. We performed experiments using replicate populations of a male-dimorphic mite, *Rhizoglyphus robini*, to test if prevalence of an elaborate, sexually selected weapon affected the risk of extinction under gradual temperature increase (2°C per generation). As temperature increased, individual survival decreased, but this effect was much more dramatic in populations with high weapon prevalence, compared to populations in which weapon expression was low. Consequently, the former was more prone to extinction than the latter. Extinctions occurred despite partial suppression of the weapon expression at increased temperatures and were not explained by increased male mortality. Our results provide the first, to our knowledge, experimental evidence demonstrating a dramatic effect of elaborated sexual traits on the risk of extinction under environmental challenge.

### **P64: THE GENETIC ARCHITECTURE OF SEXUALLY-SELECTED WEAPON IN THE BULB MITE**

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Alternative reproductive phenotypes (ARPs) represent one of the most remarkable examples of variation within sexes with the potential to both reflect and shape genetic variance across genomes, influencing the rates of adaptation, speciation, and extinction. However, to investigate how ARPs contribute to the evolutionary potential of populations requires a comprehensive understanding of their genetic architecture, which is the case for only a limited number of species. Here, we investigated the genomic basis of ARPs determination in bulb mites (*Rhizoglyphus robini*), a species with two distinct male phenotypes: fighters, with an enlarged third pair of legs for securing access to females by eliminating rivals, and non-aggressive scramblers, whose legs remain unmodified. Through whole-genome sequencing of pools of scambler and fighter males, we have identified a 4-Mb region exhibiting significant divergence between these morphs, spanning approximately 1.5 thousand genes. This remarkable genetic differentiation was further

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corroborated through an analysis of SNP composition of inbred lines selected for either fighter or scrambler males. Our recently constructed linkage map indicates a nearly complete suppression of recombination in this region in males, suggesting that the morph-determining region in bulb mites operates as a supergene. Our results provide significant insight into evolution of complex phenotypes and the maintenance of large structural variation.

### **P65: GENETIC CO-STRUCTURE IN THE BANK VOLES-BORRELIA HOST-PATHOGEN SYSTEM**

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Theory from co-evolutionary dynamics of host-pathogen interactions predicts that genetic diversity of pathogens is influenced by their host diversity and distribution, leading to congruent population structures between hosts and their pathogens. While host-pathogen co-structures were investigated in some systems using neutral, whole-genome markers, studies directly involving interacting resistance/infection genes are lacking but have potential to uncover otherwise hidden patterns. Here, I investigate and compare population structures in *Borrelia afzelii*, one of the causing agents of Lyme disease, and their host bank voles (*Myodes glareolus*), using samples of the latter collected across transects in northern Poland. We focus analyses on interacting genes for which differentiation was observed: the Complement Factor H (CFH) and CFH-related (CFHRs), regulators of immune responses in vertebrates; and the Complement Regulator-Acquiring Surface Proteins (CRASPs), which interact with CFH and CFHRs to inhibit vertebrates' immune responses. Preliminary results show evidence of structure in CFH and CFHRs in bank voles, with two distinct clades arising in the east (Eastern) and in the west (Carpathian), separated by an admixed region in the middle. Instead, we did not find clear structures in the borrelian CRASPs, probably due to *B. afzelii* being generalist and able to infect multiple vertebrate species. This study furthers our understanding of host-pathogen co-evolution and of the factors associated with pathogen diversity and distribution, with potential relevance to human epidemiology. Future studies will involve more sampling locations over west-east transects in Poland and will aim to detect signatures of positive selection in these and other interacting gene pairs.

### **P66: THE IMPORTANCE OF INTEGRATIVE TAXONOMY: UNCOVERING MULTIPLE SPECIES IN AN ALLEGEDLY MONOTYPIC GENUS**

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Taxonomy of microscopic invertebrates, such as tardigrades, is challenging due to a small number of taxonomically informative characters. Recent advances, mainly thanks to the combined use of molecular techniques and traditional methods, expose further numerous taxonomic challenges, both natural (such as species crypsis, overlap of intra- and inter-specific variability in morphological traits) as well as anthropogenic (many outdated and incomplete descriptions based only on morphological). New research opportunities are associated with an increasing amount of information, which allows to expose and describe new species with unprecedented precision, which translates to much more accurate inference in other fields that rely on precise taxonomic identifications, such as biogeography, ecology and physiology.

The genus *Richtersius* is an excellent example of problems in tardigrade taxonomy. For many decades the genus remained monotypic, containing only *R. coronifer*. A century after it was described, integrative analyses of several populations traditionally identified as *R. coronifer* indicated that species are hidden within the genus.

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In this study, a phylogenetic analysis of *Richtersius* reveals a new tardigrade species from Greece, *Richtersius tertius*. The description is based on morphological and morphometric analysis using light and scanning electron microscopy as well as genetic analysis based on four molecular markers (DNA sequences of three nuclear, i.e., 18S rRNA, 28S rRNA, ITS-2 and one mitochondrial COI fragment). Morphological and morphometric differences, together with genetic comparisons, provide independent verifications of *Richtersius tertius* as a species new to science. The results presented here contribute further to the recognition of the morphological variability and biodiversity within *Richtersius*.

### **P67: PHYLOGENY OF THE GENUS RHYZOBIOUS COLEOPTERA: COCCINELLIDAE: COCCIDULINI) – PRELIMINARY STUDY**

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Ladybird beetles (Coccinellidae) are one of the best recognized groups of beetles. Despite of many research, their classification and phylogeny still remains unclear. One of the most problematic groups within this family is tribe Coccidulini, which includes around 30 extant genera. The largest Coccidulini genus is *Rhyzobius*, which was taxonomically revised in 2010, and includes now 109 living and 5 extinct species. *Rhyzobius* is widely distributed in the Old World, but its greatest diversity is in Australian region. Recent molecular research questioned its monophyly. The aim of this work is to test monophyly and reconstruct phylogeny of the genus *Rhyzobius*. Research is based on wide spectrum of data: morphological (materials from whole distribution range), molecular (analysis of mitogenomes), and fossil data (fossils records from Baltic amber and amber from Oise in France). As a preliminary study genera *Coccidula* from Palaearctic and *Adoxellus* from New Zealand were revised, as well as new species of *Rhyzobius* from New Guinea were described. That research is a first step to understand the morphological diversity of the tribe and may lead to further phylogenetic studies.

### **P68: EVOLUTIONARY TRADE-OFFS CONSTRAINING THE MHC GENE EXPANSION: BEYOND SIMPLE TCR DEPLETION MODEL**

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The major histocompatibility complex (MHC) molecules present pathogen-derived antigens to T cells, thus initiating adaptive immune response in vertebrates. Co-evolutionary dynamics between hosts and pathogens generate and maintain huge allelic polymorphism of MHC-encoding genes, yet, individuals possess only a few functional MHC loci. Thus, paradoxically, individuals can only use a fraction of the adaptive diversity present at the population level. T-cell receptor (TCR) depletion hypothesis posits that this limitation results from an evolutionary trade-off between pathogen recognition and self-tolerance, as an increased MHC diversity might enhance negative selection and deletion of T cells, leading to a depletion of TCR repertoires. However, generality of this long-standing hypothesis was recently questioned in a study that correlated an intra-individual MHC diversity with total TCR repertoires in a laboratory-bred bank voles. It supported its predictions for MHC class I (presenting cytosolic antigens to cytotoxic CD8<sup>+</sup> T cells) but not class II (that presents extracellular antigens to helper CD4<sup>+</sup> T cells).

