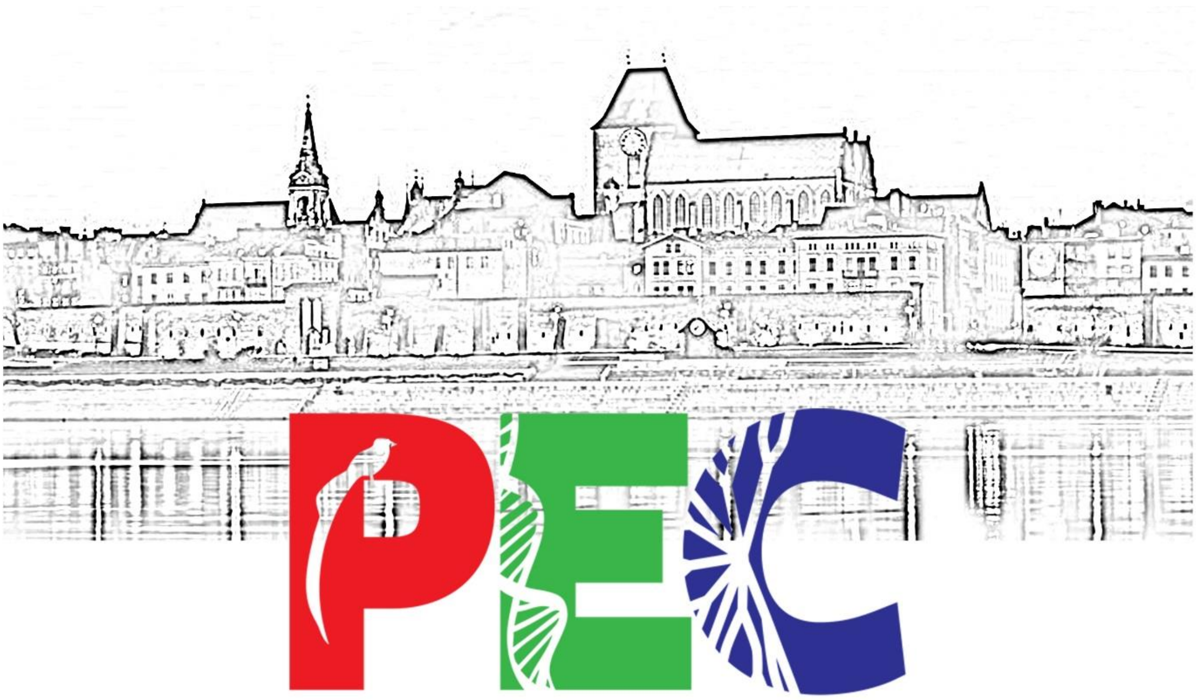

The 8th POLISH EVOLUTIONARY CONFERENCE

19 - 21 SEPTEMBER 2022
TORUŃ, POLAND

PROGRAM AND ABSTRACT BOOK

NICOLAUS COPERNICUS UNIVERSITY IN TORUŃ
Faculty of Biological and Veterinary Sciences

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POLISH ACADEMY of SCIENCES

FUNDACJA AKADEMIA BIOLOGII I OCHRONY ŚRODOWISKA

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The author of PEC logo is Szymon Drobniak

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Abstracts are arranged in alphabetical order according to the presenting author.

Presenting authors are indicated in bold font.

PROGRAM

8th Polish Evolutionary Conference

19-21 September 2022

19 September (Monday)

12:00 - 15:00	Registration
15:00 – 15:15	Opening of the conference

Plenary lecture I	Chair: *Rafał Zwolak*
15:15 – 16:15	***Elizabeth Crone***: How do host plants limit butterflies in highly fragmented landscapes?

Session 1	Chair: *Krzysztof Kowalski*
16:15 – 16:35	***Martyna Wirowska***: Successful finding of ephemeral food resources is associated with proactive personality in wild tree-dwelling rodent – edible dormouse
16:35 – 16:55	***Rafał Zwolak***: Ectoparasites do not affect seed dispersal behavior of their rodent hosts
16:55 – 17:15	***Aleksandra Wróbel***: The role of granivorous rodents in montane tree recruitment: climate change scenario
17:15 – 17:35	***Gema Trigos Peral***: Effect of urbanization on life history traits of the common garden ant *Lasius niger*
17:35 – 17:55	***Krzysztof Deoniziak***: Plastic not so fantastic: microplastic ingestion by Common Blackbirds and Song Thrushes
17:55 – 18:15	***Sabina Nowak***: Mortality of wolves *Canis lupus* in human-dominated landscapes of Poland

20 September (Tuesday)

8:00 – 8:30	Registration

Plenary lecture II	Chair: *Michał Ronikier*
8:30 – 9:30	***Christian Brochmann***: Recent and rapid speciation at the extremes: from the Arctic to tropical alpine Africa

Session 2	Chair: *Krystyna Nadachowska-Brzyska*
9:30 – 9:50	***Wiesław Babik***: Coevolution between MHC Class I and Antigen-Processing Genes in salamanders

9:50 – 10:10	***Tomasz Gaczorek***: Adaptive introgression of MHC genes in Podarcis lizards and Triturus newts
10:10 – 10:30	***Jacek Radwan***: Long term patterns of association between MHC and helminth burdens in the bank vole support Red Queen dynamics

10:30 – 11:00 Coffee break

Session 3	Chair: *Aneta Książek*
11:00 – 11:20	***Maciej Ejsmond***: Adaptive immune response selects for increased body size
11:20 – 11:40	***Antoni Żygadło***: Between big and small – how conditions of Temperature-Size Rule performance dictate optimal body size, the case of Lecane inermis (Rotifera, Monogononta)
11:40 – 12:00	***Sebastain Chmielewski***: Genomic evidence that a sexually selected trait captures genome-wide variation and facilitates the purging of genetic load
12:00 – 12:20	***Junchen Deng***: Genome comparison reveals inversions and alternative evolutionary history of nutritional endosymbionts in planthoppers (Hemiptera: Fulgoromorpha)
12:20 – 12:40	***Piotr Zieliński***: Inferring species demographic history using inversion rich genomes: the case of the spruce bark beetle
12:40 – 13:00	***Markéta Harazim***: Natural selection in Cetacean immunogenome, and its relation to morbillivirus infection susceptibility

13:00 – 14:00 Lunch break

Plenary lecture III	Chair: *Werner Ulrich*
14:00 – 15:00	***Spyros Sfenthourakis***: Darwin in the eastern Mediterranean islands: a science fiction story

Session 4	Chair: *Magdalena Witek*
15:00 – 15:20	***Dominika Wloch-Salamon***: Transition to quiescence as an eco-evolutionary process creating diversity within yeast population
15:20 – 15:40	***Monika Opalek***: How can phenotypic heterogeneity be advantageous in starvation? Studying quiescence in *Saccharomyces cerevisiae* yeast populations
15:40 – 16:00	***Bogna Smug***: Lag phase length as a determinant of microbial fitness. The overview of approaches and a new online tool.

16:00 – 18:30	**Poster session**

21 September (Wenesday)

8:00 – 8:30	Registration

Plenary lecture IV	Chair: *Wiesław Babik*
8:30 – 9:30	***Nicholas Barton***: Genetic analysis of a flower colour hybrid zone in snapdragons

Session 5	Chair: *Andrzej Grzywacz*
9:30 – 9:50	***Katarzyna Malinowska***: Making virtual species less virtual by reverse engineering spatiotemporal ecological models
9:50 – 10:10	***Werner Ulrich***: Identifying the drivers of trait change: Does Price partitioning work?
10:10 – 10:30	***Bogdan Jaroszewicz***: National parks enhance wealth of the surrounding municipalities

10:30 – 11:00 Coffee break

Session 6	Chair: *Edyta Sadowska*
11:00 – 11:20	***Sylwia Buczyńska***: Daily energy expenditures in reproducing laboratory mice selected for high and low basal metabolism rate (BMR)
11:20 – 11:40	***Piotr Minias***: Trade-offs in the evolution of the avian immune system
11:40 – 12:00	***Alaa Hseiky***: Testing the thrifty and spendthrift genotype hypotheses: A pilot study on the adverse effects of Western Diet in bank voles
12:00 – 12:20	***Ireneusz Ruczyński***: From energy constrains to sociality in male bats
12:20 – 12:40	***Viktor Kovalov***: Songbirds adjust oxygen carrying capacity through modulation of the number rather than the size of erythrocytes
12:40 – 13:00	***Marta Grosiak***: Can heat dissipation limit (HDL) theory explain reproductive ageing?

13:00 – 14:00 Lunch break

Session 7	Chair: *Robert Mysłajek*
14:00 – 14:20	***Małgorzata Lipowska***: Testing the hologenome concept: a nature vs nurture experiment on bank voles from a selection experiment
14:20 – 14:40	***Agata Plesnar-Bielak***: Physiological and molecular mechanisms of variation in male reproductive success - a case of 6Pgdh gene
14:40 – 15:00	***Małgorzata Pilot***: Implications of hybridization between wolves and dogs for the evolution of behavioural traits

15:00 – 15:20	***Daniel Sánchez García***: Short-time evolution in the morphology of the myrmecophilous *Maculinea teleius* butterfly
15:20 – 15:40	***Maciej Szewczyk***: Analysis of genetic structure and diversity of grey wolf (*Canis lupus*) paternal lineages in central and eastern Europe – preliminary results
15:40 – 16:00	***Joanna Palka***: Repeatability crisis in evolutionary biology – lessons from experimental evolution programme on *C. elegans*

16:00 – 16:15 Closing of the conference

PLENARY LECTURES

Genetic analysis of a flower colour hybrid zone in snapdragons

Barton Nicholas H., Surendranadh S. and S. Stankowski S.
The Institute of Science and Technology, Austria

The snapdragon Antirrhinum majus includes subspecies that differ in flower colour. In joint work with David Field (Univ. of Vienna) and Enrico Coen (John Innes Institute, Norwich), we have made an intensive study of a narrow hybrid zone that separates yellow and magenta flowers. Pooled sequence data shows that selection likely acts on just a few genes involved with flower colour, and prevents gene flow only across a very small region of genome. Sharp clines at flower colour loci allow us to estimate selection and gene flow, whilst a pedigree gives us direct estimates of dispersal and fitness. This study shows how a variety of techniques can be combined to understand a striking natural phenomenon.

Recent and rapid speciation at the extremes: from the Arctic to tropical alpine Africa

Brochmann Christian
Natural History Museum, University of Oslo, Norway

New evidence suggests that extreme environments such as the Arctic and high-alpine Africa excel in terms of high speciation rates as well as high extinction rates. Only few plant species - as recognized taxonomically - can tolerate the harsh conditions in these areas. In contrast to the Arctic flora, which is well known to be young and virtually devoid of endemic taxa, the afroalpine flora is famous for its high endemism (~70%) and spectacular giant rosette plants, and believed to be much older. However, our recent analyses of dated phylogenies of 20% of the afroalpine flora show that species accumulation is accelerating towards the present. Taken together with reports of extremely low within-population genetic diversity and recent intermountain population divergence, this suggests that the afroalpine flora is young, disturbed and unsaturated, shaped by cycles of colonization, speciation, and extinction during the Pleistocene (PNAS 2022 https://doi.org/10.1073/pnas.2112737119; Alpine Botany 2022 https://doi.org/10.1007/s00035-021-00256-9). In the Arctic, where the flora contains little endemism in terms of morphologically recognized taxa, there is increasing evidence for surprisingly high endemism in terms of reproductively isolated but morphologically cryptic species. Postzygotic reproductive isolation has developed multiple times within taxonomic species belonging to several distant lineages, and this may have happened over just a few millennia (e.g. PNAS 2006 https://doi.org/10.1073%2Fpnas.0510270103; Ann. Bot. 2021 https://doi.org/10.1093/aob/mcab128). We currently address whether the high speciation rates in Arctic and afroalpine plants, and thus most likely high extinction rates, are driven by bottlenecking during the Pleistocene glacial cycles and/or by selfing mating systems.

How do host plants limit butterflies in highly fragmented landscapes?

Crone Elizabeth
University of California, Davis CA USA

Insect herbivores can be limited by host plants in two ways: density-dependent competition for food resources or density independent search time limitation. Our understanding of density-dependent host plant limitation is relatively well developed and well integrated into conservation plans for at-risk insects. Search time limitation, a density-independent process, is much less well developed. Here, I explore both mechanisms using empirically based models of butterfly population dynamics. These mechanisms differ fundamentally in their predictions: resource competition leads to matching of herbivore densities to host plant densities, and visible competition via consumption of host plants. Search time limitation leads to changes in population growth rate that can cause herbivore numbers to decline when host plant densities are constant. Search time limitation also implies that host plants can limit herbivores, even when many individual plants are uneaten. To make these models concrete, I discuss the implications of search time limitation for restoring monarch butterflies in North America, and for integrating butterfly habitat into human dominated landscapes.

Darwin in the eastern Mediterranean islands: a science fiction story

Sfenthourakis Spyros
Department of Biological Sciences, University of Cyprus, 1 Panepistimiou Ave., 2109 Aglantzia, Lefkosia, Cyprus

What if Darwin had visited the islands of the eastern Mediterranean islands instead of the Galapagos? Would he have arrived to the same ideas regarding natural selection? This imaginary scenario can spark explorations that lead to a better understanding of eco-evolutionary processes that lead to community assembly in insular ecosystems in the cases of continental islands that are usually much more complex than oceanic in both history and structure. What patterns can we see in the divergence among species and populations of the eastern Mediterranean archipelagos, such as the Aegean meta-archipelago? Can we see something similar to the well-known Galapagos tortoise case or is it much more difficult to identify consistent examples of gradual, small-scale differentiation among neighboring insular populations? Is natural selection the main driver of divergence among such insular lineages or do we see other evolutionary processes taking the lead? In this talk, I'll discuss examples of evolutionary diversification among insular lineages of various taxa, focusing on the Aegean archipelagos but including also other eastern Mediterranean islands, that reveal a complex mix of patterns and processes. Of special interest are the cases of apparent non-adaptive radiations and of cryptic lineage divergence, as well as the complex responses to paleogeographic, paleoecological, and historical events, all of which make a puzzle that might have fettered understanding of basic evolutionary mechanisms before the development of modern evolutionary synthesis. On the other hand, these cases show that the eco-evolutionary dynamics in these mostly, but not exclusively, continental archipelagos make them an all-important model system for a comprehensive study of biodiversity patterns and processes, an essential complement of the much celebrated studies in the various types of oceanic archipelagos.

CONTRIBUTED TALKS

Coevolution between MHC Class I and Antigen-Processing Genes in salamanders

Palomar G.[1], Dudek K.[1], Migalska M.[1], Arntzen J.W.[2,3], Ficetola G.F.[4,5], Jelić D.[6], Jockusch E.[7], Martinez-Solano I.[8], Matsunami M.[9], Shaffer H.B.[10,11], Voros J.[12], Waldman B.[13,14], Wielstra B.[2,3] and **Babik W.**[1]

1. Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Kraków, Poland; 2. Naturalis Biodiversity Center, Leiden, The Netherlands; 3. Institute of Biology, Leiden University, Leiden, The Netherlands; 4. Department of Environmental Sciences and Policy, University of Milan, Milan, Italy; 5. Laboratoire d'Ecologie Alpine (LECA), CNRS, Universite Grenoble Alpes and Universite Savoie Mont Blanc, Grenoble, France; 6. Croatian Institute for Biodiversity, Zagreb, Croatia; 7. Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT, USA; 8. Museo Nacional de Ciencias Naturales (MNCN), Consejo Superior de Investigaciones Cientificas (CSIC), Madrid, Spain; 9. Department of Advanced Genomic and Laboratory Medicine, Graduate School of Medicine, University of the Ryukyus, Nishihara-cho, Japan; 10. Department of Ecology and Evolutionary Biology, University of California, Los Angeles, Los Angeles, CA, USA; 11. La Kretz Center for California Conservation Science, Institute of the Environment and Sustainability, University of California, Los Angeles, Los Angeles, CA, USA; 12. Department of Zoology, Hungarian Natural History Museum, Budapest, Hungary; 13. Department of Integrative Biology, Oklahoma State University, Stillwater, OK, USA; 14. School of Biological Sciences, Seoul National University, Seoul, South Korea

Proteins encoded by antigen-processing genes (APGs) provide major histocompatibility complex (MHC) class I (MHC-I) with antigenic peptides. In mammals, polymorphic multigenic MHC-I family is served by monomorphic APGs, whereas in certain nonmammalian species both MHC-I and APGs are polymorphic and coevolve within stable haplotypes. Coevolution was suggested as an ancestral gnathostome feature, presumably enabling only a single highly expressed classical MHC-I gene. In this view coevolution, while optimizing some aspects of adaptive immunity, would also limit its flexibility by preventing the expansion of classical MHC-I into a multigene family. However, some nonmammalian taxa, such as salamanders, have multiple highly expressed MHC-I genes, suggesting either that coevolution is relaxed or that it does not prevent the establishment of multigene MHC-I. To distinguish between these two alternatives, we use salamanders (30 species from 16 genera representing six families) to test, within a comparative framework, a major prediction of the coevolution hypothesis: the positive correlation between MHC-I and APG diversity. We found that MHC-I diversity explained both within-individual and species-wide diversity of two APGs, TAP1 and TAP2, supporting their coevolution with MHC-I, whereas no consistent effect was detected for the other three APGs (PSMB8, PSMB9, and TAPBP). Our results imply that although coevolution occurs in salamanders, it does not preclude the expansion of the MHC-I gene family. Contrary to the previous suggestions, nonmammalian vertebrates thus may be able to accommodate diverse selection pressures with flexibility granted by rapid expansion or contraction of the MHC-I family, while retaining the benefits of coevolution between MHC-I and TAPs.

Daily energy expenditures in reproducing laboratory mice selected for high and low basal metabolism rate (BMR)

S. Buczyńska[1], A. Książek[1], P. Brzęk[1], S. Maciak[1], M. Konarzewski[1] and J.R. Speakman[2, 3, 4]
1. University of Białystok, Faculty of Biology, Department of Evolutionary and Physiological Ecology, Ciołkowskiego 1J, 15-245, Białystok; 2. Shenzhen Key Laboratory of Metabolic Health, Center of Energy Metabolism and Reproduction, Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences, Shenzhen, China; 3. Institute of Biological and Environmental Sciences, University of Aberdeen, Aberdeen, UK 4. State Key Laboratory of Molecular Developmental Biology, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing, China

The heat dissipation limitation hypothesis (HDL) suggests that animals' energy budgets are limited by the ability to dissipate body heat to avoid detrimental overheating. To date, it has been exclusively tested under peak metabolic demands mostly in lactating mice, with a mixed results. To further test it, we compared the daily energy expenditures (DEE, measured with doubly labelled water, DLW) at peak lactation and the litter mass (being a proxy for the parental effort) in laboratory mice selected for divergence in basal metabolism rate (H-BMR and L-BMR line types) in two complementary experiments. We exposed the lactating dams with their litters to a high ambient temperature of 30°C (23°C as a control), then we manipulated their abilities to dissipate heat (with a fur shaving at the 1st experiment and burdened the dams with KLH injection in the 2nd study). In the 1st trial, at both temperatures the H-BMR mother mice had higher DEE than the L-BMR mice. Fur removal did not affect the DEE in both line types, even though shaved H-BMR mother mice raised bigger litters at 23°C. Contrary, in the 2nd experiment the effect of an immune challenge on DEE was significant. This result was additionally supported by the trade-off between the parental effort and an immune response in the H-BMR mice exposed to 23°C (which was not apparent in both line types exposed to 30°C). In both experiments, we observed a positive correlation between the litter mass and DEE only in the H-BMR mother mice at 23°C. We therefore demonstrated the temperature-dependent trade-off between the parental effort and an immune response at peak lactation. Moreover, our results showed that fur shaving is ineffective in testing the HDL predictions, at least in our animal model.

Genomic evidence that a sexually selected trait captures genome-wide variation and facilitates the purging of genetic load

Parrett J.M.[1], **Chmielewski S.**[1], Aydogdu E.[2], Łukasiewicz A.[1], Rombauts S.[2], Szubert-Kruszyńska A.[1], Babik W.[3], Konczal M.[1] and Radwan J.[1]
1. Evolutionary Biology Group, Adam Mickiewicz University; 2. VIB Center for Plant Systems Biology Department of Plant Biotechnology and Bioinformatics, Ghent University Bioinformatics Institute Ghent, Ghent University; 3. Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University

The evolution of costly traits like deer antlers and peacock trains, which drove the formation of Darwinian sexual selection theory, has been hypothesised to both reflect and affect patterns of genetic variance across the genome, but direct tests are missing. Here, we used an evolve and re-sequence approach to reveal patterns of genome-wide diversity associated with the expression of a sexually-selected weapon that is dimorphic among males of the bulb mite, *Rhizoglyphus robini*. Populations selected for the weapon showed reduced genome-wide diversity compared to populations selected against the weapon, particularly in terms of the number of segregating non-synonymous positions, indicating enhanced purifying selection. This increased purifying selection reduced inbreeding depression, but outbred female fitness did not improve, possibly because any benefits were offset by increased sexual antagonism. The majority of single nucleotide polymorphisms (SNPs) that consistently diverged in response to selection were initially rare and overrepresented in exons, and enriched in regions under balancing or relaxed selection, suggesting they are likely moderately deleterious variants. These diverged SNPs were scattered across the genome, further demonstrating that selection for or against the weapon and the associated changes to the mating system can both capture and influence genome-wide variation.

Genome comparison reveals inversions and alternative evolutionary history of nutritional endosymbionts in planthoppers (Hemiptera: Fulgoromorpha)

Junchen Deng[1], Diego C. Franco[1], Anna Michalik[2], Gordon M. Bennett[3], Monika Prus[1] and Piotr Łukasik[1]
1.Institute of Environmental Sciences, Faculty of Biology, Jagiellonian University, Gronostajowa 7, 30-387 Kraków, Poland; 2. Department of Developmental Biology and Morphology of Invertebrates, Institute of Zoology and Biomedical Research, Faculty of Biology, Jagiellonian University, Gronostajowa 9, 30-387 Kraków, Poland; 3. Department of Life and Environmental Sciences, University of California, Merced, Merced, California, USA

The ancient endosymbiont Sulcia and possibly a single betaproteobacterial companion have co-diversified with Auchenorrhyncha (Hemiptera: Suborder) for ~300 million years. The suborder split early into Cicadomorpha and Fulgoromorpha, along with the diversification of the betaproteobacterium into Nasuia/Zinderia and Vidania, respectively, in these two clades. The dominant nutritional role of Vidania over Sulcia and its lack of an alternative genetic code relative to Nasuia/Zinderia suggested a different symbiotic history in Fulgoromorpha (planthoppers). However, genomic studies of symbionts are scarce in planthoppers, hindering the further investigation of the symbiosis origin. Here, we characterized Sulcia and Vidania genomes from three Pyrops planthoppers (family Fulgoridae) and investigated their evolutionary history with comparative genomics tools. In Pyrops, Vidania plays a major nutritional role by providing seven out of ten essential amino acids, which has been also described in other planthopper species. The genome comparison of Sulcia lineages across Auchenorrhyncha superfamilies confirmed the conserved genome organization but identified multiple independent rearrangements, including one occurring in an early ancestor of either Cicadomorpha or Fulgoromorpha. In beta-symbionts, Nasuia, Zinderia, and Vidania showed perfect genome synteny within each of them but an almost lack of synteny between them, questioning their common origin. However, our latest beta-symbiont phylogeny still supports a monophyletic group of beta-symbionts. These results suggest an alternative evolutionary history as opposed to the conventional view of evolution in these highly reduced genomes.

Plastic not so fantastic: microplastic ingestion by Common Blackbirds and Song Thrushes

Deoniziak K.[1], Cichowska A.[1], Niedźwiedzki S.[2] and Pol W.[3]
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Plastic usually refers to a wide group of synthetic polymer-based materials, which can be easily processed and shaped using heat, and thanks to their properties, have been widely used in our daily lives since the 1950s. Unfortunately, currently produced plastics are not biodegradable in a reasonable timeframe under natural conditions. Rather, they undergo disintegration and degradation into microscopic plastic particles known as microplastics and nanoplastics, gradually accumulating in the environment. This has led to the recognition of microplastic pollution as one of the leading global conservation issues. Microplastics generate various physical and toxicological effects on wildlife, which have received significant scientific and conservation-based attention. However, most research to date has been conducted in aquatic environments, while terrestrial ecosystems are still underrepresented. In this study we investigated the potential of thrushes, a group of songbirds with an exceptionally terrestrial lifestyle and wide distribution range, to be used as a proxy of microplastic contamination in terrestrial ecosystems. Hence, we analysed the gastrointestinal tracts of Common Blackbirds (*Turdus merula*) and Song Thrushes (*Turdus philomelos*) in search of microplastics and assessed whether their contamination differed regarding the age of the birds and the time of year. We used birds that had died as a result of collision with anthropogenic surfaces, which were sampled during wildlife monitoring of anthropogenic infrastructures. We found that all the analysed individuals contained microplastics in their gastrointestinal tracts, mostly consisting of transparent fibers below 1mm in size. However, we found no seasonal or age-related differences in microplastic ingestion in either species. Slight discrepancies in microplastic ingestion observed between the studied species may be related to differences in their foraging strategies and habitat utilization. While our results show an ubiquity of microplastics in terrestrial environments, they also indicate that thrushes may be used as indicators of microplastic pollution in terrestrial ecosystems.

Adaptive immune response selects for increased body size

Ejsmond M.J.[1*], Radwan J.[2], Ejsmond A.[3,4], Gaczorek T.[1] and Babik W.[1]
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The emergence of adaptive immunity, which is pathogen-specific and enables immunological memory, is considered a major evolutionary innovation of vertebrates. Proteins of the Major Histocompatibility Complex (MHC) initiate the adaptive immune response by presenting pathogen-derived antigenic peptides to T cells. MHC genes are characterized by extraordinary polymorphism, the result of balancing selection driven by host-pathogen coevolution. However, the effect of these processes on the evolution of host life-histories remains unknown. Here, we model how host MHC–pathogen coevolution—and its concomitant impact on host mortality—can affect the evolution of host life-histories, as represented by body size at maturity. Life histories were compared in scenarios with and without adaptive immune response under equal mortality rates. We show that host-pathogen coevolutionary dynamics select for postponed maturation and increased body size; the Red Queen process generates linkage disequilibrium between immunocompetent MHC alleles and the maturation-postponing alleles of physically unlinked genes that determine body size at maturation. Particularly large body size was attained when pathogens mutated slowly, thus allowing the advantage of resistant MHC alleles to last over multiple generations. Our work suggests that the adaptive immune response, mediated by polymorphic MHC genes, may drive the evolution of host body size. This form of adaptive immunity may have thus predisposed vertebrates to evolve large body size and exhibit the macroevolutionary patterns of increasing body size over time that have been detected in comparative studies.

Adaptive introgression of MHC genes in Podarcis lizards and Triturus newts

Gaczorek, T.S.[1], Dudek, K.[1], Arntzen, J.W.[2], Caeiro-Diaz, G.[3], Chechetkin, M.[1], Crochet, P.A.[4], Marszałek, M.[1], Pinho, C.[3], Wielstra, B.[2] and Babik, W.[1]

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The Major Histocompatibility Complex (MHC) is the key component of adaptive immunity and contains the most polymorphic genes in the vertebrate genome. Its extraordinary diversity is driven mostly by host-pathogen coevolution with novel or rare alleles being favoured under Red Queen host-pathogen dynamics. Because novel MHC alleles may be easily acquired by introgression from related species, MHC introgression is likely to be adaptive, however, its extent and prevalence remain an open question. In this study, we tested for MHC introgression in six hybrid zones formed by six Triturus newt species and in six zones formed by seven species of Podarcis lizards. We sequenced and genotyped the variable second exons of the MHC class I and II genes and compared their interspecific similarity at various distances from the centres of the hybrid zones. We found evidence for introgression of both MHC classes in the most examined hybrid zones, with some support for a more substantial class I introgression. Furthermore, the overall MHC allele sharing outside the hybrid zones was elevated between pairs of Triturus species with abutting ranges, regardless of the phylogenetic distance between them. No effect of past hybrid zone movement on MHC allele sharing was found. Finally, using the available genome-wide data, we demonstrated that MHC introgression was more extensive than genome-wide introgression, suggesting its adaptive potential. Our study thus provides evidence for the prevalence of MHC introgression in multiple Triturus and Podarcis hybrid zones, pointing to adaptive MHC introgression between divergent hybridizing species as a widespread phenomenon.

Can heat dissipation limit (HDL) theory explain reproductive ageing?

Grosiak, M., Koteja, P. and Sadowska, E.T.
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It is well known that both reproductive performance and thermoregulatory capability of mammals decrease with age. The reproductive period of mammals is energetically demanding, especially during lactation. According to the heat dissipation limit theory (HDL), the capacity to dissipate heat limits the reproductive effort. The main aim of this study is to test a novel hypothesis that the age-related decline in reproductive performance is due to the age-related decrease of the capacity to dissipate heat. We also hypothesized that the limiting mechanism is more severe in animals with high rates of metabolism. The research is based on a model of experimental evolution, lines of bank voles (*Myodes glareolus*) selected for high swim-induced rate of aerobic metabolism (which have also increased basal and average daily metabolic rates) and unselected control lines. Measurements of peak-lactation reproductive and metabolic traits were performed on 350 adult females from three age classes: young (3.0 – 4.7 months), middle-aged (6.8 – 10.8 months) and old (13.8 – 22.8 months). Half of females were shaved to relieve them from the heat dissipation limitation. Old females had a decreased litter size, mass, and growth rate. Fur removal increased the peak-lactation food consumption and, only in females with large litters, also milk production. However, we did not find the age-related differences in these traits. The peak-lactation average daily metabolic rate (ADMR) was higher in shaved than in unshaved mothers, and this difference was more profound among old than young and middle-aged ones. Selected voles had higher litter size and mass, the litters growth rate, food consumption, AMDR and metabolizable energy intake than voles from the control lines. The results support the HDL theory, but not the hypotheses linking the reproductive ageing with either thermoregulatory capability deterioration or genetically based differences in metabolic rate.

Testing the thrifty and spendthrift genotype hypotheses: A pilot study on the adverse effects of Western Diet in bank voles

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Obesity and co-occurring disorders have become a common problem, particularly in the western societies. Although the immediate causes seem obvious – easy access to the so-called “western diet” (WD), rich in fats and simple sugars, combined with reduced locomotor activity – the reasons why humans are vulnerable to such conditions remain subject of discussion. The ultimate objective of our research project is to test the “thrifty genotype” hypothesis, and its logical complement, the “spendthrift genotype” hypothesis, using an experimental evolution model: the multidirectional artificial selection on bank voles, with lines characterised by different metabolic properties. The aim of this pilot experiment was to choose for the main project a WD diet of marked adverse effects, but not leading to the animal suffering. Four days after weaning, voles from non-selected control lines were assigned to either a standard diet (SD) or one of six versions of WD (different percentages of fat, sucrose, and cholesterol). The voles were monitored till adulthood, and finally several physiological performance traits and body composition were analyzed. Surprisingly, neither the body mass, fat content nor the blood glucose were elevated by the WD. This shows that the voles are more resistant to the WD than e.g., laboratory mice, which develop obesity and severe metabolic syndrome with such WDs. Thus, bank voles seem to represent a spendthrift genotype compared to the mice. However, the maximum aerobic exercise metabolism was decreased by the WD. Furthermore, the liver and spleen were enlarged in the WD groups, especially those with cholesterol supplementation. Similarly, several biochemical markers in blood plasma indicated a compromised liver and kidney function. Thus, testing for differences among the distinctly selected lines of voles in response to the extreme version of WD (21% fat, 30% sucrose, 0.5% cholesterol) will provide a tool for testing the thrifty and spendthrift.