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Here we expand beyond immunogenetics and look into how diversity of each MHC class influences both numbers and TCR repertoire size of the responding T cell subsets in voles. Our findings suggest that the MHC class I expansion may be limited by diminishing T cell counts, rather than by directly depleting the TCR richness of CD8+ T cells. In contrast, negative effects of MHC class II diversity on CD4+ T cell counts might be counterbalanced by a relative enrichment of TCR diversity of CD4+ T cells, arguing against a universal TCR depletion model.

### **P69: VARIABILITY OF EVOLUTIONARILY IMPORTANT GENES (MHC) IN NON-PASSERIFORMES**

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The major histocompatibility complex is a group of genes encoding MHC molecules (Major Histocompatibility Complex), i.e. cell surface proteins that play a key role in the adaptive immune system. MHC genes are considered to be one of the most important genes in evolutionary terms, also playing an important role in mating and individual recognition in some species.

The genes encoding MHC molecules are the most polymorphic region of the genome. A characteristic feature of these genes is a significant differentiation of polymorphism between species. Due to multiple duplications, the MHC region may have multiple alleles within a locus. The greatest polymorphism was observed in passerine birds (Passeriformes). Significantly fewer genes and lower polymorphisms were found in the non-Passeriformes group. It is a systematically heterogeneous group formed by all orders of birds not belonging to passerines. The genetic architecture of the MHC genes of this group has not yet been compared. However, it can be expected that due to such a large diversity of the group resulting from the different phylogenetic background, there will be large differences in the level of polymorphism of species belonging to different orders.

The aim of the study was to compare the variability of MHC genes in different species and non-Passeriformes orders. MHC class I sequences of 36 species and MHC class II sequences of 120 species available in the NCBI database were analysed. A phylogenetic tree was constructed and sequence polymorphism and selection acting on MHC genes in different orders of birds were analysed.

### **P70: SOSNOWSKY'S HOGWEED HERACLEUM SOSNOWSKYI INVASION FAVOURS EUROPEAN HONEYBEES APIS MELLIFERA OVER OTHER POLLINATORS DEPENDING ON ITS SEVERITY AND TRAITS**

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Pollinators, for example, the generalist European honeybee *Apis mellifera*, can attend the flowering invasive plants, although invasions are also responsible for pollinators' decline. There is a lack of studies assessing what traits of invasive plants attract pollinating insects. The study investigated whether areas invaded by Sosnowsky's hogweed *Heracleum sosnowskyi* attracted honeybees and reduced the abundance of other pollinators, and the influence of traits of the invader. Pollinator surveys were at 34 hogweed sites in southern Poland, with each site containing three study plots with varying invasion severity (uninvaded, less invaded, severely invaded). Honeybees were up to four and three times more abundant in severely invaded than uninvaded and less invaded plots, respectively, but their abundance did not differ between less invaded and uninvaded plots. All studied hogweed traits (i.e., number, coverage, height, flowering) with the highest values attracted honeybees in less invaded and severely invaded plots and other pollinators (i.e., non-*Apis* bees and wasps, Diptera, Coleoptera) in the less invaded plots. The abundance of honeybees

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decreased when pollinated hogweed flowers became more frequent and the abundance of other pollinators increased at the same time (mainly Coleoptera insects in less invaded plots and non-*Apis* bees and wasps in severe invasion). Honeybees were highly attracted by the traits of invasive plant species reflecting severe invasion at the expense of other less favored pollinators that competed with generalists for the same resources in the invaded areas. This is important, as nowadays the invasive hogweeds can experience a rapid evolution impacting the declining pollinators.

### **P71: PHYLOGENY AND EVOLUTIONARY HISTORY OF THE GENUS *SERGIA* (CAMPANULACEAE) AND ITS RESPONSE TO THE CLIMATE CHANGES PREDICTED FOR THE MOUNTAINS OF CENTRAL ASIA (A WORLD BIODIVERSITY HOTSPOT)**

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Ongoing climate change is a significant threat that impacts the range dynamics of cold-adapted alpine species and in consequence, biodiversity loss. In this study, we used molecular data (ITS, cpDNA, genome-wide SNP genotyping) to reconstruct the phylogenetic relationship and estimate the divergence time of *S. regelii* and *S. sewerzowii*, against the backdrop of other Campanulaceae species from the region. We modelled present and future potential distribution of the two endemic species associated with rocky habitats in the Mountains of Central Asia to illustrate the evolutionary history and differences in their environmental niches. The results reveal that the studied species are Miocene relicts, which diverged from a common ancestor ca. 12.06 Mya. Our results show evidence for the polyphyletic nature of the genus *Sergia*. The future distribution model demonstrates a dramatic loss of *S. regelii* habitats with a shift of suitable habitats to higher elevations, while the potential range of *S. sewerzowii* increases and shifts to the north. The predicted distribution changes are based on the fact that *S. regelii* prefers much higher elevations than *S. sewerzowii* and is adapted to lower temperatures. The deep analyses of niche preferences and evolutionary history of the endemic genus *Sergia* presented here cast light on the phylogeny of Campanulaceae species in the Central Asian mountains and will help to more precisely assess the risk of species extinction in this world biodiversity hotspot.

The student was funded by the project entitled “ATUT PhD Programme in Biology”. The project is co-financed by the European Union under the European Social Fund – Operational Programme Knowledge Education Development.

### **P72: GENETIC DIVERSITY OF HYBRID ZONES OF SCOTS PINE AND ITS CLOSE RELATIVES**

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Pines are often characterized as species with weak reproductive isolation. Therefore, closely related species, such as *Pinus sylvestris* L. and pines from the *Pinus mugo* complex (*P. mugo* T. and *P. uliginosa* N.), can undergo introgression and produce hybrids in areas with suitable climate conditions where parent species come into secondary contact. The main focus of this study was to analyze the genetic diversity and relations between pines from three hybrid zones located in southern Poland – Błędne Skały, Torfowisko pod Zieleńcem and Bór na Czerwonem. Samples from more than a thousand individuals from all phenotypes were collected in hybrid zones. Several allopatric populations of pure pine species were added as references samples. Two different approaches were employed – SNaPshot genotyping for mitochondrial and chloroplast DNA markers and nuclear DNA microsatellite (SSR) markers. Both methods proved to be

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highly efficient. Close genetic relationships are clearly visible in both sets of markers, particularly in the *P. mugo* complex. The results also show a slight difference between the approaches: mitochondrial markers better represent geographic differences, whereas nuclear SSRs show a clearer differentiation between species. The study indicates that hybridization proceeds in the investigated populations but its patterns are site specific.