National parks enhance wealth of the surrounding municipalities

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Establishment of protected areas is an effective way to deal with degradation of ecosystems and loss of biodiversity. However, it is often controversial at the local level and rises protests of local authorities worrying about economic losses. That is why creation of a national park (NP) requires in Poland the consent of the council of local government, which effectively gives them the right of veto against such development. In result, any NP has been established in our country since 2001. Despite of the same arguments used in public dispute over and over again robust studies documenting the economic impacts of Polish NPs are rare. We used publicly available data of the Statistics Poland (Główny Urząd Statystyczny) on the income of Polish local municipalities (gmina) to determine how their economic wealth in 1995-2020 was related to the percentage of land protected in the limits of NPs. Analysis was performed for all municipalities hosting the NP in their limits. The adjacent municipalities were used as control group. To generate rigorous impact estimates, we modeled economic outcomes as a function of the percentage of land protected in the limits of NP, type of municipality (rural, mixed, urban) and type of NP (seashore, lowland, mountain). Contrary to common narratives of local authorities that national parks depress economic growth, percentage of land protected was associated with a modest increase in the mean income per capita of gmina in all Polish NPs, does not matter their type. Our results suggest that establishing of NPs is in the best interest of local communities as they deliver not just ecosystem services and increase health benefits but also enhance economic wealth of host municipalities.

Songbirds adjust oxygen carrying capacity through modulation of the number rather than the size of erythrocytes

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Birds rely on aerobic metabolism as the main source of energy for their physical performance. Thus, the supply of oxygen is crucial to maintain proper functioning. Over a lifetime, birds experience changing energy demands, which require adjustment of the metabolic machinery. One way to adjust is to modulate oxygen carrying capacity (OCC) described as the amount of oxygen transported within the bloodstream. Among birds, hemoglobin is the only carrying molecule for respiratory gases, it is exclusively located in erythrocytes, and hemoglobin concentration in blood is known to affect OCC. Thus, we may expect hemoglobin concentration to play a key role in regulating the level of metabolism. However, little is known about the underlying cellular mechanisms – erythrocyte size and numbers – controlling blood hemoglobin concentration. To investigate what parameter hemoglobin concentration depends on, we analyzed relationship among hematological variables. We conducted a correlation analysis between four directly measured hematological variables – hemoglobin concentration, hematocrit, erythrocyte number and erythrocyte size – for 698 individuals from three avian species – zebra finch (*Taeniopygia guttata*), great tit (*Parus major*), and common starling (*Sturnus vulgaris*) – sampled under various physiological conditions, both in the laboratory and free-living. We found that hemoglobin concentration correlates positively with erythrocyte number but not with erythrocyte size. In addition, there is a strong positive correlation between hemoglobin concentration and hematocrit. At the same time, erythrocyte number shows a weak negative correlation with erythrocyte size. All the findings listed are uniform for each species, as well as for the combined dataset. These results indicate that among cellular parameters only erythrocyte number affects concentration of hemoglobin; we propose that erythrocyte number modulation serves as a mechanism affecting OCC to adjust metabolism level. We also speculate that changes in erythrocyte number on a population level might be an evolutionary pathway to adapt to changed energy demands.

Testing the hologenome concept: a nature vs nurture 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's fitness. The microbiome structure can result from an interplay of 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 can preferably maintain a specific microbiome. The general concept can be tested with experimental evolution approach. Here we performed a cross-fostering 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. During a feeding trial performed on young, still growing voles, the H-line animals had a more positive body mass balance than the C-line ones both on standard (p=0.001) and on low-quality diet (p=0.005), with no effect of foster mother type (p≥0.3). Apparent digestibility of either diet was not affected by selection (p≥0.5), but the H-line animals were able to increase their food consumption of low-quality diet more than the C-line ones (p=0.008). Body mass change and food consumption during the feeding trial were not correlated with the caecal microbiome alpha-diversity indexes (p≥0.06), but higher OTU number and Chao1 diversity index were associated with higher digestibility of both diet types (p≤0.001). However, selection affected only the Pielou evenness, which was higher in animals reared by the H-line foster mother and fed the low-quality diet (p=0.025). Therefore, although caecal microbiome diversity contributes to the ability to absorb nutrients from food, the effects of selection were achieved by modifications of quantity of food processed rather than quality of its digestion, and did not involve meaningful changes in the microbiome diversity. Thus, the results have not provided an evidence supporting the hologenome concept.

Making virtual species less virtual by reverse engineering spatiotemporal ecological models

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The virtual ecologist approach is an extremely useful tool in ecological research, as it allows for testing different methodological aspects of species distribution modeling. However, simulation methods used so far lack solutions that provide high biological realism and account for spatiotemporal variability in population densities. Therefore, we developed a virtual species generation method that is characterized by high realism and reflects as faithfully as possible the characteristics of the original system. The framework consists of the following steps: fitting a generalized additive mixed model (GAMM) to real monitoring data, simulating a virtual species while keeping the most important features of the original system (such as abundance-environment relationship, spatial and temporal autocorrelation, random spatial variability), generating virtual ecologist data, fitting the GAMM model again, and evaluation. The effectiveness of the presented approach has been

tested on large-scale (whole country of Poland) and long-term (20 years) bird abundance monitoring data. We have shown that the designed method replicates well the properties of the original system. The study was supported by the National Science Centre, Poland (grant no. 2018/29/B/NZ8/00066).

Natural selection in Cetacean immunogenome, and its relation to morbillivirus infection susceptibility

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The Cetacean morbillivirus (CeMV) is an infective agent of marine mammals causative of multiple well known epizootics, and contributing factor in the decline of some cetacean species. Differences of disease outcome between cetacean species, range from high mortality epizootics to absence of detected cases, suggests disease resistance is possibly influenced by species specific evolutionary mechanisms. If specific species have developed some type of immune resistance to the virus, such signals should be detectable in cetacean immuno-genomes. Genomic information can then be integrated with known patterns of Morbillivirus resistance in different cetacean host species, to identify candidate genes involved in susceptibility to this disease. We retrieved full genome sequences of 35 cetacean species from publicly available databases We compiled a list of over 1500 genes with known function in immune system, and retrieved the homologous coding gene sequence from each cetacean genome. The sequence alignments were then tested for signals of natural selection, using model-based dN/dS methods. In this presentation, we will show preliminary results of this analyses, focusing on signatures of selection across immune genes in cetaceans, and the potential functional mechanisms of tolerance or resistance to CeMV in different species.

Trade-offs in the evolution of the avian immune system

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Vertebrates rely on both innate and acquired branches of the immune system to optimally defend themselves against infections. However, the development, maintenance, and use of the immune system are costly in terms of energy and biochemical substrates. Resources invested in the immune defence could be otherwise allocated to other physiological processes, including growth and reproduction. Thus, animals are expected to optimize (rather than maximize) their investment in each branch of the immune system and, consequently, the evolution of innate and acquired immune defences may be shaped by resource allocation trade-offs. Here, we used phylogenetically-informed comparative analyses to test for associations between components of the innate and acquired branches of the avian immune system. We found a negative association between the level of natural antibodies (innate immune system) and structural complexity of the major histocompatibility complex (MHC) region (acquired immune system). Our results provide the first phylogenetically robust evidence for an evolutionary trade-off between the innate and acquired branches of the avian immune system, where the development of a complex acquired immune system was accompanied by an apparent downregulation of the innate immune system.

Mortality of wolves *Canis lupus* in human-dominated landscapes of Poland

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The recovery of wolf population across human-dominated landscapes of central Europe coincides with an increasing human-caused mortality of wolves, which level remains unknown. In Poland, where the species is strictly protected since 1998, and its current range covers all larger forests, we opportunistically collected data on wolves illegally shot, snared and hit by vehicles from 2002 to 2021, revealing their geographical extent, seasonal variation, sex and age structure. Furthermore, we estimated wolf mortality rate due to illegal shooting on the basis of 16 GPS/GSM collared by us individuals between 2014 and 2020. We recorded 63 illegally shot, 41 snared and 272 wolves killed by vehicles on roads. The majority (70%) were illegally killed between 2017 and 2021, also most of wolves (75%) died on roads during this period. The sex structure was similar between shot and snared individuals, while males prevailed (61%) among road casualties. In all groups, the individuals between one and three-years old prevailed, although there were 21 (33%) pups among shot wolves and 77 (29%) pups among roadkills. The road mortality was the highest in October-December (31%) and February-March (23%) and wolves mainly died on national roads (57%). Out of 16 GPS/GSM collared wolves; six were shot giving the mortality rate of 0.33 per year. Simulations revealed that the minimum number of wolves illegally shot in Poland annually is 147. In six out of seven cases, in which the person who shot a wolf was eventually sentenced, hunters were responsible.

How can phenotypic heterogeneity be advantageous in starvation? Studying quiescence in Saccharomyces cerevisiae yeast populations

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Environmentally driven phenotypic heterogeneity is widespread among clonal microbial populations, as it provides fitness advantage via various social strategies, e.g. bet-hedging, cross-feeding, and division of labour. Clonal populations of Saccharomyces cerevisiae laboratory strains can differentiate into at least two phenotypically distinct cell types when exposed to starvation. A fraction of cells actively cease growth, exit the mitotic cell cycle, and enter a reversible growth-arrested state - quiescence (Q cells). The other cells (non-quiescent, NQ) do not undergo directional changes and stop at various stages of the cell cycle when nutrients are depleted. Q cells are resistant to multiple kinds of stress (long-term starvation, heat shock, antifungals) and are considered as ones that enable the population's survival. However, we recently showed that the coexistence of Q and NQ cells can provide a fitness advantage, since Q cells survive long starvation better, while NQ cells start to proliferate faster if the starvation period is short (Opalek et al. 2022). Currently, we are running an experimental evolution aiming to explore the adaptative value of Q:NQ ratio in a variety of ecological scenarios and starvation regimes. Keywords: phenotypic heterogeneity, experimental evolution, quiescence, Saccharomyces cerevisiae, fitness References: Opalek, M., Smug, B., Doebeli, M., & Wloch-Salamon, D. (2022). On the Ecological Significance of Phenotypic Heterogeneity in Microbial Populations Undergoing Starvation. Microbiology Spectrum. https://doi.org/10.1128/spectrum.00450-21

Repeatability crisis in evolutionary biology – lessons from experimental evolution programme on *C. elegans*

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Experimental evolution (EE) is a powerful research framework for gaining insights into a wide range of biological questions. The great strength of this approach lies in using replicated and controlled experiments to directly track, in real time, changes in fitness (or any other trait of interest), occurring in response to specified environmental conditions. We have designed a long-term and highly replicated experimental evolution project using C. elegans. One of the primary aims of this study was investigating the impact of reproductive system on adaptation and diversification of initially (nearly) identical populations. Unexpectedly, however, the programme has led us far beyond the specific biological questions which had initially motivated it. Striking level of non-replication we encountered when collecting fitness data after ca. 100 generations of experimental evolution forced us to delve into literature concerning the repeatability crisis in modern science. Here, we outline our project and the problems with repeatability in trait measures, based on both our original data and the overview of the literature in the field. We highlight the importance of replicating experiments which, however, is very rarely done in the field, as our literature overview has shown. We conclude that the repeatability crisis is currently severely undermining the reliability of published research results and conclusions, which requires immediate attention and action.

Effect of urbanization on life history traits of the common garden ant *Lasius niger*

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Urbanization is known to lead drastic changes in local habitat features at both biotic and abiotic levels. Temperatures are higher in urban areas (urban heat island effect) and the food sources might be poorer since the homogenization of the habitat decreases both the plant and animal diversity and abundance. In the case of poikilothermic, stationary organisms which physiological traits are strongly linked to the environmental features, these changes can strongly influence the dynamic of their populations and even their survival. In our study, by using *Lasius niger* ant as a model organism, we carry out field and laboratory studies to test the effect of urbanization on life history traits of ants. Specifically, we have tested for differences in foraging activity, nutritional choices and fat content of the individuals coming from urban and natural populations of this ant species. The results from the field and laboratory assays show that the ant foraging is positively influenced by the higher temperatures and the light pollution present in cities influence positively. Moreover, at the laboratory, the total ant consumption was significantly higher for the sugar source than for proteins or proteins+fat sources. This preference for sugar vs proteins+fat tends to be stronger in the urban colonies, whereas no differences were found in the case of sugar vs proteins sources. Finally, the fat content of gynes (young queens) collected from colonies living in natural habitats was significantly higher than for urban gynes whereas no significant differences were found in the case of workers. To summarize, our results show how crucial traits linked to the species survival like foraging, food intake or body fat content of the reproductive cast can be affected by the urban conditions.

Implications of hybridization between wolves and dogs for the evolution of behavioural traits

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The process of animal domestication involved behavioural adaptations to new ecological niches created by humans. Introgressive hybridization between domestic animals and their wild relatives is therefore likely to alter behavioural traits, but little is known about the behavioural effects of hybridization. We assessed introgression patterns in admixed populations of Eurasian wolves and free-ranging dogs (FRDs) to identify genes and associated phenotypic traits under adaptive introgression. For this purpose, we analysed genes located within chromosomal regions showing significant overrepresentation of hybrid ancestry. We found 16 such regions containing 72 genes in wolves and 21 regions containing 311 genes in FRDs. In wolves, the gene ontology (GO) enrichment analysis revealed overrepresentation of only one biological process, the glutamate reuptake. Genes involved in glutamate metabolism were previously shown to play a major role in dog domestication, and therefore the overrepresentation of dog-derived variants of such genes may suggest the presence of dog-like behavioural traits in admixed wolf populations. In FRDs, we identified a larger set of enriched GO terms, most of which were associated with clustered protocadherins (PCDH) that play a key role in many neurodevelopmental processes, including axon guidance, synapse formation and dendritic self-avoidance. In earlier studies, PCDHs displayed differential expression between domesticated and wild populations of several mammalian species, as well as between tame and aggressive experimental populations. The overrepresentation of wolf-derived PCDHs variants may therefore attenuate the behavioural effects of domestication in FRDs that are less desirable in free-living populations. Overall, our results suggest that wolf-dog hybridization may modify behavioural traits in both canids.

Physiological and molecular mechanisms of variation in male reproductive success - a case of 6Pgdh gene

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Sexual selection has been a focus of researchers for decades, but there are surprisingly few systems in which specific physiological mechanisms of variation in male reproductive success can be linked to their genetic basis. Allele polymorphism in 6-phosphogluconate dehydrogenase (6Pgdh) in the bulb mite *Rhizoglyphus robini* is a striking example of a single gene involved in sexual selection and conflict. Males bearing the “winning” 6Pgdh allele (S) gain higher reproductive success than males lacking it and mating with S-bearing males decreases female fecundity. In our study, we look for the proximate mechanisms

driving variation in fitness of males differing in 6Pgdh genotype using phenotypic assays and transcriptomics. 6Pgdh is an enzyme in pentose phosphate cycle, a glucose converting pathway, generating NADPH and affecting the rate of nucleic acid, lipids and protein synthesis. Based on these functions, 6Pgdh polymorphism has been suggested to influence metabolic processes, cell division rates and hence the rate of spermatogenesis. The S allele has also been hypothesized to make males more active, increasing male efficiency in locating female partners. To test these hypotheses we analyzed phenotypic differences between males of different 6Pdgh genotypes. Males with the S allele produced more sperm and copulated more frequently. However, increased copulation frequency was not associated with greater mobility of these males, suggesting they might be more efficient in detecting females and/or forcing them to copulate, rather than just more active. Then, we analyzed gene expression patterns of the FF and SS males to identify physiological pathways differentially affected by alternative alleles of 6Pgdh. We found nearly 3500 gene models differentially expressed between FF and SS males, with significant enrichment in gene ontology categories associated with protein metabolism, zinc ion binding and DNA integration, suggesting these processes contribute to variation in male reproductive success associated with 6Pgdh polymorphism.

Long term patterns of association between MHC and helminth burdens in the bank vole support Red Queen dynamics

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Major histocompatibility complex (MHC) genes encode proteins crucial for adaptive immunity of vertebrates. Negative frequency-dependent selection (NFDS), resulting from adaptation of parasites to common MHC types, has been hypothesized to maintain high, functionally relevant polymorphism of MHC, but demonstration of this relationship has remained elusive. In particular, differentiation of NFDS from fluctuating selection, resulting from changes in parasite communities in time and space (FS), has proved difficult in short-term studies. Here, we used temporal data, accumulated through long-term monitoring of helminths infecting bank voles (*Myodes glareolus*), to test specific predictions of NFDS on MHC class II. Data were collected in three, moderately genetically differentiated subpopulations in Poland, which were characterized by some stable spatiotemporal helminth communities but also events indicating introduction of new species and loss of others. We found a complex association between individual MHC diversity and species richness, where intermediate numbers of DRB supertypes correlated with lowest species richness, but the opposite was true for DQB supertypes—arguing against universal selection for immunogenetic optimality. We also showed that particular MHC supertypes explain a portion of the variance in prevalence and abundance of helminths, but this effect was subpopulation-specific, which is consistent with both NFDS and FS. Finally, in line with NFDS, we found that certain helminths that have recently colonized or spread in a given subpopulation, more frequently or intensely infected voles with MHC supertypes that have been common in the recent past. Overall, our results highlight complex spatial and temporal patterns of MHC-parasite associations, the latter being consistent with Red Queen coevolutionary dynamics.

From energy constrains to sociality in male bats

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Bats are one of the most social mammals. Although they present high diversity of social systems, practically in all species, only females form groups, and these are maternal colonies, while adult males are typically solitary. There are just a few temperate-zone bat species in which male groups have been observed. So the question is, what evolutionary mechanisms influenced the emergence of the sociality of males? The phylogenetic analysis indicates that male sociality is usually short-lived, overlaps with the time of spermatogenesis, and occurs in species that feed on ephemeral insects. Thus, their food appears en masse but is unpredictable in time and space. It suggests that male sociality occurs in species facing extremely high fluctuations in food availability. Therefore, we have hypothesized that group formation may respond to high energy demands and may buffer potential energy limitations. Individuals facing a shortage in food abundance or unfavorable weather conditions may have significantly reduced reproductive parameters, such as sperm production rate. We assumed that the sociality of males could significantly improve the energy balance by reducing the costs of maintaining a relatively high temperature during spermatogenesis and increasing foraging efficiency by hunting in a group. We tested our hypothesis in a unique combination of field studies and laboratory experiments using *Vespertilio murinus* males (species with male colonies). Laboratory experiments showed that both limited food availability and lower ambient temperature significantly slowed sperm production rate. Field observations showed that the more unfavorable weather and reduced food availability, the more individuals were in colonies. We showed that solitary individuals keep high body temperature and metabolism as males in a group, but they pay a much higher energy price. Energy savings in group-living

individuals and the observed behavior of males during hunting indicate that social behavior can compensate for the negative effects of energy restrictions.

Short-time evolution in the morphology of the myrmecophilous *Maculinea teleius* butterfly

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The butterfly *Maculinea teleius* is a social parasites of Myrmica ants which larvae live and feed inside ant colonies. In the Netherlands this species became extinct and a successful reintroduction in Moerputten nature reserve was performed in 1990 by using eighty-six butterflies from a source population located in Poland. The aim of our research was to study the putative changes which may have happened in butterfly weight, thorax width and wing morphometrics over 30 years, both in Polish and Dutch populations. Since a part of butterflies died during the initial transportation to the Netherlands, and then they were stored as cabin specimens, we used them to compare changes in wing morphometrics between source population from 1990 and from 2019/2020. The weight and thorax width from the butterflies of the two current populations were measured in the field during the butterfly flight peak period by using a portable balance and a precision calliper. Additionally, the right and left hind wing of each butterfly, including the butterflies from the source population (Poland 1990) were photographed to study wing morphometrics. We analysed 14 landmarks and 18 semi-landmarks per wing to assess the size and shape of wings. Our results showed that the body mass of the Polish females is significantly larger than Dutch females, while both females and males have a bigger thorax width in the current Polish population. Polish butterflies from the current population have also bigger wing size than butterflies from the Netherlands and from butterflies from the source Polish population (from 1990). However, there is not difference in the ratio of wing size/body mass between current Polish and Dutch population. This short-time evolution in body characteristics may be explained by changes in habitat, which could have affected dispersal capabilities and conditions of butterfly larval development.

Lag phase length as a determinant of microbial fitness. The overview of approaches and a new online tool.

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Microbial populations grown in liquid culture are often tracked in time and their population size can be represented by a growth curve, typically divided into the following phases: (1) the lag phase, when cells adjust to a new environment before they start dividing, (2) the exponential growth phase when cells divide with maximal rate, (3) the stationary phase, when cells cease divisions due to nutrients depletion, and (4) the death phase where population's density drops due to the cell death. Most of the studies focus on the exponential phase and use the maximum division rate as a measure of fitness. We, however, want to draw attention to the lag length which is equally important to predict the stress or fitness of microbial populations. However, quantifying the lag phase length may be challenging and method dependent. We discuss some of the frequently used methods, and we point out to possible challenges and inconsistencies between them. To further help to calculate and consistently report the lag phase length we have developed a freely accessible web server (https://microbialgrowth.shinyapps.io/lag_calulator/) where the lag length can be calculated based on the user-specified growth curve data, for various methods, parameters, and data pre-processing techniques.

Analysis of genetic structure and diversity of grey wolf (*Canis lupus*) paternal lineages in central and eastern Europe – preliminary results

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The grey wolf (*Canis lupus*) is an iconic apex predator species that plays a key ecological role in many ecosystems and thus its ecology, behavior and genetics have been extensively studied. However, most genetic studies analyzed biparentally inherited autosomal markers or maternally inherited mtDNA. Analysis of paternally inherited Y chromosome markers should provide necessary complement to such studies, but previously these markers have been used mostly in local-scale research or wolf-dog hybridization studies. Aim of our study is to assess the diversity of wolf paternal lineages across Europe. We hypothesize that in continuous wolf range, this diversity is significantly higher than reported for isolated populations studied before. Moreover, as the results of some telemetric and genetic research on wolves suggest that dispersal in this species may be male biased, we hypothesize that wolf populations are less spatially structured on the level of paternally inherited markers compared to mtDNA and autosomal DNA. Our preliminary results seem to support these hypotheses. In ca. 300 analyzed samples from central and eastern Europe (Poland, Belarus, Russia, Ukraine and the Baltic countries) we have found nearly 30 Y-STR haplotypes, over 2.5 fold more than reported in previous studies restricted to smaller areas. Interestingly, in around 40 Polish samples analyzed, we detected 10 haplotypes, indicating that the diversity of paternal lineages significantly exceeds this of mtDNA lineages. Moreover, we found several haplotypes that are widespread over vast areas of central and eastern Europe, e.g. a haplotype shared between the Polish, northern Russian and Caucasus wolf populations. On the other hand, we have detected a peculiar group of closely related private haplotypes in Belarus, indicating presence of local genetic structure within the European Plain. To further explore this phenomenon, we plan to analyze a larger dataset of wolf samples and use Y-SNP markers that should provide a "phylogenetic backbone" allowing arrangement of Y-STR haplotypes into haplogroups.

Identifying the drivers of trait change: Does Price partitioning work?

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The Price equation of evolutionary biology, and extension of Fisher's fundamental theorem, describes the change in character expression within a population in terms of average character values and the covariance of character values and fitness. It has become a standard tool in the study of animal and plant community functioning. Nevertheless. the approach has been highly controversial, and critics have argued that Price partitions are not statistically independent and lack a simple, unequivocal interpretation, or even become meaningless, making functional inferences challenging. In this talk, I shortly introduce into the Price approach, discuss the recent controversy around Price partitioning in functional ecology, and present a new solution of the Price equation that allows for a partitioning of changes in trait expression into richness, abundances and interaction parts. I compare this approach to other partitioning methods (ANOVA, beta diversity), highlight possible pitfalls and problems with non-independencies, and demonstrate the potential advantages of the method using a worked example from primary plant succession.

Successful finding of ephemeral food resources is associated with proactive personality in wild tree-dwelling rodent – edible dormouse

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The variation in animal personality is thought to be shaped by complex evolutionary mechanisms involving interaction between energy allocation and resource acquisition. However, still little is known about potential linkage between animal personality and food resource acquisition in free-ranging animals. We hypothesized that consistent individual differences in behaviour affects the probability of finding ephemeral food resources. By performing a quasi-experiment with 'random-walking-feeders' we assessed the use of unexpected food resources in the natural habitat occupied by a tree-dwelling mammal – edible dormouse *Glis glis*. To assess whether male dormice show consistent individual variation in behaviour, repeated open-field tests were conducted. Our study indicate that proactive personality is positively correlated, independently of age and body size, with the probability of finding unpredictable food resources in a natural environment. This supports the hypothesis that inter-individual variation in resource acquisition, not only energy allocation, can mediate the fitness-personality linkage.

Transition to quiescence as an eco-evolutionary process creating diversity within yeast population

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Microbial communities are ubiquitous in almost every niche on Earth. However most cells spend the majority of their life in the non-proliferating, low metabolism, quiescent state. Transition to this state is crucial for microorganisms to survive long starvation periods and restart divisions afterwards. This is why research on quiescent cell adaptation and evolution although difficult is important to understand the microbial world dynamics. After first signal of glucose limitation, a fraction of the initially clonal non-quiescent (NQ) Saccharomyces cerevisiae populations diverse and enter the quiescent state (Q). Results of our mathematical model support hypothesis that such phenotypic heterogeneity can be understood as an example of bet hedging where different phenotypes provide fitness advantages depending on the environmental conditions: duration of the starvation period, the length of the lag and regrowth phase, and the complexity of the starvation environment. Applying various duration of starvation and re-growth periods we observed adaptation of experimental yeast as a changed Q/NQ balance within the population. Serial enrichment of Q or NQ cells followed by whole genome sequencing allowed us to identify several mutation in genes that are presumably important for such transition in yeast cells. Analysis of the mutational spectrum allow us to identify SPS external amino acid sensing pathway as one of the mechanisms influencing transition to quiescence.

The role of granivorous rodents in montane tree recruitment: climate change scenario

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Spotted nutcrackers (*Nucifraga caryocatactes*) are known as crucial seed disperser of Arolla pine (*Pinus cembra*) in montane ecosystems, but recent studies suggest that granivorous rodents pilfer most seeds cached by nutcrackers. Traditionally, granivorous rodents have been thought to act as strict seed predators limiting Arolla pine recruitment. Yet, small mammals may in fact be secondary dispersers who transport some of the pilfered seeds to microsites favorable for pine recruitment, or conditional mutualists, whose role switches between seed predation and seed dispersal depending on ecological conditions. If this is the case, pine-nutcracker mutualistic interactions may be considered a more complex diplochory pine-nutcracker-rodent system. However, the fate of pine seeds removed by small mammals is still unknown. We combined seed fate experiments, seed pilferage experiments and seedling emergence 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. All these experiments and measurements were conducted at four elevations, including: two below the treeline, one at the tree line and one above the tree line. The project is still ongoing and we will present the data obtained during two first field seasons. Here, we want to elucidate the role of granivorous rodents in tree recruitment in montane ecosystems and to provide an experimental evaluation how this role changes along an elevation gradient. This knowledge will improve predictions on the effects of climate change on tree recruitment, under the assumption that climatic zones will move upwards with global warming. The contribution of granivorous rodents in forest regeneration now revealed at lower elevations (where rodents are currently abundant) can represent the future picture of seed dispersal mechanisms at higher elevations (where the abundance of rodents is increasing due to global warming).

Inferring species demographic history using inversion rich genomes: the case of the spruce bark beetle.

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Studies on the demographic history of species and populations using whole genome data can provide quantitative information about the population parameters of biological relevance i.e. size changes, time of divergence and rates of gene flow. However, to obtain reliable estimates one need to use data which are not affected by selection. While removing coding regions seems to be the state of the art in demographic inferences it is not obvious how to treat genomic regions showing different genomic arrangements. Here we use genome wide data from over 300 bark beetle (*Ips typhogaphus*) individuals, from 23 populations sampled across its European range to reconstruct species demographic history. We assessed if the demographic model of spruce bark beetle is similar to its host plant Norway spruce. To perform these analyses, we used Pairwise Sequentially Markovian Coalescent (PSMC) model and coalescent-based simulation method based on site frequency spectrum (SFS). We accounted for several large inversions identified in the bark beetle genome and performed demographic inferences for datasets with and without inversions. We assessed if the demographic model of spruce bark beetle is similar to its host plant Norway spruce. PSMC analysis suggest that populations of spruce bark beetle went through a serious change in the effective population size over time, reaching highest effective population size just before the Last Glacial Period. Demographic parameters inferred by the analyses with and without inverted regions differ. Therefore, our results demonstrate the importance of recognizing and taking into account species genomic architecture before the demographic inferences, since using data from rearranged regions might heavily bias the estimates.

Ectoparasites do not affect seed dispersal behavior of their rodent hosts

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Ectoparasites are supposed to “drive hosts to distraction”, which makes foraging more risky for the hosts, and reduces its intensity. If this is the case, ectoparasites can affect key trophic interactions of their hosts. One of such interactions is animal-mediated seed dispersal. Many plants rely on animals for seed dispersal, thus ectoparasite-driven changes in animal foraging patterns could affect plant regeneration. We tested this notion in a field experiment on yellow-necked mice (*Apodemus flavicollis*) foraging on pedunculate oak (*Quercus robur*) acorns. We treated 306 mice at three field sites with an antiparasitic medication (“Frontline”), while 297 mice at another three sites received control treatment (paraffin oil). In comparison with control, the antiparasitic treatment reduced the average (per host) abundance of fleas by 69% and the abundance of ticks by 32%. Contrary to our predictions, the ectoparasite reductions had no clear influence on most parameters of seed dispersal (dispersal distance, the proportion of seeds cached vs. eaten, the probability of partial acorn consumption, etc.). Instead, seed dispersal characteristics varied with the abundance of mice. Intriguingly, the antiparasitic treatment appeared to result in higher mouse densities in the treated relatively to the control sites. Thus, if ectoparasites affect foraging of their seed-dispersing hosts, the impact occurs through their effects on host abundance rather than effects on host behavior.

Between big and small – how conditions of Temperature-Size Rule performance dictate optimal body size, the case of *Lecane inermis* (Rotifera, Monogononta)

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The temperature-Size Rule (TSR) is a well-established phenomenon to describe the growth response of ectotherms to temperature. TSR predicts a negative correlation between body size to increasing temperature. Nevertheless, there are limits to plastic body size response. In consequence, the TSR could only be applied within a specific optimal thermal range which is determined by the minimum and optimum temperatures for performance directly referred to as fitness. In this study, we aimed to examine the optimal thermal range for nine parthenogenetic populations of *Lecane inermis* (Rotifera, Monogononta). Each population had known thermal preference, being either generalist or specialist; cold- or warm-preferring. Each population of *L. inermis* was exposed to six thermal regimes from 10°C to 35°C. The response trait was body size. Additionally, the population growth rate was estimated as a fitness measure to establish the population-specific optimal thermal range and to enable the interpretation of the significance of possible differences in TSR patterns-. The results confirmed predictions that the populations that prefer cooler conditions exhibited ranges of TSR shifted to lower temperatures, whereas the populations that prefer warmer conditions achieved ranges of TSR shifted to higher temperatures. Optimal thermal ranges for the TSR differ from the thermal preferences of examined populations. Results show that it is important to take thermal preferences into account while planning the studies on the plastic body size response to temperature changes. Even closely related organisms may differ in the thermal ranges within which they can plastically respond to the environment.