### **P73: UNRAVELLING THE EVOLUTIONARY RELATIONSHIPS AND SPECIATION PATTERNS OF EUROPEAN PINE TAXA**

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Delimiting closely related species that share an evolutionary history and genetic variation can pose significant challenges. However, studying such species is invaluable as it provides unique insights into the mechanisms of speciation and how species maintain their integrity despite gene flow and adaptive divergence. Our aim was to unravel the phylogenetic relationships among closely related pines from the *Pinus mugo* complex and *P. sylvestris*, while exploring various scenarios of speciation within this group. Accurate species delineation would greatly enhance our understanding of the genomic divergence history and help identify regions under selection that contribute to species integrity and local adaptation. We analyzed sequence variation data from multiple neutral genes, reconstructed phylogenies, and utilized a coalescent modelling approach to investigate reticulation events in the evolutionary history of pines. Our findings revealed a substantial overlap of neutral variation within the *P. mugo* complex, providing evidence of multiple instances of interspecific gene flow during species divergence. We rejected the pure hybrid speciation model for *P. uliginosa* and discovered that *P. mugo* and *P. uncinata* are sister species, with *P. uliginosa* as the basal lineage. We also observed asymmetrical migration between them following their divergence. The extent of gene flow between species varied significantly, with a consistently stronger flow from representatives of the *P. mugo* complex to *P. sylvestris* compared to the opposite direction. These results highlight the prominent role of reticulation evolution in forest trees and establish a genetic framework for studying species integrity maintained by selection and local adaptation.

### **P74: CLIMATE CHANGE IMPACT ON FOREST PHYTOCOENOSES OF UKRAINE**

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Climate change poses a particular threat to Ukrainian forests, particularly biodiversity, and the sustainability of agroforestry landscapes. At the same time, forests can prevent climate change or mitigate its consequences.

The climate change impact in the 21st century on Ukrainian forest is modeled using A1B climate scenario of the Intergovernmental Panel on Climate Change (AR 4). The viability of populations of six main forest-forming species with a long development cycle: *Pinus sylvestris* L., *Quercus robur* L., *Fagus sylvatica* L., *Picea abies* (L.) H. Karst., *Betula pendula* Roth, *Alnus glutinosa* (L.) Gaertn. is considered based on the assessment of bioecological characteristics according to climate humidity, continentality and cryo climate

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indicators. Based on the developed modeling methods the vulnerability of forest phytocenoses of Ukraine to climate change was assessed.

Climate humidity appeared to be the primary limiting factor for the survival of forest-forming species. Water stress is the main factor restricting the forest's spread and resilience. The projected decrease in climate humidity will lead to a significant narrowing of the optimal growth zone of the studied species, its shifting northward and increasing in areas with arid conditions unfavorable for forests. It will result in a decrease in productivity, reproduction, and resistance of studied species to pests and diseases, an increase in forest fires and deforestation risk in the 21st century.

To prevent such consequences adaptation measures are required, namely preservation of genetic reserves of the main forest-forming species, expansion of protected areas, reforestation, and forestry management based on principles close to nature.

### **P75: HOW WELL CAN PLANT SUCCESSION DESCRIBE SHORT CLIMATIC OSCILLATIONS IN THE QUATERNARY?**

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The Quaternary climate is characterised by alternating phases of cooling (glaciations) and warming (interglacials). Among these periods, Marine Isotope Stage 11 (MIS 11) stands out as an intriguing period in the Middle Pleistocene due to its resemblance to the orbital configuration of the Holocene. Remarkably, MIS 11 experienced a relatively stable climate with warm and moist conditions, featuring a global temperature increase of approximately 1.5–2°C above pre-industrial levels. In Polish stratigraphy, the substage "c" of MIS 11 corresponds to the Masovian Interglacial.

This study aims to comprehensively understand vegetation changes during the Masovian Interglacial by employing high-resolution palynological data obtained from five newly examined profiles in Eastern Poland. The research emphasises periods of climatic oscillations, meticulously recognised in this investigation. All geological profiles analysed are situated in the Southern Podlasie Lowland, an area known for its abundant MIS 11c lacustrine deposits.

Drawing on new material we propose a revised duration of the Masovian Interglacial, estimating it to span approximately 18,000 years. This study achieves a more accurate reconstruction of the vegetation during the Masovian Interglacial utilising the REVEALS model. Notably, our findings highlight the increased importance of larch (*Larix*) and riparian communities during the early Interglacial. Furthermore, the REVEALS model confirms the dominance of fir (*Abies*) during the Younger Holsteinian Oscillation (YHO), indicating its expansion in the region and its ability to thrive in nutrient-depleted soils. Additionally, the results of the NMDS analysis suggest that YHO triggered the transformation of oak-hornbeam forests toward a more thermophilic variant.

The student was funded by the project entitled "ATUT PhD Programme in Biology". The project is co-financed by the European Union under the European Social Fund – Operational Programme Knowledge Education Development.

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## **P76: INVESTIGATING THE IMPACT OF ENTOMOPATHOGENIC FUNGUS BEAUVERIA BASSIANA INFECTION ON REPRODUCTION AND ADULT, MORTALITY IN REPRODUCTIVELY NAIVE TROPICAL CRICKETS (GRYLLODES SIGILLATUS)**

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This study examines the influence of *Beauveria bassiana* infection on reproduction and adult mortality in reproductively naive tropical crickets (*Gryllobates sigillatus*). The methodology employed in this research aims to understand the effects of reproductive status and infection on the reproductive fitness and survival of the crickets. In the experimental design, replicates consist of a population of 20 individuals to reflect the promiscuous nature of the species. Reproductively naive adults of both sexes are infected with *B. bassiana* for 10 days prior to mating or remaining reproductively naive. Each treatment consists of 20 individuals, and the surviving individuals after the infection period are selected for further analysis. To isolate the effects of reproductive status and infection, different treatments are implemented. These treatments include combinations of infected and control males and females, both in the reproducing and reproductively naive groups. Each treatment is replicated 10 times to ensure statistical reliability. Throughout the study, the reproductive output and adult mortality of the infected and control individuals are closely monitored. The number of offspring produced by the females and the survival rates of the adults are recorded. By comparing the reproductive success and lifespan among the different treatments, the impact of *B. bassiana* infection on the reproductive fitness and adult mortality of reproductively naive tropical crickets can be assessed. The findings from this research will contribute to our understanding of the ecological and evolutionary consequences of pathogen exposure in tropical cricket populations, the insights gained will inform the development of targeted biological pest control.

## **P77: INVESTIGATING SEXUAL DIMORPHISM OF TROPICAL HOUSE CRICKET (GRYLLODES SIGILLATUS) IN RESPONSE TO INFECTION BY ENTOMOPATHOGENIC FUNGUS BEAUVERIA BASSIANA**

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Sexual dimorphism can be observed in almost all traits, including in the two main components of adaptation - reproduction and survival. The sexes differ in external mortality, an important component of which is that caused by pathogens.

Aim of examining the susceptibility of male and female *Gryllobates sigillatus* to infection by *Beauveria bassiana* is to unravel the potential variations in adaptive strategies between the sexes. According to life-strategy theory, if more energy is spent on survival, less can be spent on reproduction. Elucidating sex-specific responses to *B. bassiana*, paves the way to more efficient pest management approaches targeting specific populations.

Previous studies on *G. sigillatus* - a promiscuous species with males having substantial parental investment challenges to a degree Darwin-Bateman paradigm (which became controversial in recent years). Research on sexual dimorphism, especially in response to pathogens in insects, is limited. Authors of this study hope to contribute to the topic of host-parasite interactions as well as to ongoing discussion on sexual selection. Experiment aims to reflect natural conditions where crickets can choose their mates. Tests will involve populations of 20 individuals of both sexes Infected for 10 days prior to mating. Surviving infected individuals will be further analysed. Treatments will include various combinations of infected and control crickets of both sexes with each treatment being repeated 10 times. Reproduction will be counted both as the number of individuals that hatch from eggs (hatchability) and the number of offspring that reach sexual maturity. Offspring per female, from the entire reproductive period, will be counted.

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## **P78: BEETLE ELYTRA: EVOLUTION, MODIFICATIONS AND BIOLOGICAL FUNCTIONS**

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The transformation of fore wings into rigid covers, known as elytra, was a groundbreaking morphological adaptation that has contributed to beetles' amazing evolutionary success. Nonetheless, knowledge of the functional characteristics of these structures is still patchy and dispersed throughout a wide range of studies. We have compiled the most recent information on the evolution, development, modifications, and biological functions of this critical evolutionary novelty. The formation of elytra occurred during the early evolution of Coleoptera, most likely during the Carboniferous period, and was achieved through the gradual process of progressive forewing sclerotization and the formation of inward-directed epipleura and a secluded sub-elytral space. The elytra of several extant beetle lineages have been significantly modified. Multiple surface alterations, a hard connection or fusion of the elytra, or partial or total reduction are examples of this. Mechanical protection of hind wings and body, anti-predator strategies, thermoregulation and water saving, water harvesting, flight, hind wing folding, diving and swimming, self-cleaning and burrow cleaning, phoresy of symbiotic organisms, mating and courtship, and acoustic communication are all functions of beetle elytra. We believe that the elytra's ability to perform multiple roles has greatly contributed to the beetles' extraordinary diversity.

## **P79: COMING OUT FROM THE SHADOWS: CHEMICAL STRATEGY OF A FACULTATIVE SLAVE-MAKING ANT SPECIES FORMICA SANGUINEA**

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Obligate slave-making ant species often develop chemical camouflage to deceive the recognition system of their host species. Recent studies on *Formica sanguinea* support the idea that facultative slave-making species also face selective pressure to maintain species-specific recognition labels. These studies reveal that *F. sanguinea* manipulates the cuticular hydrocarbon (CHC) profiles of their slaves, making them chemically similar to the parasites. However, this strategy may fail when slave-makers are in the minority, particularly during the early stages of colony development after a newly-mated parasite queen usurps the host colony. To understand the chemical strategy employed by parasitic ants during this stage, we analyzed CHC profiles of ants from incipient and maturing *F. sanguinea* colonies. Over time, we observed an increase in the proportion of compounds characteristic of *F. sanguinea*, positively correlated with the proportion of slave-making workers in the colony. Additionally, we found that young *F. sanguinea* workers (callows) had a lower proportion of compounds distinguishing them from *F. fusca* ants compared to older individuals. The ability to mimic recognition cues of the slaves appears to be acquired during preimaginal life, possibly at the larval stage through the ingestion of CHCs transferred with food by nursing workers. This gradual change of chemical identity allows slaves to familiarize themselves with and learn new recognition cues. The initial chemical camouflage of slave-making ants is crucial in subduing the intrinsic aggression of host ants in response to parasite cues as supported by a few records of aggression from slaves towards *F. sanguinea* ants in our experimental colonies.

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## **P80: THE MECHANISM OF RESCUE ACTIONS IN MANICA RUBIDA ANTS**

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Communication plays a major role in animals' survival. One can reasonably expect that animals also use communication in the context of rescue behaviour, i.e. when one individual helps another one in a life-threatening situation. Such behaviour is common in group-living animals, where communication is also advanced. Some species of ants have evolved the stridulatory organ - a morphological structure that enables the emission of vibroacoustic signals called stridulations. The functional importance of these signals remains understudied. Here, we tested whether stridulations play a role in the context of rescue occurring between nestmates when one of them is trapped. As a study model, we chose the ant *Manica rubida*, characterized by the ability to rescue and produce intense sounds. Our aim was to find out whether workers react to species-specific sounds and whether these sounds elicit rescue actions. The results of the playback experiment showed that *Manica rubida* ants react not only to sounds produced by nestmates but also to white noise, enhancing recruitment behaviours. Furthermore, ants were more prone to rescue nestmates whose abdomens were left free to move than individuals with the abdomens blocked. We suggest that allowing the ants to have the abdomens free, allowed them to both emit vibroacoustic signals and spread pheromones more effectively. Still, other types of signals, such as chemical substances, require further research attention as a multimodal system is likely to occur in the context of rescue behaviour elicitation. Our findings bring methodological value for further studies on communication in social insects.

## **P81: UNVEILING SPECIES DIVERSITY OF DAY ACTIVE MOTHS IN THE TROPICAL ANDES: THE SCORDYLIODES GENUS (LEPIDOPTERA, GEOMETRIDAE: LARENTIINAE)**

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The Andes, known as a biodiversity hotspot, still harbour a poorly understood Lepidoptera fauna. In this study, we investigated the *Scordyliodes* genus, a group of diurnal moths that inhabit the cloud forests of the Andes. So far, only four species belonging to this genus were described, but the real number of species within this genus is much more higher than assumed. By employing an integrative taxonomy approach, including morphological (wing color pattern) anatomical (genitalia), and molecular (a fragment of cytochrome oxidase subunit I gene, COI) data, we aimed to reveal the true species diversity within this genus.

Our results demonstrated a remarkable three-fold increase in the recognized number of *Scordyliodes* species, compared to previous assessments. On the basis of the studied material, twelve new *Scordyliodes* species were distinguished. Molecular analysis revealed a strong correlation between species distribution and geographic isolation. Natural barriers between populations influenced molecular, colour pattern, and genitalia variations, providing information on the evolutionary history of the Andes.

This study highlights the importance of considering diurnal moths within the diversity of Andean Lepidoptera and emphasizes the importance of integrating multiple data sources for a comprehensive understanding of the natural history. By expanding our knowledge of *Scordyliodes* species diversity, we contribute to the broader understanding of Lepidoptera biodiversity in the Andes. Our findings underscore the complex interplay between species, their habitats, and historical processes in shaping the remarkable biodiversity of this region.

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## **P82: THE SLIMY BASTARDS – UNCOVERING THE HIDDEN DIVERSITY WITHIN TAXONOMICALLY CHALLENGING GENUS OF TERRESTRIAL SLUGS (GASTROPODA: AGRIOLIMACIDAE: DEROCERAS)**

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*Deroceras* Rafinesque, 1820, represents the most diverse genus of slugs, comprising a remarkable variety of over 100 species, accounting for approximately 90% of all Agriolimacidae taxa. While several of these species exhibit restricted ranges on specific islands or geographical regions, a few possess wide distributions and hold economic importance. However, despite its significance, the GenBank database presently contains sequences for only 14 species within the *Deroceras* genus, representing a mere fraction of the recognized taxa within this group. Consequently, the precise phylogenetic relationships among *Deroceras* species remain largely elusive.