POSTERS

P1. Consequences of hybridization in mammals: a systematic review

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Hybridization, defined as breeding between two distinct taxonomic units, can have an important effect on the evolutionary patterns in cross-breeding taxa. Although interspecific hybridization has frequently been considered as a maladaptive process, which threatens species genetic integrity and survival via genetic swamping and outbreeding depression, in some cases hybridization can introduce novel adaptive variation and increase fitness. Most studies to date focused on documenting hybridization events and analyzing their causes, while relatively little is known about the consequences of hybridization and its impact on the parental species. To address this knowledge gap, we conducted a systematic review of studies on hybridization in mammals published in 2010–2021, and identified 115 relevant studies. Of 13 categories of hybridization consequences described in these studies, the most common negative consequence (21% of studies) was genetic swamping and the most common positive consequence (8%) was the gain of novel adaptive variation. The total frequency of negative consequences (49%) was higher than positive (13%) and neutral (38%) consequences. These frequencies are biased by the detection possibilities of microsatellite loci, the most common genetic markers used in the papers assessed. As negative outcomes are typically easier to demonstrate than positive ones (e.g., extinction vs hybrid speciation), they may be over-represented in publications. Transition towards genomic studies involving both neutral and adaptive variation will provide a better insight into the real impacts of hybridization.

P2. The diversity and spatiotemporal distribution of microbiota associated with *Macrosteles leafhoppers* (Hemiptera: Cicadellidae)

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Microbial symbionts play important roles in insect biology, but their diversity, distribution, and dynamics over time across host populations is poorly understood. We surveyed the spatio-temporal distribution of bacterial symbionts in several species of the broadly distributed, diverse, and economically significant leafhopper genus Macrosteles, with emphasis on *Macrosteles laevis*. Amplicon sequencing of the Cytochrome oxidase I (COI) gene allowed us to distinguish species, revealed lack of strong genetic differentiation across *M. laevis* populations combined with significant levels of heteroplasmy, and multiple cases of parasitoid infections. 16S rRNA amplicon sequencing data confirmed the omnipresence of the ancient nutritional endosymbionts Sulcia and Nasuia and a high, but variable prevalence of Arsenophonus, previously shown to colonise Sulcia cells. Other abundant symbionts included Rickettsia, Wolbachia and a previously unreported symbiont in Auchenorrhyncha, Ca. Lariskella. Further, we detected the known plant pathogen phytoplasma in 31 specimens, or 8.5% of samples. However, there was no discernable patterns in the symbiont prevalence among *M. laevis* populations, or associations between the presence of different symbionts. Combined, our data show how the simultaneous characterization of host and symbiont marker gene amplicons in large insect collections can reveal patterns critical for the understanding of their significance.

P3. Asymmetry in the thermal sensitivity of predator and prey performance may explain T-S and Bergmann's rules in zooplankton

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Numerous studies have demonstrated an inverse correlation between ambient temperature and body size in various ectotherms. This pattern could be explained by the greater temperature effect on the predator's foraging rate and, in turn, on the mortality rate in comparison to the birth rate in prey populations. While a number of studies have revealed that the latter effect is close to the one anticipated by the Q10 = 2 assumption, the hypothesis would be confirmed if the effect of temperature on the foraging rate of the predator was greater than Q10 = 2. This could occur either when the thermal sensitivity of the predator's standard metabolic rate (SMR) is greater than this prediction or when the traits relevant for performance, mainly the mobility of both the predator and its prey, are affected asymmetrically by the elevated temperature. To test this hypothesis, we compared the capture rate and SMR of two fish species (rudd and Malabar danio) and several parameters characterising the mobility of the fish and their planktonic prey (Daphnia) at different temperatures. The results confirmed our hypothesis, as the capture rate increased with rising temperatures much more than expected from the Q10 = 2 assumption, particularly for danio. Such a great effect cannot be explained by the thermal sensitivity of SMR alone, since the Q10 for SMR was around a mere 2. The most likely explanation seems to be a much greater increase of mobility and, in turn, reaction field volume of the fish than of its planktonic prey at elevated temperatures, which improves its attack rate more than predicted by the Q10 = 2 assumption. This mechanism may be responsible not only for the smaller mean body size but also the lower density of zooplankton populations and communities at an elevated temperature, and hypothetically could be observed in other predator-prey interfaces. The research was financed by the National Science Centre, projects no. 2016/23/D/NZ8/03532 and 2019/35/B/NZ8/04523.

P4. Mechanisms determining predatory behavior: a project on experimentally evolved populations of bank voles

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One of the major challenges in evolutionary physiology is explaining the mechanisms behind complex adaptations' evolution. These adaptations are often associated with extensive changes at all levels of an animal's organization, from molecules to morphology and behavior. Predatory behavior is one of such complex adaptations and is important not only from an ecological and evolutionary context but also from a biomedical perspective, because of its plausible relevance to pathological aggression in humans. Interestingly, little is known about the mechanisms controlling predatory aggression. A powerful method to study the genetic, physiological, and neurobiological basis of behavioral diversity is to compare lines of animals selected for the behavioral trait of interest. We will use the laboratory evolved populations (>30 generations) of bank voles (*Myodes glareolus*), selected to hunt crickets (Predatory lines), and random-bred control lines (Control lines). We will perform detailed analyses of hunting behavior to verify that evolution in the Predatory lines not only increased motivation to attack (predatory drive) but also improved hunting skills (time to catch cricket in successful trials). Immediately after the cricket hunting tests, the corticosterone levels will be measured to check if coping with stress contributes to an increase in predatory behavior. We will identify whether selection for increased predatory behavior altered the levels of key hormones such as testosterone, prolactin, estradiol, insulin, and leptin. To identify the differentially neural circuit activation in the Predatory and Control voles, the brains will be processed to measure the expression levels of C-fos. The brain regions, central amygdala, which plays a central role in motivation to pursue prey, and ventrolateral caudoputamen, which orchestrate the sequence of hunting movements, will be used to determine the concentration of neurotransmitters. Together, our results will provide insights into the neuronal and hormonal mechanisms underlying predatory behavior and its main components: motivation and skill.

P5. Structure remodeling and changes of lipid peroxidation in the brown adipose tissue of the bank voles (*Myodes glareolus*) under different conditions of photoperiod and ambient temperature

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Brown adipose tissue (BAT) plays an important role in thermoregulatory heat production of small mammals and its thermoregulatory potential may change with changes in the photoperiod and temperature. The aim of this study was to investigate the effect of photoperiod and ambient temperature on the BAT structure (tissue mass, cell size and lipid droplet size). Additionally, the intensity of lipid peroxidation as an indicator of the intensity of metabolic processes in the cell was analyzed. Bank voles were held under short (SD) or long (LD) photoperiod in 20°C or 5°C, creating four experimental groups (LP20, SP20, SP5 and LP5). Both under the influence of short photoperiod (SP20) and low temperature (LP5), a reduction of the lipid droplet size was observed, which seems to be a key mechanism of increasing thermogenic potential of BAT. This is confirmed by the negative correlation between the intensity of lipid peroxidation and the droplet size in the tissue. The smallest lipid droplets were observed in SP5 group. Additionally in this group (SP5), BAT-building cells were the smallest. Our results therefore indicate, that winter reduction of BAT weight in the bank vole is the effect of both lipid droplet size remodeling and cell size reduction. Only a slight decrease in BAT mass in LP5 group suggests the existence of mechanisms of lipid stories refuel in long photoperiod and/or less use of the BAT potential. The explanation of the differences in the influence of photoperiod and temperature on the mass control mechanisms, properties and activity of the BAT requires additional studies of the tissue lipid and protein composition.

P6. Do changes in heat loss capacity affect oxidative stress in lactating females of laboratory mice with different levels of basal metabolic rate?

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Heat dissipation limit (HDL) hypothesis predicts that the sustained metabolic rate of endotherms can be limited by their capacity to dissipate heat. This effect should be particularly evident during lactation, when the costs of reproduction, expressed as sustained metabolic rate of females, are high. At the molecular level such costs manifest as elevated oxidative stress (OS). However, the significance of both the HDL and OS as the costs of reproduction is controversial. We studied females of laboratory mice from two lines, divergently selected towards either high or low level of basal metabolic rate (BMR), and differing with the level of obligatory heat production and lactation performance. In three experiments, we manipulated the level of heat production and/or the capacity to

heat loss in lactating females by exposing them to different ambient temperatures (23 °C or 30 °C) combined with shaving and/or an immune challenge. We then quantified the magnitude of oxidative damage to lipids and the level of glutathione (antioxidant) in livers. We found no clear effect of all experimental factors on analyzed parameters in both lines of mice. However, the within-group variation in the increase of litter mass during lactation was correlated positively in two experiments with oxidative damage in mothers nursing those litters, and correlated negatively in another experiment with mother's glutathione level. We conclude that changes in the capacity of heat dissipation had no effect on OS in lactating females. Strikingly, this is another study when mice selected for high BMR were not more sensitivity to changes in heat dissipation as could be predicted by HDL. However, our results confirm that higher reproductive effort can be related to elevated OS, although our experimental setup did not allow us to analyze the causality of this relationship.

P7. What the small rotifer species *Lecane inermis* can teach us about the role of oxygen in the response of body size to temperature

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The role of oxygen in the body size response to temperature was first proposed on theoretical grounds and then began to be tested empirically. Although far from a consensus on how universal these mechanisms are among different groups of organisms, one species in particular seems to stand out in terms of how well understood are the proximate and ultimate mechanisms responsible for temperature-dependent body size regulation. That species is the rotifer *Lecane inermis*. To date, it is known that, for this species, decreasing body size with temperature is an adaptation to decreasing oxygen availability under high temperature conditions. It is also known how the plastic response of adjusting body size to temperature is controlled, and the conditions under which it can occur have been recognized. How different types of standard diet can affect this response has also been investigated. Finally, the response to changing temperature (and with it, to oxygenic conditions) has been examined at various levels, including processes occurring at the mitochondrial level. It appears that the totality of the results collected to date for this species informs us about how changes in temperature and oxygen conditions can affect relatively simple ectothermic organisms, which allows us to plan similar studies on organisms that have more complex mechanisms for regulating body size, and perhaps enable further predictions about how global warming may affect living organisms in general.

P8. Do animal personality impact seed dispersal?

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Behavioural syndromes, also known as animal personalities, are sets of correlated behaviours that are consistent over time and across different ecological situations. Typically, we distinguish two endpoints of animal personalities (with many intermediate types): proactive – fast-exploring, bold and aggressive individuals, and reactive – slow-exploring, cautious, and non-aggressive individuals. Animal personality, along with other traits such as sex, body mass or reproductive status, can impact individual's foraging strategies. Foraging strategies of granivores can determine whether an animal acts as a mutualist or a predator in a plant-animal interaction. According to the literature, bold and fast-exploring animals should cache seeds more frequently while shy individuals should consume seeds close to the parent trees. The aim of this study is to investigate the impact of boldness of yellow-necked mouse (*Apodemus flavicollis*) on common oak (*Quercus robur*) seed dispersal. We conducted our study in "Zielonka" Forest. Study sites consisted of 100 traps of type "dziekanówka", placed at 10-m spacing. Each trapped individual underwent two tests assessing behavioural syndrome: an open-field test and struggle rate in a fabric bag. We tagged all individuals with 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. Contrary to our predictions, exploration rate did not impact whether an individual consumed or cached encountered acorns, and was not linked to acorn dispersal distance. However, foraging on seeds was affected by individual traits such as body mass and sex.

P9. Diversity and introgression of MHC genes in the Iberian Podarcis species complex.

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The Major Histocompatibility Complex (MHC) is a group of genes involved in the adaptive immune response of jawed vertebrates. It has long been a subject of interest in genetics and evolutionary biology due to its extreme diversity and presumably complex evolution. Apart from host-pathogen co-evolution and the retention of ancestral polymorphism, a potential source of MHC diversity is adaptive introgression, in which related species exchange MHC alleles despite strong reproductive isolation. The Iberian Podarcis lizard complex is a good study system to test this possibility, as it includes several species which currently show little hybridization and form multiple contact zones. To assess the diversity and introgression of MHC, we sampled over 600 individuals from 7 species, then sequenced and genotyped the variable second exon of class I and II of MHC. We found extreme diversity (over a thousand alleles coming from several genes for each MHC class) across the complex, with allelic diversity somewhat positively correlated with population size. MHC allele sharing between species ranged from 0 to 13 percent, while a very small (21 individuals out of 535 successfully genotyped) number of admixed individuals was detected via genome-wide sequencing. We detected multiple codons under positive selection in both MHC classes that somewhat correlated with putative peptide-binding sites. We detected significant MHC introgression across multiple contact zones which, considering very low overall hybridization, points to adaptive introgression of MHC. These results add to the gradually accumulating evidence for MHC continuing to introgress even at late stages of speciation, driven presumably through the novel allele advantage.

P10. Weather and reproduction in an urban bird

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A growing number of animal species use human-dominated areas as a novel habitat for reproduction and other activities. Specific features of urban habitats may modulate the effects of environmental conditions on bird reproductive success. We conducted a long-term monitoring to investigate associations between basic weather parameters (temperature and precipitation) and reproductive performance in an urban population of the Eurasian Coot. Our results revealed a complex nature of weather-dependent variation in coot breeding success. The mean daily temperature during chick-rearing period was recognized as a key determinant of coot reproductive output, but the direction of this effect varied between the stages of chick development. We also found an unexpected relationship between the mean daily precipitation level at the early chick-rearing stage and the number of raised chicks in study population. We conclude that our results may reflect a unique structure of urban habitat and specific behavioral responses of urban coots to environmental conditions.

P11. Nest characteristics in Great Tits *Parus major* and Blue Tits *Cyanistes caeruleus*: a long-term study

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Reproduction is often described as one of the most energetically costly stages of the life-cycle of an organism. In birds, the time of reproduction is divided into several smaller periods, like: choosing a partner, nest construction, defense of the breeding territory, egg laying, incubation and chick rearing. In secondary cavity-nesters parents may reduce the cost of clutch incubation by constructing an insulated nest that may efficiently buffer fluctuations of the temperature of an outside world. We present results concerning nest parameters and their impact on breeding characteristics in Great Tits (*Parus major*) and Blue Tits (*Cyanistes caeruleus*) in central Poland over a six year period, 2012–2017, in a deciduous forest and an urban parkland. We found that Blue Tit nests were higher and heavier than Great Tit nests. There were no differences in nest hight and nest mass between two habitats in Blue Tits, but Great Tits nests were highter in the forest than in the parkland. Potential impacts of the local climate and predation risks on the species-specific expression of the nest parameters are discussed.

P12. Social intraspecific and interspecies learning of Prussian carp *Carassius gibelio*

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Alien species invasions are one of the most serious threats to global biodiversity. Alien species, introduced by humans into new areas threaten native species, changed native ecosystems and can lead to not only to native species extinction, but economic problems as well. One of the environments particularly vulnerable to the uncontrolled spread of alien species are freshwater ecosystems, which are now recognized as the most degraded ecosystems in the world. Progressive changes, such as rising temperatures, increasing pollution and eutrophication of waters, can effectively accelerate biological invasions and lead to the elimination of native, narrowly specialized species in favor of widely specialized alien species that quickly adapt to new environments. One of the most important factors determining the success of invasions by vertebrates, including fish, is their ability to learn, individually and socially. Individual and social learning of fish, as components of phenotypic plasticity, enhance feeding efficiency and thus survival in new and/or unstable environments. Species with higher learning rates are potentially better competitors for food or shelter resources, which may consequently facilitate biological dispersal and domination of more habitats. The literature lacks detailed studies on the social learning ability of invasive fish species and data on whether invasive species can effectively learn from representatives of another species. The aim of this study was to investigate whether the teacher species affects the learning efficiency of the invasive freshwater Prussian carp *Carassius gibelio*. The study group of invasive fishes foraged more efficiently than self-learning individuals, with both intra- and interspecies social learning being equally effective. The obtained results prove the ability of this invasive species to acquire and use information from the observations of representatives of another species. Such a strategy may be beneficial for the colonization of unknown areas and even crucial in the initial stages of invasion.

P13. Testing the thrifty and spendthrift genotype hypotheses: The experimental evolution model system and the plan of a "nature – nurture" experiment on bank voles

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Obesity and co-occurring disorders have become a common problem. Among the well-documented causes are a) the so-called "western diet" (WD), rich in fats and simple sugars, combined with b) reduced locomotor activity. Many hypotheses were proposed to answer why we are vulnerable to such conditions. The "thrifty genotype" hypothesis assumes that natural selection allowed our body to efficiently store fat reserves when food was abundant to endure the time of food shortage. Nowadays, however, with easy access to food, fat is continuously stored, which leads to various disorders. If the hypothesis is correct, its logical counterpart, the "spendthrift genotype" hypothesis, should be also true: animals that evolved high metabolic performance under no food-access restrictions should be less vulnerable to the adverse effect of such an excess. These hypotheses are simultaneously studied based on an experimental evolution approach - an artificial selection on bank voles. The experiment comprise lines selected in 3 selection directions: "Herbivorous lines" with the ability to grow on low-quality herbivorous diet, "Aerobic lines" with higher aerobic metabolism during swimming, and "Predatory lines" with a propensity to hunt crickets; and unselected Control lines. Both the Aerobic and the Predatory lines represent the spendthrift genotype, while the Herbivorous lines the thrifty genotype. Six days after weaning, voles from all the lines were given either WD (21% fat, 30% sucrose, 0.5% cholesterol) or standard diet for more than two months. At the age of 96-107 days, several metabolic and locomotor performance traits were analyzed, mass of internal organs and fat pads was measured, and blood parameters analyzed to asses lipid profile and markers of liver and kidney function. If the thrifty-spendthrift hypotheses are correct, the adverse effects of WD will be more profound in the Herbivorous, and less profound in the Aerobic and Predatory lines, compared to the Control lines.

P14. The impact of anthropogenic pollution and urbanization on avian colouration: a meta-analysis

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Brilliant, amazingly diverse bird colour ornaments were one of the crucial cues that led Darwin to the idea of sexual selection. Although avian coloration plays multiple functions, including concealment, thermoregulation or advertisement as a distasteful prey, the quality-signalling role in sexual selection attracted most of the researchers' attention. Sexually selected ornaments are thought to be more susceptible to external stressors than naturally selected traits, and as such, they might be used as a litmus test for environmental quality. For this reason, the last two decades brought numerous studies on the impact of anthropogenic pollution on the expression of various avian colour traits. Here, we applied a meta-analytical approach to summarize their results and examine if there is an interaction between the mechanism of colour production (carotenoid-based, melanin-based and structural) and the type of anthropogenic factors (categorized as heavy metals, PCBs, urbanization or other). Following the assumption of heightened condition-dependence of ornaments under sexual selection pressure, we also expected the magnitude of effect sizes to be higher in males. The overall effect size was significantly negative, which provides the support for the general detrimental effect of anthropogenic pollutants on avian colouration. Contrary to expectations, we found no interaction between pollution types and colour-producing mechanisms. However, there were significant differences in sensitivity between colour-producing mechanisms, with carotenoid-based colouration being the most fragile for anthropogenic environmental disturbances. Moreover, in contrast to predictions, we observed no sex-specific effect, which, may result from a large pool of studies in which males and females were not treated separately. Importantly, we identified a publication gap concerning structural colouration, which, compared to pigment-based colouration, remains markedly understudied and, thus, should become the priority for future research. Finally, we would like to call for the unification of methods used for colour quantification in ecological research to ensure comparability of results between studies.

P15. Development of a novel molecular tool for a common avian ectoparasite

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Louse flies, also known as keds (Diptera: Hippoboscidae), are hematophagous, viviparous ectoparasites of birds and mammals. Recent checklists indicate 29 species within Ornithomya genus, six of which can be defined as avian polixenic parasites. Taking into account their potential role as vectors of various bloodborne pathogens it is surprising, that the studies concerning louse flies are so scarce. There are only few molecular studies focused on their phylogeny, diversity, population genetics and interactions with different hosts. Especially the louse flies that are avian parasites may strongly impact wildlife and poultry production. Such studies focus on developing molecular methods detecting pathogens secondary transmitted by keds as host species (e.g. Bartonella spp.) or between species on which keds prey.

Here, we present the new microsatellite loci for *O. avicularia*. Using the next-generation sequencing, we received 126269 prospective microsatellite loci, and among them, we selected 26 most promising. We developed primers and started testing their potential to amplify on 26 individuals of *Ornithomya avicularia* collected mainly during different bird-ringing schemes in Poland. After setting the optimal reaction protocols, we genotyped the product to check the polymorphism. From the initial 26 loci, 20 markers were polymorphic and did not show signs of a null allele and Hardy-Weinberg equilibrium aberrations. The number of alleles varies between 2 and 23 per loci. In the next step, we will investigate the population genetic structure of O. avicularia, using developed markers as a molecular tool. We plan to cross test developed markers on closely related species, like *Ornithomya chloropus* to test their capability to amplify and potential polymorphism.

P16. Saccharomyces sp. from Białowieża National Park temperate forests

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Saccharomyces cerevisiae yeast has been associated with human activities for at least 10K years and there are many domesticated breeds characteristics of food and beverages. However, *S. cerevisae* and closely related species can be isolated from wild natural niches, specially from oaks and related trees in primary forest. The discovery of South East Asia as the birth place of S. cerevisiae is proposed a single out-of-China event that founded the rest of the world population. This has originated wild populations that are mostly in the north hemisphere. Within ongoing project there are currently sampling and sequencing Saccharomyces yeasts in different part of Europe to try to reconstruct both the pre-domestication and domestication phases. Białowieża Forest represent a unique place to reconstruct *S. cerevisiae* history after the initial out-of-China event. Given its history and geographic location, Białowieża Forest might represent a reservoir of the *S. cerevisiae* lineage that was dispersed from China. We aim to isolate and genome sequence Saccharomyces yeasts associated with plants and soil to unveil the species history during its dispersal in the European continent.

P17. The combined effect of an elevated temperature and the presence of hypoxia on the interspecific competition of Daphnia

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An apparent decrease in individual body size among a variety of aquatic ectotherms as well as the mean body size of their populations, either spatially or temporally, have been revealed in numerous studies. In the case of zooplankton communities, one of the most likely explanations of these patterns is the relative decrease of the competitive abilities of larger- over smaller-bodied species because the production (i.e. growth and reproduction) of individuals of larger species is more limited due to their greater susceptibility to decreased oxygen at an elevated temperature either through a decreased oxygen concentration or increased oxygen demands (due to an accelerated metabolism). To test this, we performed competitive experiments at high and low oxygen concentrations (8.0 and 3.0 mg O2 L-1) at two temperatures (23 and 13 ºC) with two pairs of zooplankton species differing in body size: *Daphnia longispina* (smaller-bodied) and *D. pulex* (larger-bodied), as well as *D. pulex* (smaller-bodied) and *D. magna* (larger-bodied). In the case of *D. longispina* and *D. pulex*, our hypothesis was not confirmed, since larger-bodied species competitively excluded the smaller one in all of the experimental treatments. Although in the case of *D. pulex* and *D. magna*, both species successfully coexisted for a very long period of time in all of the treatments, their relative densities were affected by both experimental variables. According to our hypothesis, temperature favoured smaller-bodied species. Contrary to the hypothesis, low oxygen concentration had the opposite effect, which may be attributed to a greater concentration of hemoglobin in the body tissues of *D. magna* than in *D. pulex*. The research was financed by the National Science Centre, projects no. 2016/23/D/NZ8/03532 and 2019/35/B/NZ8/04523.

P18. Age, fungal infection and immune investment in foragers and intra-nidal workers of Myrmica ants

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Social insects like ants are living in densely populated colonies in which individuals frequently interact with many nest-mates that favours fungus or bacterial growth and can elevate infection risks. Different members of the colony can widely differ in the conditions they are exposed to, depending on their age and mostly on the task that they perform in the colony. Foragers that are working outside of the nest in order to search for food are more exposed to various risks, including infection, compared to intra-nidal workers. Therefore, we can expect different immune investment in these two groups of colony members. In our study, we used *Myrmica scabrinodis* ants to test the individual immune defence of foragers (old workers) and young intra-nidal workers from two colony types: either infected or uninfected by laboulbenial fungus *Rickia wasmannii*. As a measure of immune defence, we assessed the level of phenoloxidase - the enzyme involved in the melanization of pathogens – in its active form and as the total level which includes the active phenoloxidase and its inactive precursor – prophenoloxidase. We found that the infection status of the colony did not explain the variation in either the active or total phenoloxidase levels. However, the total level of phenoloxidase was explained by age. Specifically, older individuals had higher levels of total phenoloxidase than young individuals. This age-specific pattern in immune defence may be explained by differences in immune investment strategies between young and old individuals, which evolved in response to differences in infection risks between these age groups.

P19. Origin of the Eurasian lynx population in the Roztocze region, south-east Poland

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Genetic analyses can provide important insights into processes that shape population structure of protected species. To better understand the origin and connectivity of Eurasian lynx (Lynx lynx) inhabiting previously unstudied Roztocze region (south-east Poland), we analysed both tissue and non-invasive samples using microsatellite DNA loci and a portion of the mtDNA control region. Our results showed that lynx population in Roztocze is genetically distinct from the Carpathian population and clustered with individuals from a Baltic population. Interestingly, analyses of microsatellite loci grouped individuals from Roztocze into separate cluster, distinct from groups previously described in north-east Poland, although genetic distance between them is weak.

P20. Relation between different niche dimensions: positive feedback or trade-offs?

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Ecological niche is inherently multidimensional, and interactions of organisms with their surroundings and resources measured via different niche dimensions may be subjected to different selective pressures. Therefore, to study niche breadth evolution, it is critical to consider reciprocal relationships between different environmental variables by which a niche is characterized. Primarily, it is crucial to learn: (i) whether broadening a niche in one dimension will result in broadening a niche in another dimension (i.e., feedback resulting in evolution of ecological generalists) or (ii) if there are trade-offs between the evolution of a niche in different dimensions (i.e., generalization in one dimension resulting in specialization in another dimension). Generally, the majority of experimental studies investigating niche breadth has focused on responses of organisms adapting to variation within a single environmental dimension. These studies have improved our understanding of the evolution of niche breadth, but many gaps remain in explaining the interactions between different niche dimensions. This presentation reviews literature on relationships between different niche dimensions. Both scenarios, feedback or trade-offs, are possible outcomes when organisms adapt to different environmental resources. Understanding the complexity of such interactions and multidimensionality of niches is of paramount importance when studying the evolution of niche breadth and ecological specialization. The study was financially supported by the National Science Centre in Poland (grants no. 2021/41/B/NZ8/01703 and 2018/29/B/NZ8/00066).

P21. rangr: An R package for mechanistic, spatially explicit simulation of species range dynamics

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Data originating from citizen science and wildlife monitoring programmes pose a great analytical challenge. They usually have complicated, multivariate and hierarchical structure which is a result of spatial and temporal replication, hundreds of recorded species and many observers involved. Despite a relatively low signal-to-noise ratio and considerable observational error, these kinds of data are an extremely useful, and sometimes the only, source of ecological information. Therefore, they are widely used in

scientific research and conservation. In this study, we present rangr, an open-source R package designed to simulate species range dynamics. This tool mimics the essential processes that shape population numbers and spatial distributions: local dynamics, dispersal and habitat selection. Simulations may be conducted in a spatially-explicit and dynamic environment, which facilitates population projections as they respond to climate or land-use changes. By using different sampling schemes and observational error distributions, the structure of the original survey data can be reproduced or a purely random sampling can be mimicked. Some of the key features of rangr are its high flexibility and customisability, which guarantees that the simulation can be tailored to meet specific research needs. For instance, the user can choose between different types of dynamics (including Allee effects), modes of dispersal and dispersal kernels, detectability functions, or levels of stochasticity. To improve scalability, the R code is optimised to support parallelization and efficient memory management. The study was supported by the National Science Centre, Poland (grant no. 2018/29/B/NZ8/00066).

P22. Just showy or simply honest? Signaling of the floral reward in yellow iris (*Iris pseudacorus* L.)

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Pollinators are often unable to directly assess the quality and quantity of rewards offered by flowers. As a result, the interaction between plants and pollinators is frequently mediated by the expression of rewards advertising signals. Since pollinators visit flowers for rewards, they should prefer so-called ‘honest floral signals’ that indicate the reward properties. To gain more insight into the factors shaping plant-pollinator interaction we tested the relation between the visual features of Iris pseudacorus flowers (i.e., tepals diameter and length, the size of the spot) and the properties of the food reward offered. Additionally, we experimentally changed flowers’ features, which potentially play an important role in plant-pollinator communication (tepals shortening or covering the spot on the tepals). We also assessed the frequency of pollinator visits and their reproductive success in non-modified and experimentally changed flowers. Our results indicate that flower traits are a good predictor of reward properties. The spot on the tepal is a good indicator of the nectar volume and we found several correlations between flower size and the sugar or amino acids amount. However, the size of studied flower traits does not influence the frequency of pollinator visits and the seedset. However, covering the spot on the tepal resulted in a lower frequency of visits. Thus, by analysing collected data we can infer that some flower features may be an honest signal for pollinators, however, A. mellifera, responsible for more than 80% of the visits, does not use it while foraging.

P23. Population genomics of Carpathians and Apennines populations of spruce bark beetle

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Spruce bark beetle (*Ips typographus*) is the most destructive pest of Norway spruce (*Picea abies*) forests and occurs in all forests where this tree species is present. Under special conditions spruce bark beetle can outbreak, resulting in mass infestations of Norway spruce forests. Despite the ecological and economic importance of *Ips typographus*, hardly any studies have been carried out on its genome-wide variation, particularly in the populations of Carpathians and Apennines, where Picea abies forms a distinct genetic linage. In the present study, we use whole-genome resequencing data and apply state-of-the-art population genetics analysis to examine levels of genetic variation of Carpathians and Apennines spruce bark beetle populations. We are particularly interested in determining if mountain range populations are genetically distinct from other spruce bark beetle populations, and if do they have distinct signatures of local adaptations and different selection patterns. Additionally, using our high coverage sequencing data we assess variation in microbiota and nematode infestation among populations across species range. The results of the study will provide a comprehensive description of the whole genome variation across species range – the information still lacking but necessary to be able to combine extensive ecological information with genetic resources to provide insights on the dynamics of pest outbreaks in forest ecosystems.

P24. Main course or side dish – wolf *Canis lupus* predation on Eurasian beavers *Castor fiber* in central Europe

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Although the grey wolf (*Canis lupus*) is mainly considered as predator of ungulates, it shows natural adaptability to forage on various animals or even plants. Factors influencing its dietary flexibility, however, remain poorly understood. In central Europe wolves prey primarily on roe deer (*Capreolus capreolus*), red deer (*Cervus elaphus*) and wild boars (*Sus scrofa*), but locally the Eurasian beaver (Castor fiber) become an important item of their diet. We compiled the dietary data from 21 study areas incorporating 6199 scat samples collected between 1985 and 2020 in Poland to investigate diet of grey wolves on regional and national scales and with regard to seasonal and habitat variations. The percentage of the beaver in the diet of adult wolves differed significantly among all studies ranging from 0 to 46% of consumed biomass. Furthermore, despite low consumption of beavers by adults, its share in the diet of pups may be substantial. Wolves consumed more beavers in NE Poland, where landscape is richer in features supporting beavers persistence, e.g. marshes. This food item is also more frequent in the wolf diet in drier seasons when the water table is low. Dietary plasticity of wolves may support recovery of wolf population across central and western Europe, and underscores its status as an opportunistic species which is likely to be robust to ongoing environmental changes.