The primary objective of this research was to unravel the phylogeny of *Deroceras* by conducting analyses on two mitochondrial markers (COI, 16S rRNA) and two nuclear markers (28S rRNA, histone 3). To accomplish this, specimens from the natural history collections of German and Polish museums, specifically Görlitz, Dresden, Frankfurt am Main, Stuttgart, and Wrocław (Poland), were examined. In addition to elucidating the relationships among the investigated taxa, this study significantly contributes to species identification through the establishment of a comprehensive DNA library for the studied species.

Acknowledgements: This research received support from the SYNTHESYS+ project <http://www.synthesys.info/> which is financed by European Community Research Infrastructure Action under the H2020 Integrating Activities Programme, Project number 823827.

## **P83: CONVERGENT EVOLUTION OF RARE DARK, UV-ABSORBING CUTICULAR PIGMENTATION IN A NEW AFRO-ORIENTAL HETEROTARDIGRADE SPECIES COMPLEX**

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Green, brown and black pigments are uncommon in the typically yellow to orange Echiniscidae (one of the most diverse groups of limnoterrestrial tardigrades). Only one heterotardigrade genus, *Viridiscus*, has been known to exhibit cuticular colouration which varies from a light through dark green to almost black. In our current study, we discover a new echiniscid lineage from the primeval subtropical and tropical rainforests of India and Tanzania, comprising three species with a caramel/brown body. At first glance *Viridiscus* and the new species complex may be mistaken for each other, as both of them lack trunk appendages and share dark cuticular pigmentation. However, a closer inspection of the dorsal cuticular sculpture and molecular phylogenetic analyses indicate that the new complex belongs within the *Echiniscus spinulosus* morphogroup, which exhibits typical orange pigmentation. An ultra violet microscopy (UVM) analysis revealed that the cuticular green colouration in *Viridiscus* and brown in the new species complex absorbs UV light, which suggests an adaptive character of the dark pigmentation in both lineages. Thus, the presence of UV-absorbing dark pigments in two indirectly related lineages is evidence for the convergence of dark cuticular colouration in limno-terrestrial heterotardigrades. This study, by exposing cases of species crypsis, also provides a clear case of the critical role of DNA barcoding in an accurate estimation of tardigrade species richness.

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## **P84: RELEVANCE AND PHYLOGENETIC POSITION OF THE GENUS MILNESIOIDES CLAXTON, 1999 (TARDIGRADA)**

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Even though relationships between the major tardigrade lineages seem to be solved, there are still a number of rare, very often morphologically unique, groups of which the phyletic position is unknown and pivotal for our understanding of tardigrade evolution. One of the two eutardigrade orders, the order Apochela comprises four genera: Milnesium, Limmenius, Milnesioides, and Bergtrollus. Whereas Milnesium is found throughout the globe and there are ample genetic data for many of its numerous species, the remaining apochelan genera are monotypic, have very limited geographic ranges and have never been sequenced, so their phyletic positions are uncertain. Moreover, the recent discovery of a new African Milnesium species, characterised by an elongated head with a “snout” and a very long buccal tube, challenged the validity of Milnesioides. A discovery of two populations of Milnesioides from Western Australia offers a unique opportunity to pinpoint the phyletic position and test the validity of the mysterious genus. We sequenced several genetic markers (18S and 28S rRNA, ITS-2 and COI) and imaged the newly found populations in light microscopy, and compared them with the published Milnesium dataset, including the African long-tubed Milnesium. Our Bayesian inference phylogeny showed, with high support, that Milnesioides is a sister lineage to all remaining Milnesium species, supporting the validity of both genera. Moreover, our data strongly suggest the presence of more than one Milnesioides species.

## **P85: TARDIGRADE AUGEAN STABLES – A CHALLENGING PHYLOGENY AND TAXONOMY OF THE FAMILY RAMAZZOTTIIDAE (EUTARDIGRADA)**

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Tardigrades, commonly known as water bears, are a diverse group of microscopic invertebrates. Taxonomy of these ubiquitous tiny animals is often perplexing due to imprecise species description, scarcity of genetic data, and undersampling. The cosmopolitan family Ramazzottiidae, encompassing misidentified model species used in biomedical and astrobiological research, is no exception in this regard. In this study, we carried out the most extensive phylogenetic analysis of this family to date, with new molecular data obtained from poorly sampled regions. Based on the integrative taxonomy approach, we have delineated two new species complexes, one Neotropical and the other – Afro-Oriental. The taxonomic status of the two lineages, however, could not be strictly defined due to both inaccurate and/or outdated species descriptions which do not sufficiently address intra- and inter-specific variation and due to extremely scarce currently available genetic data associated with morphotype. Our results also strongly suggest that a recently erected ramazzottiid genus, Cryoconicus, which exhibits unique phenotypic adaptations to glacier habitats, is invalid, as it breaks the monophyly of Ramazzottius. This example of anacladogenesis is cautionary in terms of erecting new genera with limited genetic data. In addition to identifying the issues with ramazzottiid phylogeny and systematics, we also suggest solutions that could elucidate the current understating of the evolution of the family.

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## **P86: PHYLOGEOGRAPHY AND MORPHOLOGICAL EVOLUTION OF THE GENUS BARBARIA (HETEROTARDIGRADA)**

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Tardigrades, also known as “water bears”, are an understudied phylum of micrometazoans, especially outside the Palaearctic (where most tardigradologists are based). Here, we have analysed the evolutionary history of a recently erected genus *Barbaria*, an emblematic tardigrade group for the South American fauna. The phylogenetic relationships in the genus have so far been completely unknown, but the discovery of two new species (*B. paucigranulata*, *B. weglarskae*), together with new genetic data (18S, 28S rRNA, ITS-1, ITS-2 and COI) for further six species, not only allowed for a greater understanding of the differences between species, but also for reconstructing morphological evolution in *Barbaria*, thanks to which we were able to formulate several hypotheses of the evolution of taxonomically significant characters in this lineage. We concluded that the genus is most likely limited to the Neotropics, Antarctica and southern parts of the Nearctic, and that alleged records of *Barbaria* spp. from other parts of the world are invalid. The ancestral state reconstruction analysis revealed that last common ancestor of the genus probably exhibited well-developed dorsal pillars and pores, making the *B. bigranulata*, the type species for the genus, the closest extant morphotype to the reconstructed ancestral state. Interestingly, the ancestor of *Barbaria* exhibited also weakly sculptured pedal plates on legs I–III, i.e. with endocuticular pillars and pseudopores, a character that has only recently been recognised as taxonomically informative. The findings are discussed in the context of the phylogeny of the *Echiniscus* evolutionary line.

## **P87: PATTERNS OF EVOLUTION WITHIN TARDIGRADA (ECDYSOZOA: PANARTHROPODA) UNVEILED BY TIME-CALIBRATED MULTILOCUS PHYLOGENY**

**Alejandro López López<sup>1</sup>, Piotr Gąsiorek<sup>1</sup>, Witold Morek<sup>1</sup>, Pritam Kumar Dey<sup>1</sup>, Łukasz Michalczyk<sup>1</sup>**

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Tardigrades, also known as “water bears” or “moss piglets”, most known due to their outstanding capabilities for withstand extreme environmental conditions, constitute a micrometazoan phylum with a global distribution, both in marine and terrestrial habitats. While numerous studies have explored the phylogenetic relationships within specific groups of tardigrades, only a few works have addressed the systematics and evolution of the phylum, albeit using incomplete or flawed matrices or unreliable methods and models.

In this work, we carry out a phylogenetic analysis of the phylum Tardigrada using a carefully assembled matrix composed of five nuclear and mitochondrial DNA fragments, including all groups of tardigrades for which reliable molecular data is available. Our analysis reconstructs the timeline of major events of morphological and ecological evolution of tardigrades, showing how the acquisition of new characters or shifts in their lifestyles can be correlated to major events in the history of Earth. Our phylogenetic tree sheds a new light on the evolution of these organisms and will serve as an essential framework for future studies.

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## **P88: PERSONALITY AND PARASITES: LINKS BETWEEN OPEN FIELD ACTIVITY, SPACE USE, AND PARASITE LOADS IN YELLOW-NECKED MICE (APODEMUS FLAVICOLLIS)**

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Inter-individual differences in behavior, known as animal personalities, are hypothesized to affect host-parasite interactions. Researchers have been attributing higher prevalence and infestation intensity to higher activity measured in the experimental arena, under the assumption that the test results reflect animal activity in its natural habitat and, consequently, higher risk of parasitism. To investigate this subject, we conducted live-trapping, repeated behavioral tests, and parasite collection in a wild population of *Apodemus flavicollis*. We found that BLUPs (Best Linear Unbiased Predictors) derived from a measure of activity during the open-field tests were not associated with parasite loads. However, open field activity was linked with space use parameters: higher BLUPs were associated with increased trap diversity, trappability, and larger home range sizes. Furthermore, the indices of space use were positively associated with flea, but not tick, mite, or helminth burdens. In conclusion, while behavioral characteristics do seem to influence an animal's use of space and therefore, potentially, its exposure to certain types of parasites, these factors do not directly translate into greater parasite loads. Our findings challenge previous assumptions that higher activity levels, as measured in experimental arenas, are indicative of higher parasitic infestations.

## **P89: AROLLA PINE (PINUS CEMBRA L.) AND GRANIVOROUS RODENTS: DO THEY PLAY BY THE NUMBERS?**

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Foraging decisions of rodents are dependent on their abundances and seed availability. Lower seed:rodent ratio usually results in higher predation and pilferage rates while higher seed:rodent ratio usually promotes caching, thus, seed dispersal. Consequently, plant-granivorous rodent interactions cannot be categorized as simply mutualistic or antagonistic, but are located at some point along a mutualism–antagonism continuum that shifts with ecological conditions. Climate change can indirectly affect tree recruitment by shifting distribution of granivores, altering patterns of seed fate. Our research objective is to elucidate the role of granivorous rodents in Arolla pine (*Pinus cembra*) recruitment in montane ecosystems and to provide an experimental evaluation how this role changes along an elevation gradient and along with fluctuating seed production.

We combined comprehensive experiments conducted in the field. In addition, we monitored seed crop and natural regeneration of Arolla pine as well as measured abundance and diversity of rodents. The project is still ongoing and we will present the data obtained during three field seasons. At this point, we revealed that changes in rodent abundances strongly correspond with fluctuations in tree seed production. In turn, this has a crucial effect on the fate of pine seeds, although it is altitude-dependent.

Our research will help to reveal how complex plant-animal interactions respond to a potential increase in temperature with climate change, and contribute to a deeper understanding of the causes and consequences of mechanisms participating in distributional shifts. This understanding is crucial if we want to predict the environmental impacts of climate change.

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## **P90: RECONSTRUCTING SPECIES DISTRIBUTION AND INTRA-SPECIES DIVERSITY OF SWEDISH AUCHENORRHYNCHA BASED ON MALAISE TRAP SAMPLING**

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Insects remain an understudied group despite their diverse and critical roles in terrestrial ecosystems. Our understanding of the diversity and distribution of species, the intra-species genetic diversity, and their importance in response and adaptation to rapid environmental changes of the Anthropocene era, are very incomplete. Malaise traps have proved to be an effective sampling method for biodiversity assessment, capturing a relatively unbiased sample from several insect clades, including the hemipteran suborder Auchenorrhyncha, comprising several economically significant species. Here, we ask how effective Malaise traps capture the geographical distribution of species and intra-species diversity of Swedish Auchenorrhyncha.

Through individual barcoding of over 1000 Auchenorrhyncha specimens extracted from Malaise traps from across Sweden, we find that only a relatively small proportion of an estimated 420 spp. is represented in the collection. The collection is dominated by a few species known to be abundant across Sweden, mostly representing the family Cicadellidae, with long-winged species particularly common. We also find distinct spatial and temporal patterns in the diversity and distribution of species. Within several species sampled from across different geographic areas, we observe diversity within the COI gene sequence, suggestive of limited dispersal rates and different evolutionary histories. Furthermore, in several cases, COI data indicate infections with heritable facultative endosymbiont Wolbachia, with substantial variation in genotype associations and prevalence across species and populations.

Combined, the data show that Malaise trap sampling and individual-specimen barcoding can be an effective strategy for monitoring specific target groups of Swedish Auchenorrhyncha but not necessarily the total diversity.

## **P91: GENOMIC CONSEQUENCES OF ARTIFICIAL TRANSLOCATION, ADMIXTURE AND POPULATION REPLACEMENT IN THE TRINIDADIAN GUPPIES**

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Gene flow between recently diverged populations can homogenize genomes and reverse changes accumulated during early stages of speciation. Human activities, including translocations between previously isolated populations, increase the rates of such processes, potentially threatening biodiversity and local adaptation. On the other hand, admixed populations can benefit from receiving genetic variants that are adaptive. To explore the relative importance of negative and positive effects, we investigated the genomic consequences of a recent translocation of guppies (*Poecilia reticulata*) between two river drainages in Trinidad. Since a translocation event in 1957, introduced guppies spread down the river, replacing phenotypically similar populations. We sequenced around 200 individuals to explore how genetic variation is affected by admixture and recombination to create geographic and genomic landscape patterns. Our results confirmed mitochondrial sequence divergence between the drainages ( $d_{xy} = 0.03$ ). Nuclear divergence is smaller (average  $d_{xy} = 0.008$ ), and strongly correlates with recombination rate and within population nucleotide diversity. The results give clear evidence that invaders mixed with local populations. Indeed, despite a severe bottleneck, translocated genetic material now dominates the recipient river, and

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only a small fraction of contemporary genomes likely originate wholly from native populations. Genotypes originating from translocated individuals were identified within several rivers of the same drainage, suggesting that these populations may widely become replaced by alien genetic material. Thus, in this system, without strong barriers to gene flow, locally adapted genotypes were not preserved.