P25. High prevalence of polymorphic inversions in the most destructive forest pest in Europe

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Single nucleotide polymorphisms have often been markers of choice in studies investigating neutral and adaptive genome-wide variation patterns. However, growing empirical evidence, facilitated by technological and methodological advances, suggests that structural variants play crucial roles in adaptation and speciation processes. In particular, polymorphic inversions seem to be underlying the maintenance of complex phenotypes present in many species. Here, we examine the genome-wide variation in the most aggressive pest of European forests: spruce bark beetle (*Ips typographus*). We sampled >200 individuals from 18 populations across species range, including rarely outbreaking populations from Scandinavia and frequently outbreaking populations from Central Europe. We found high within-species variation and significant but weak differentiation among populations across species range. Interestingly, we discovered over a dozen polymorphic inversions that cover more than 25% of the species genome. The inversions differ in size and age but most of them are present in all sampled populations. One inversion is associated with sex chromosome and detected only in Scandinavian populations and 3 smaller inversions show significant geographical clines across species range. The high prevalence of polymorphic inversions make spruce bark beetle one of the most variable species in terms of inversion polymorphisms described so far and raises the questions of its genome dynamics and inversions role in its adaptation.

P26. Biological clocks in the wild: Does artificial light at night disturb development in a migratory bird?

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Biological clocks play a key role in maintaining vital functions and are synchronised with environmental cues, primarily light. Artificial light at night (ALAN) is nowadays a major anthropogenic factor disrupting these cues and possibly affecting physiology and behaviour. Many studies reported effects of light pollution on circadian clock disruption in captive animals. Yet, very little is known about the impact of ALAN on wild populations in an evolutionarily relevant context. In particular, ALAN presents a real-life threat to

migratory animals. In this study we are exploring the effects of ALAN exposure on circadian clock functioning at early life in a free-ranging migratory bird: the collared flycatcher (*Ficedula albicollis*). During 2021 and 2022 breeding seasons, we experimentally introduced ALAN to nestboxes occupied by flycatchers on the island of Gotland, Sweden. We quantified growth (i.e., body mass and structural size: tarsus, wing chord and 3rd primary feather length), fledging success, as well as time spent in the nest by nestlings from experimental and control (naturally dark at night) groups. In our study we are evaluating circadian gene expression (CLOCK, ARNTL, PER2, CRY1) in order to link the disruptions in their expression to the observed developmental differences. As such, our research will provide a comprehensive insight into the impact of ALAN on early life history traits depending on circadian clocks in birds.

P27. Handgrip strength and oxidative stress markers in men

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According to evolutionary hypothesis, androgen-dependent traits are costly to develop and therefore the levels of their expression might reflect biological quality in males. The results of studies testing if physiological cost of androgens are linked to immunosuppression are still inconclusive. It is likely that other factors might be involved in signaling role of testosterone-dependent traits. In accordance to Oxidative Handicap Hypothesis (OHH), testosterone stimulates production of reactive oxygen species (ROS) and therefore only those men who are able to effectively neutralize ROS (and maintain low levels of oxidative stress) can maintain high testosterone level. Handgrip strength (HGS) is highly sexually dimorphic trait and it also depends on currently circulating androgens level. Several studies link HGS to general health, reproductive success, immunity but those linking HGS with oxidative stress (OS) are still limited. In this study we try to verify the OHH on a group of 158 healthy men aged 29 - 44. HGS was measured from each hand by dynamometer (the maximum value was used). Serum levels of DNA/RNA oxidative damage markers were measured by ELISA. Testosterone levels, BMI, smoking status, supplements use, sport activity and chronic illnesses were also controlled. OS markers were not related to HGS (also when controlling for confounders), but were marginally significantly related ($r = -0.14$, $p = 0.077$) to testosterone level. Our results do not confirm OHH assumption in the studied sample. OS levels might be, however, insufficient to evaluate the biological condition, as individuals with different ROS production might present similar OS levels (depending on individual's antioxidant potential). Further studies testing OHH should include the levels of both OS and antioxidants. Founded by National Science Centre, Poland; grant no 2017/27/B/NZ8/00500

P28. Pollination in a big city - pollen grains movements in the strict city center during different parts of the flowering season

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Cities are the fastest-growing ecosystems, with the increase of urbanization influencing many ecological interactions, for example, pollination. We still do not fully understand the influence of urbanization on this plant-animal interaction. Our research was the first attempt to track pollen grain movements in urbanized areas using quantum dots and the first study testing the frequency of pollinators' visits in isolated patches of urban greenery in different parts of the flowering season. We studied *Fritillaria imperialis* (early spring) and Hemerocallis sp. (midsummer). Study sites, located in the city center (Warsaw), were islands of green areas surrounded by impervious areas. The frequency of pollinators visits differed in the flowering season and early in the spring was positively correlated with increasing temperatures. Our study showed frequent pollen transfer between small, isolated patches with flowering plants. We observed a correlation of pollen movement between populations with the proportion of green areas, however, it depended on the species and the direction of pollen transfer. Pollen deposition on the stigma was strongly influenced by the pollinator behaviour, i.e., in the case of plant species with pollen grains used as a primary reward for pollinators (*F. imperialis*), pollen deposition on stigmas was several times higher when compared to the species with nectar as a primary reward (Hemerocallis). New tools that allow tracking pollen grains movements may help to enhance the role of cities in biodiversity conservation and demonstrate that formulating recommendations for wildlife conservation activities in cities requires a broad and innovative approach to the problem.

P29. Studying bacterial-fungal interactions (BFI) of the dry-aged beef (DAB) improves understanding of microbiome functioning

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Fungi and bacteria often co-occur in different environments, forming habitat-specific microbial communities, sometimes creating multi-species consortia. Although understanding how these microorganisms function in the network and how they adapt to specific environmental conditions is crucial in learning how they function in the environment, it remains poorly studied. Fungi from the Mucoraceae family are known to form close interactions with bacteria. Some of them (*Thamnidium, Mucor,* and

Helicostylum) are also commonly isolated from protein-rich substrates, such as dry-aged beef (DAB). Dry aging is a method of storing beef under refrigeration and exposed to air flow over several weeks. This process occurs partially due to the enzymatic activity of microorganisms. Although some colagenses encoding genes were detected in symbiotic bacteria, little is known about the bacterial-fungal succession of DAB. Therefore, we decided to find how the occurrence of *T. elegans, M. flavus and H. pulchrum* fungal strains affects the bacterial communities of DAB after 28 days. The changes in prokaryotic microbiome were monitored using next generation amplicon sequencing and bioinformatics pipeline. Results indicate that the taxonomic composition of bacteria is variable. Proteobacteria and Firmicutes, naturally occurring on meat, dominated across the samples. Unidentified species were also abundant, especially with *M. flavus*. Although no human pathogenic bacteria were identified in analysed samples we tested the survival of *Listeria monocytogenes, Salmonella enterica* and *Lactobacillus plantarum* on DAB inoculated with fungi. Mycobiota developing on DAB do not inhibit bacterial growth. Moreover, *T. elegans* WA18081 promoted bacterial development. Hyphae can serve as an additional source of water for bacterial cells survival, likewise bacteria cells transmission can occur via fungal highways. Although the stable fungal communities found on DAB are affecting variable bacterial ones, this relation seems to be much more complicated than expected. The further understanding of this interkingdom interaction may also have industrial applications.

P30. Does daylight affect multimodal parent-offspring communication in Great Tits?

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The evolution of nestlings' detectability and signaling is complex. Nestlings solicit parents' attention by vocalization, movement, and gaping. Communication between offspring and parents is multimodal, using acoustic and visual channels. So far, we know that parental feeding activity is affected by mouth coloration. Color perception in cavities is limited due to low light levels, which may hinder the feeding process. Under dim lighting conditions, parents may need more time to assess nestling needs properly, which may reduce provisioning efficiency. This study aimed to test whether increased lighting conditions significantly affect the visual and vocal components of begging in great tit nestlings. We assumed that different luminosity in nest boxes might affect the use of different communication channels between parents and offspring. Considering the proximate mechanisms of signaling, we expected that, in changing lighting conditions, nestlings could exploit innate parental signal preferences in different ways. The use of particular communication channels may depend on the energy costs associated with a given type of signal propagation within different lighting conditions. We expected that, if possible, nestlings would reduce the less profitable signals in particular light conditions (e.g. paler flanges due to intentional pigments retraction in darkness). At the same time, we expected differences in vocal signaling between dark and bright environments. We also tested whether the change in signaling is flexible and occurs within a couple of days. We measured the response of 8 and 12 days-old nestlings of Great Tits. The study was financially supported by the Polish National Science Center no. 2020/37/N/NZ8/01345.

P31. Genetic alterations in the insulin/TOR pathway might not lead to coordinated changes in cell size among different tissues in *Drosophila melanogaster*

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Size is the fundamental feature of any cell; millions of years of evolution have led to its enormous variance across the Tree of Life. Although we still do not fully understand how cell size is determined on a molecular level, such mechanisms are now beginning to be uncovered. Recent studies have revealed the signaling pathways responsible for adjusting and maintaining the cell size of an organism, e.g. aberrations to insulin/TOR signaling may result in diseases, including diabetes and cancer. Cell size plays a huge role in evolutionary and phenotypically plastic changes in organismal body size, suggesting that cell size is under selective pressure in nature. However, we still lack a convenient model organism to study the role of cell size in the physiological and evolutionary ecology. We used *Drosophila melanogaster* flies with precise genetic alterations in the insulin/TOR pathway to check whether cell size undergoes coordinated changes in different tissues on an organismal-wide level. Our results show that Rictor Δ2 flies have smaller ommatidial cells in the eyes and smaller epidermal cells in the leg and the wing, while w*Mnt1 flies possess bigger cell sizes in the above-mentioned tissues when compared to the respective controls. Interestingly, cells of dorsal longitudinal muscles in the thorax did not appear to respond to the genetic alterations in either of the groups. The study was supported by NSC grant to MCz (OPUS 2016/21/B/NZ8/00303).

P32. Does thyroid hormones metabolism affect the development of polymorphism of winter phenotype in Siberian hamsters *Phodopus sungorus*?

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Wide spectrum of winter phenotypes can be observed within one population. Individuals responding to changes in photoperiod reduce gonads, change fur and use torpor, whereas nonresponding individuals maintain summer phenotype. Although this phenomenon is long since studied, the mechanism of its development is largely unknown. Since many of seasonal adjustments (including cessation of reproduction and heterothermy) are

determined by changes in thyroid hormones level, we hypothesized that polymorphism of winter phenotype is related to the differences of thyroid hormones metabolism in brain. To test this hypothesis, we used Siberian hamsters *Phodopus sungorus*, model species for seasonality research. We set 4 experimental groups, 10 individuals each, acclimated either to long day (control group), or to short photoperiod (experimental groups). After 14 weeks of short day acclimation we choose full responders (white fur and torpor use), nonresponders (grey and no torpor use) and partial responders (white fur but no torpor use). All animals were sacrificed and hypothalamus was dissected. We measured expression of dejonidases (dio), monocarboxylate transporter 8 (mct8), thyroid releasing hormone (trh) and somatostatin (srif) because of their importance in seasonal response. We found that dio2 was downregulated and dio3 was upregulated in full responders and partial responders, which is typical for SP response in this species. However, nonresponding individuals differed neither from control group nor from other phenotypes. Groups did not differ in mct8 and trh expression, whereas Srif was downregulated in SP, in all phenotypes. We also observed much higher variability of gene expression in nonresponders than in full responders. Lack of differences between nonresponders and control animals, similarity between nonresponders and other phenotypes and high variability within nonresponders suggest that photononresponsiveness in Phodopus has various backgrounds. This study was supported by the grant #NCN 2019/32/T/NZ8/00481.

P33. Palaeogenomics of the Central European refugia: spatio-temporal dynamics of the arctic-alpine flora between northern and temperate latitudes – a new project

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Our poster introduces a new project focused on the role of the Central European mountains (Carpathians, Sudetes) as cold- and warm period refugia and as postglacial colonization sources for cold-adapted plants in the late Quaternary. The project relies on exploring both the contemporary phylogeographical structure of selected species and the ancient genetic data acquired from mountain lake sediments in the Tatra Mts. and Karkonosze Mts. We aim to explore the role of the Central European (CE) mountains by two main approaches: (i) using metabarcoding of DNA in ancient lake sediments to gain insight into Last Glacial to Holocene changes in plant communities and assess to what extent the CE mountains efficiently ensured a long-term resilience of the arctic-alpine biota; (ii) using DNA capture techniques applied on both modern samples and a chronoseries of ancient sediments, to assess the dynamics of intraspecific genetic lineages of arctic-alpine species in time and space, and to test the role of the CE mountains in the maintenance of rare, relic lineages, and as sources of postglacial colonization. First contemporary phylogeographical data from Dryas octopetala, one of our model species, show a key importance of the Carpathians for the species' lineage diversity in Europe as this range harbored two distinct lineages absent from western Europe albeit with a limited role in postglacial recolonization of the North. First sediment cores were obtained in winter 2022 in mountain lakes of the Tatra Mts. and preliminary insight into the past communities and population genetic composition of selected species, to confront the contemporary patterns, is expected in 2023. Intraspecific data from the CE mountains will be explored in a larger geographical context through international collaboration. Research financed by the National Science Centre in Poland (project no. 2020/37/B/NZ8/03307).

P34. How do seed limitation and negative density dependence shape the recruitment of native and invasive tree species?

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Alien species often outcompete native species at the recruitment stage. Enemy Release Hypothesis (ERH) suggests that the release from natural enemies that alien plants experience in the new range could determine this advantage. Yet, the ability to tolerate or compensate for the damage can be more important than the sheer magnitude of consumption. The aim of this project is to evaluate how seed limitation and density dependence shape the effect that mortality caused by herbivores has on the recruitment process of alien vs native tree species. We hypothesize that the recruitment advantage of invasive alien trees, if occurring, can be due to strong seed limitation and weak density dependence and/or to damage tolerance. Therefore, invasive alien trees could have an advantage during recruitment even if ERH (measured by the magnitude of consumption) is not supported. Our study is ongoing. We are performing three different tests. 1. Alien red oak vs native sessile oak seed rain measurement: we used acorn traps to compare the magnitude of seed rain produced by red oak and native oak. In 2021, alien red oak produced significantly more acorns than native sessile oak (p-value = 0.007). We will repeat the data collection for two more years. 2. Red oak vs sessile oak seed experiment: for each species, we added seeds at 10 different density levels crossed with 2 treatments (granivore exclusion and control) to measure the degree of seed limitation and mortality caused by granivores. We will collect data from this experiment in late June 2022. 3. Multispecies seedling experiment: in autumn 2022 we will plant seedlings of several common native and invasive trees at 9 different densities crossed with 2 treatments (herbivore exclusion, control) to measure the extent of seedling mortality caused by density dependence and herbivores.

P35. Symbiotic Entomortierella – a supplementary food source for red wood ants (preliminary studies)?

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Entomortierella is one of the fungal genera recently determined in the study of the Mortierellaceae phylogeny. The etymology of the name: entomon- refers to a frequent isolation of this genus representatives from insects. However, a determination of any explicit insect-Entomortierella interaction is still missing. In our previous studies on the mycobiota of *Formica polyctena*, we have shown that species of Entomortierella are present in the ants' environment. Precisely, we have isolated those strains from: the ants' cadavers, infrabuccal pellets, and mound material. Interestingly, it is known that many species of Entomortierella produce a great abundance of enlarged cells filled with liquid droplets, which could possibly work as a supplementary food source. However, the questions of ants feeding on Entomortierella hyphae and such hyphae nutritional value for ants are still open. In order to find answers for those questions we are using both behavioral and biochemistry approach. In the behavioral part of the study, we analyzed and compared *F. polyctena* behavior towards hyphae of E. beljakovae and closely related soil-borne M. alpina. In the field, ants from 25 nests were introduced to fungal colonies growing on two different media: one rich with aminoacids and the other rich with glucose. In the rich with aminoacids setup, we have observed *F. polyctena* workers feeding on E. beljakovae hyphae and a tendency of ants to prefer this hyphae over M. alpina. In the biochemistry part, using HPLC method we are analyzing and comparing sugars and aminoacids profiles of ant-isolated and soil-isolated strains of both E. beljakovae and M. alpina. Observed in our study F. polyctena ants' interest towards Entomortierella representatives suggest an occurrence of a previously unknown ant-fungal interaction, which needs further research to be fully understood.