### **P92: ESTIMATING GENETIC LOAD IN NATURAL POPULATIONS OF GUPPIES (*POECILIA RETICULATA*)**

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Genetic load (GL) is a relative measure of average population genotype fitness while compared to the optimal fitness. Since high load is often observed in small, declining populations, GL is of high importance in conservation biology, especially in genetic rescue efforts. Apart from population size, there are other demographic factors that may affect GL and how certain processes influence accumulation of deleterious (harmful) mutations is still not completely clear. It has been reported that population expansion may be followed by an increase in GL, especially at the expansion front, where the population is sparse. However, there are studies which state otherwise – due to increased selection strength during expansion, GL should be decreased. In our analysis we strive to shed some light onto processes accompanying population expansion in 210 guppy samples across 20 natural populations. Guppy genomes were mapped to reference (15x mean coverage) and polymorphic sites were phased using ancestral sequence. We are now screening the genomes for deleterious variation using GL measures like “conservation score”, level of mutation deleteriousness and ratio of non-synonymous to synonymous polymorphisms. Our next step will be comparing populations from different sites while considering their previously reported demographic history. We plan to focus on one river in particular - Turure in Trinidad, where fish were introduced 70 years ago and where expansion continues to this day. In summary, in this ongoing project, we aim to find how different demographic processes, including expansion and gene-flow affects GL accumulation.

### **P93: CRYPTIC DIVERSITY IN *PERFORATELLA* AND *EUOMPHALIA* SNAILS**

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In recent years, molecular studies have uncovered vast amounts of previously unknown cryptic diversity. Cryptic species are impossible to identify based only on morphology. As they only differ molecularly, even detailed morphological studies show no differences between them. Two other types of cryptic taxa are also distinguished: semicryptic species and pseudocryptic species. Semicryptic species cannot be identified solely on the basis of morphology, but can be identified based on their geographical origin or population characteristics. Pseudocryptic species are highly similar, but can be identified by detailed morphological studies, after detecting their molecular distinctness. One of the methods of identification of cryptic species is DNA barcoding. This simple method, even despite its limitations, may be the first step to recognizing new, unknown species as well as determining the scale and the geographic patterns of cryptic diversity. The existence of cryptic diversity applies not only to obscure, rare species, but also to well-known, relatively large species, such as *Fruticicola* snails. An increasing number of studies have shown that there is a large amount of unknown cryptic diversity in other land snails. Some examples have been detected in *Perforatella* and *Euomphalia*. Both of these genera come from the family Hygromiidae and live in wooded areas in Central Europe. Even simple DNA barcoding showed the possibility of cryptic species detection for these taxa. The study of cryptic diversity is also important for biodiversity protection. As it is not possible to protect the species that are unknown, any research on this topic is extremely valuable.

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## P94: ACETAMIPRID – EFFECTS ON LIFE HISTORY AND BEHAVIOR OF ANTLIONS

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Acetamiprid is a widely used and cheap insecticide, effective across a wide range of crops and ornamental plants. Its main targets are sucking and biting insects and their larvae. Its non-selective neurotoxic mode of action as neonicotinoid poses a risk to all animals within its range of application. Contaminated runoff can carry the toxin even beyond the immediate area potentially affecting a wide range of non-target species. Antlion larvae are widespread representatives of ground-dwelling insects that not only do not interact with target plants but also cannot escape from the affected area. Surprisingly, no research has been done on the effects of acetamiprid on this family of insects. This study aims at testing for the effects of neonicotinoids on life history of *Myrmeleon formicarius*, common in Europe and North America. We studied immediate (within few hours), medium-term (within days), and long-term effects (within months) on 4th-instar larvae in response to exposure to a neonicotinoid. Therefore, we exposed one group of antlions to a manufacturer-recommended dose of Mospilan 20SP (20% acetamiprid product) through contact application, while a control group was exposed to water droplet; and quantified different behaviors, oxidative stress biomarkers (catalase, superoxidase dismutase, and thiobarbituric acid reactive substances), growth rates and survival. Preliminary results show negative effects of neonicotinoid exposure on building time and frequency of sand pits, and hunting success, and growth rate. This research will provide insight into the effects of acetamiprid exposure on life-history traits and its potential consequences in the adaptation of non-target species.

## P95: ORIGIN AND DEMOGRAPHIC HISTORY OF THE GOLDEN JACKAL (*CANIS AUREUS*)

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Ongoing rapid climate change impacts species and ecosystems, causing range shifts, extinctions, habitat loss, and the spread of invasive species. The expanding range of the golden jackal raises concerns for

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ecosystems due to uncertain effects on species interactions and pathogen transmission. Golden jackals are currently found in Europe and southern parts of Asia. Since the 1960s, jackals have been expanding from the limited coastal regions of the Mediterranean and Black Seas and rapidly reached Northern and Western Europe. Genetic studies confirm their historical northwestern expansion from Southern Europe and Caucasus, with low to moderate genetic variability in populations occurring on the continent. Dalmatian and Greek populations exhibit distinct genetic traits, potentially representing relic populations.

The evolutionary history, origin, and expansion patterns of jackals are not yet fully understood and only a few whole genomes of the species have been sequenced to date. At the present study we sequenced the whole genomes of 14 individuals from Asia and Europe with an average coverage of 37X to determine the origin, investigate phylogenetic relationships and demographic history of the species.

Preliminary analyses showed that the golden jackal experienced population increase in the Middle Pleistocene, followed by population decline during the Last Glacial Period, indicating that species dynamics was driven by climate changes. Analysis of runs of homozygosity (ROHs) showed the pattern of lowest number of ROHs in jackals from the eastern range (India, Middle East) and highest in the western range (Balkans), consistent with westward expansion and a long-term stable population in Asia.

### **P96: DEVELOPMENTAL DISORDER AND MORTALITY CAUSED BY HYBRIDISATION AND POLYPLOIDIZATION IN AN ASEXUAL FISH COMPLEX OF COBITIS GENERA.**

**Daniel Kulik<sup>1</sup>, Grzegorz Jan Skórzewski<sup>1</sup>, Karel Janko<sup>2</sup>, Dmitry Dedukh<sup>2</sup>, Anatolie Marta<sup>2</sup>, Jan Kotusz<sup>1</sup>**

<sup>1</sup> Museum of Natural History, University of Wrocław, Poland

<sup>2</sup> Laboratory of non-Mendelian Evolution, Institute of Animal Physiology and Genetics CAS, Czech Republic

One of the mechanisms responsible for increase in diversity of vertebrate species is speciation by hybridization. Spontaneous interspecific interbreeding has been observed in the reproduction of fish of the genus *Cobitis*, resulting in mixed offspring with a diploid number of chromosomes. These hybrids are capable of reproduction, only by gynogenesis; when the genetic material of the sperm is incorporated into the nucleus of the egg cell, individuals with a triploid genome are produced. A similar process occurs in triploid individuals. Moreover, these fish, together with their parental species, form balanced diploid-polyploid hybrid complexes. We examined the effects of hybridization and polyploidization on mortality, and appearance of developmental defects in *Cobitis* fish. Observations of larval development were carried out from 1 to 29 days after hatching, at 5-time intervals. Live larvae were randomly collected at 2-day intervals, while dead larvae were collected daily to document their developmental status, along with a description of visible developmental defects. The mortality rate of polyploid individuals (3n and 4n) was higher than that of diploids. There were no differences, in terms of defect frequency, between different ploidies and age classes of hybrid groups with various genotypic compositions (Biotypes). The harmfulness index calculated based on observed developmental defects was significantly higher in dead individuals in each age class (PERMANOVA). Statistically significant differences in harmfulness index values were also found between individual biotypes. However, no differences were noted between individual ploidies. The research depicted the selection against particular biotypes of *Cobitis* larvae in different age classes.

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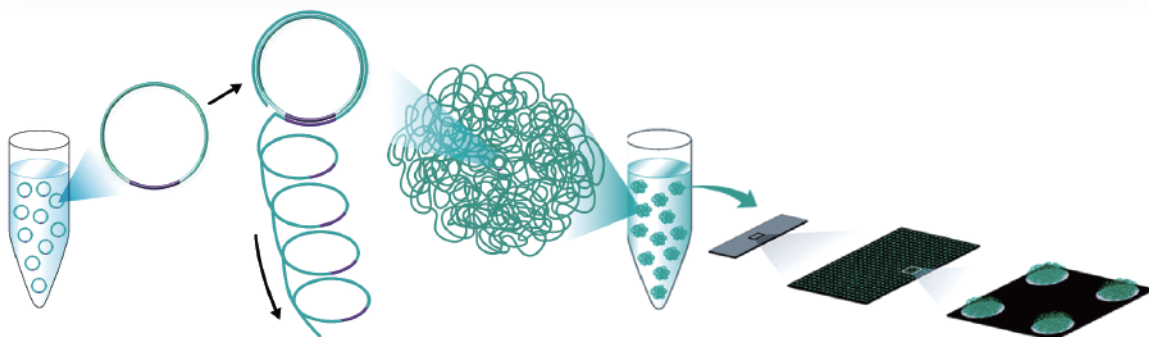
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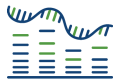
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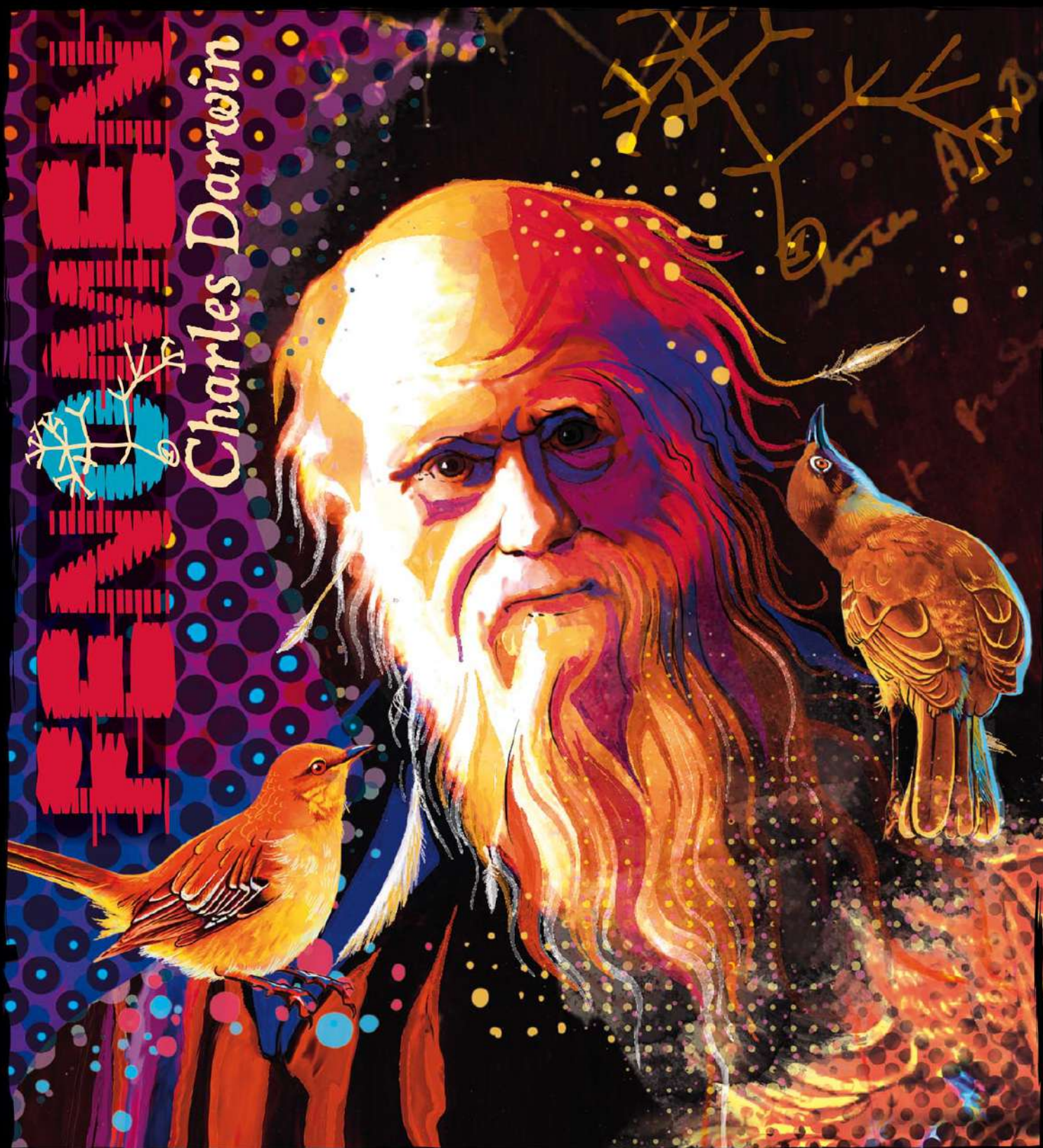
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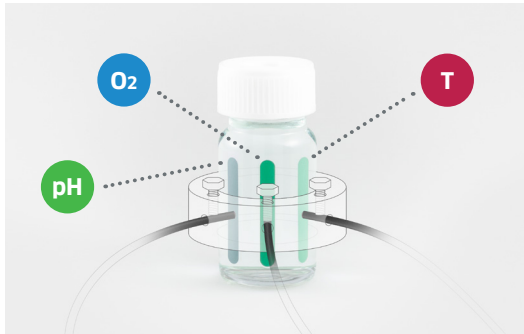


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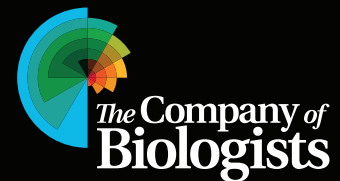


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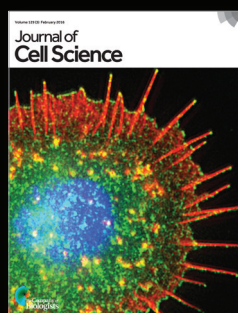
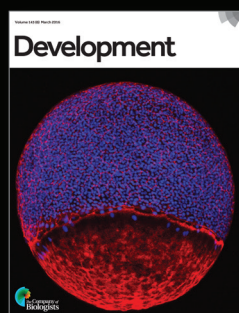
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