P36. Hybridogenesis outside metazoan world? Possibility of appearance in ciliates

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Hybridogenesis and kleptones are disputed phenomenons by embryologists, evolutionary biologists, cell biologists and geneticists. These phenomena were detected and documented in amphibians (especially Pelophylax), fishes (Tropidophoxinellus and Cobitis) and ants (Cataglyphis, Wasmannia, Pogonomyrmex). However hybridogenesis and kleptones were never described outside metazoan world - lack of such effects dispersion would be surprising due to many cytogenetics process documented in plants and Alveolata - for example, in ciliates. In last mentioned taxon it observed processes like conjugation. Interspecies conjugation was sparsely noted and, even, never experimentally inducted. Taking into consideration confrontation of two different genetical pools, kleptone origination is possible. During reconstruction of macronucleus after deleting IEES, one pool could be used to creating somatic genome. Ciliates has also great possibilities of dispersion - even in aerosole, what increase probability of confrontation diverse genetic pools. This issue can be studied experimentally on model species like Paramecium and Tetrahymena by creating chimaeras, manipulating semiochemicals or modulating developmental processes using RNA interference. In natural conditions processes of hybridogenesis and kleptone origination may have appeared on borders of species distribution and/or environments, where different species could come in contact with themselves - borders of oceanic fluxes, oceanic deeps and high attitude mountain lakes. It will be very odd, if hybridogenesis is limited to some metazoan (and mainly vertebrate) taxa.

P37. Mystery of moa birds - how many species lived in New Zealand

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Moa birds (Dinornithiformes) were flightless birds from New Zealand. Extinction treaded between 15-th and 19th century due to overhunting by native people, like many examples of Quaternary megafauna. Nowadays ten species (and one fragmentary specimen from Saint Bathans fauna) are grouped in 3 families and 6 genera. However number of these taxa is questionable. Moa probably had sexual dimorphism with bigger females like some Charadriiformes (as Jacanidae, Phalaropus and *Charadrius morinellus*). This fact may suggest polyandric reproduction system. Smaller males could be described as different species - such a mistakes took place in past. Therefore additional studies in morphology (especially morphometry and allometry) and paleo-genetics (collagen mass spectrometry and ancient DNA analysis) are essential to verify taxonomical studies of moa species and genera. Only then complete reconstruction of Dinornithiformes phylogeny will be possible.

P38. How to persist in a changing environment? Evolution of niche breadth in response to environmental heterogeneity

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All organisms face environmental variability. In extreme cases, habitats may become temporally entirely unavailable, e.g. due to seasonality, pulsed resources, or human activity. Explaining the mechanisms that allow persistence in variable environments is crucial for understanding ecosystems functioning and biodiversity maintenance. We addressed this important issue using a wheat pest of global economic importance, commonly known as wheat curl mite. Our goal was to understand how environmental heterogeneity influences wheat curl mite niche breadth expressed as its ability to utilize different host plant species. We subjected a mite population to replicated experimental evolution in a single-host environment, or in an alternation between two plant species. Next, we estimated fitness of evolving populations on a range of host plant species. Moreover, we measured mite's host-acceptance and dispersal propensity, and we characterized the seasonal pattern of host infestation based on long-term field-collected data. Our results revealed that the niche breadth evolved in response to the level of environmental variability. Stable host environments led to specialized phenotypes. The fluctuating environment expanded the niche breadth by increasing the ability of the mite to utilize different plant species, including novel ones. However, repeated experimental evolution on non-cereal host, both in stable and alternating conditions, showed that adaptation to this host is not possible. Thus, environmental heterogeneity does not always lead to the evolution of flexible host-use generalist phenotypes. Instead, a host can act as a sink habitat functioning as a temporal stepping-stone allowing for populations' persistence. Altogether, we showed that both generalization and source-sink dynamics may promote the long-term populations' persistence in variable environments. The study was financially supported by the National Science Centre in Poland (grants no. 2016/21/B/NZ8/00786 and 2017/27/N/NZ8/00305).

P39. Domain architecture shows extensive mosaicism of phage proteins engaged in host tropism

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For milions of years bacteriophages have been forced to keep the pace with evolution and diversification of bacterial receptors. We hypothesized such coevolution has shaped the domain architecture of phage proteins engaged in host tropism, like receptor-binding-proteins (RBPs). To address it, we downloaded representative genomes of phages from NCBI RefSeq and created deep HMM profiles for all proteins therein using UniClust30. We used remote homology detection (HHblits) for an all-by-all profile-profile comparison, protein domain detection using Pfam and putative function assignment to each profile using homology detection with three complementary approaches (PHROGs, GOs, PhANN). Our results show that the function of a structural protein often cannot be uniquely determined and, when using low coverage threshold, some functions (eg tail fibres and spikes) cannot be distinguished using homology-based approaches. We found that such functional ambiguity is related to domain sharing between proteins from different functional categories. We then systematically compared domain architectures of structural proteins from various functional categories. Domains found within these proteins were shared between otherwise dissimilar proteins and co-occurred in multiple combinations. Such understood mosaicism was more frequent within RBPs than other structural components like capsids or baseplates. To account for under- or overrepresentation of domain databases, we carried out an all-by-all comparison between phage proteins and found that sharing fragments between otherwise dissimilar proteins is more frequent within RBPs than other structural proteins. Altogether these results highlight the importance of the underlying protein domain architecture in RBPs in helping phages to adapt to novel bacterial surface receptors.

P40. Does it always take two to tango? Autonomous pollination in an invasive *Spirea tomentosa* L.

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The most well-known influence of invasive plant species on plant communities involves direct competition for light, nutrients, water or/and space. There is little information available about their effects on other trophic levels such as mutualistic interactions, e.g., between plants and pollinators. Since pollination is a phenomenon commonly found in almost all terrestrial ecosystems, the potential role of an invasive species may be very important. In our study we examined *Spiraea tomentosa* L. (Rosaceae), a partially invasive North American species, associated mainly with wetland habitats. We conducted our experiments on three populations in Lower Silesian Forest (Bory Dolnośląskie, Poland) in the summer of 2021. The breeding system and pollination biology of this species are still not well studied. We also do not know the potential influence of this species on the local plant-pollinator network. Our results show that *S. tomentosa* is a self-compatible species, with a great potential for spontaneous self-pollination, all studied inflorescences produced seeds without pollinators. In some studied populations we did not record differences between fruit set in control and spontaneous autogamy. Our results indicate also a low potential for influencing local plant-pollinator networks. The frequency of visits to *S. tomentosa* flowers was very low - we recorded only 57 visits for 5400 minutes of recording. Such a low frequency of insect visits may be related to the fact that studied species do not offer nectar and flower visitors collect only pollen.

P41. Always on the safe side. Autonomous selfing in *Fritillaria persica* L. - how much pollen stays on the stigma and what is the role of the potential pollinators in pollen transfer

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Understanding the reproductive biology of a given species is crucial for predicting population development and for efficient conservation activities. One of the interesting mechanisms is autonomous selfing, which occurs usually when anthers touch stigmas or when pollen falls onto the stigma of the same flower. Typically, this ability involves innovations in flower morphology and development, e.g., changes in the size or in the arrangement of reproductive elements. We studied the ability of autonomous selfing in two natural populations of *Fritillaria persica* L. (Liliaceae) in Israel (Judaean Desert and Hakoach eucalyptus forest) in spring 2022. *Fritillaria persica* is a herbaceous perennial and geophyte, with big green or purple inflorescence. In bell-shaped flowers of this species anthers move towards the style while anthesis and finally deposit pollen on the stigma. With the use of quantum dots we tracked pollen deposited autonomously on the stigma and pollen transfer within and among inflorescences. To better understand the reproductive system of *F. persica* we also tested the potential for self-pollination and plant-pollinator interaction. Our results show that the plant is self-compatible and pollen grains deposited autonomously on the stigma are often numerous and may play an important role in pollination. Less than half of the spontaneously deposited pollen stayed on the stigma, so we assume that it may play a dual role: (i) reproductive assurance and

(ii) pollen presentation. Our data also show that pollinators were more active in the eucalyptus forest, where we found *Apis mellifera* beehives, than in the Judaean Desert.

P42. Interactions between wolf and domesticated dog based on scent marking: experimental study in Kampinos National Park.

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The modern wolf (*Canis lupus*) and its domesticated form the dog (*Canis lupus familiaris*) share not only a common origin, but also a large part of the behavior. Thanks to species protection, the wolf population has increased and now wolves are observed in all bigger forest complexes in Poland. Dogs have become the most common carnivore and their population is still increasing. This led to higher possibility of meeting and interacting between these two carnivores. However, the potential negative impact of dogs on wolf conservation is still poorly understood. Scent marking is one of the most important forms of communication for canids. It is used for determination and protection of territories, synchronization of reproduction, establishment of hierarchies in groups, and formation of new pairs. Since both the wolf and the dog scent-marking plays an important role in communication, the presence of dogs in wolf territory can modify the behavior of wolves. To check it, we conducted an experiment. We tasted the presence of scent stimuli from the "new wolf" and "new dog", as well as water as a control, on the behavior of wolf families living in Kampinos National Park. Results showed that wolves respond less to scent marking from a dog than to scent marking from a wolf, but more strongly than to a control stimulus. These results suggests that the high density of dogs on wolf territory, can negatively affect the behavior of the living there wolves. All effort from the territory's residents to respond to the scent marking from the dog cannot bring the same effects as in the case of reactions to scent marking from the wolf. This indicates that managing dogs entering forest areas requires quick consideration by national authorities.

P43. Factors affecting mushroom production in mixed deciduous forests of Białowieża

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Mushroom picking is a popular activity both in economically developed countries, where their harvesting is an important recreational activeness and in developing countries, where mushrooms often are a key food and source of income. The global mushroom market was valued at USD 45.8 billion in 2020 and is expected to reach 63.24 billion by 2027. They also might become a critical source of food in a circular economy, playing a role in climate change mitigation and in buffering food shortage, as they are commonly available and contain essential nutritional substances (e.g. a complete essential amino acids profile, source of antioxidants). Despite their high importance, only a few species are cultivated, whereas most edible mushrooms are still harvested in forests. Therefore, it is crucial to understand factors affecting mushroom production. Many studies showed the key effect of weather, soil properties and stand characteristics on mushroom production, but still little is known about how tree species diversity and identity impact it. We conducted our research in Białowieża Forest on the network of plots designed to maximize tree diversity differences and minimize all other environmental factors. We collected mushrooms every ten days for two yielding seasons (July-half of November 2020-2021) to study ecological factors influencing their production. We confirmed the effect of soil properties (pH) and stand characteristics (stand basal area and cover of understorey) on mushroom productivity. There was also a strong relationship between mushroom species richness and mushroom productivity. However, we didn't reveal the direct influence of tree diversity on mushroom production. This influence was mediated via species richness, which was shaped by tree species identity and diversity, and in turn affected production of mushrooms.

P44. The effect of ambient temperature and food availability on testosterone level, basal metabolic rate, and sexual maturation in male bats

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Basal metabolic rate (BMR) defines a minimum level of energy and constitutes a large part of animal total energy expenditures. Animals' survival depends on the balance between energy input and output. The energy budgets are especially challenged during the reproduction and therefore any unfavorable change in natural environment may be critical in this period. To save energy male bats use torpor, however the decrease in body temperature may slow down processes related to sperm production. We tested the influence of two crucial environmental factors: ambient temperature and food availability on testosterone level, BMR, torpor use and rate of sexual maturation (based on testicular growth and epididymal filling). We conducted two experiments on male bats (*Vestpertillo murinus*) at the time of sperm production. In the first one we manipulated food availability (high food and low food), and in the second one ambient temperature (warm 25°C, cold 10°C). The well fed group had the highest testosterone level and highest body mass, and it was also the only one which finished the process of sperm production in a course of experiment. The testosterone level did not influence torpor use in any group. Across both 10°C and 25°C the natural testosterone level positively correlated with BMR at the early stage of sperm production. We discovered that changes in ambient temperature and food limitation slow down the process of sexual maturation in the current year. Facing the energy restrictions males decreased body temperature and testosterone production which probably inhibit the spermatogenesis.

P45. Concerted decrease in body and cell size in adult *Drosophila melanogaster* flies induced by rapamycin supplementation of larvae: similar pattern among five cell types

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Cellular composition of a body is an apparent feature of all organisms on Earth. Organisms differ in cell size between populations and species as a result of environmental conditions and evolution. This suggests that cell size is not a neutral trait. It can affect the functioning of an organism and thus undergo adaptive evolution, which is postulated by the theory of optimal cell size (TOCS). However, it is not clear whether cell size changes can occur in a coordinated way in all cell types in a body or whether they occur independently in different cell types. To address this scientific question, we measured cell size in five cell types: wing and leg epidermal cells, ommatidia, flight muscle cells, and epithelial cells that form Malpighian tubules in two phenotypes of adult *Drosophila melanogaster* flies with environmentally induced changes in cell size. To induce a small size phenotype, we used food supplemented with rapamycin during larval development. Rapamycin, an immunosuppressive drug used in human pharmacology, inhibits the TOR (target of rapamycin) pathway responsible for cell growth and proliferation. Our results showed that rapamycin supplementation reduced body size and cell size in all cell types, suggesting that the TOR pathway may play a role in coordinated changes in cell size and that such changes may contribute to changes in body size. The study was supported by the National Science Centre Poland grant to MC (OPUS 2016/21/B/NZ8/00303).

P46. Testing for the mechanisms of balancing selection maintaining 6Pgdh polymorphism in the bulb mite

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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 Phosphogluconate 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. Firstly, mites were evolved at different temperatures under equal sex ratio (24°C, 20°C, 18°C,) and at different sex ratios (male biased, equal sex ratio, female biased) at 24°C. Both temperature and sexual selection intensity affected the strength, but did not reverse selection on 6Pgdh (the S allele was favored in all the treatments). Then, we test for the effect of lower temperatures and temperature (18°C vs. 12°C) by sex ratio (female biased, equal sex ratio) interaction in a fully factorial crossed design. We also checked the change in F frequency after one generation at higher ranges of temperatures and observed a slight (but not significant) increase in F frequency at 8°C and decrease at 24°C. Our results suggest that both temperature and sexual selection intensity contribute to selection on 6Pgdh.

P47. Genomic similarities and differences among closely related bacterial strains infecting ants, beetles, fish, and whales

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Microbes dramatically affect the biology and evolution of their animal hosts, and these effects can range from pathogenic, through commensal, to mutualistic. We know that the effects of infections with related microbes can vary, depending on environmental conditions, but also on their host organisms. While some microbes have co-evolved with their host and become highly specific, others have a broad host range, colonizing different organisms and environments. Weissella ceti (Firmicutes: Lactobacillales) has a strikingly wide host range. Originally isolated from a dead beaked whale, it was later described as a pathogen of rainbow trout, and we have found it to be abundant in colonies of neotropical army ants and their associated myrmecophile beetles. Here, we asked about the genomic properties that allow this microorganism to colonize such different hosts. For this, we compared previously published and new genomic sequences of Weissella ceti strains from whale, trout, ants and their associated beetles. At 1.3-1.4 Mb, the genomes of the characterized strains are smaller than those of other Weissella species. Phylogenomic analyses, and broader comparisons based on marker gene sequences, revealed two distinct clades: one grouping strains from whale and trout (and some beetles), and another, grouping ants and most beetles. Functional comparisons revealed the ant-derived strain has more carbohydrate metabolism genes, lacks one gene related to DNA transport and genes for antibiotic resistance and cell regulation, commonly found in pathogens. Ant Weissella also lacks transposase sequences present in the other strains. These functions could offer some insight into the versatility of this microbe. Our data demonstrate that closely related microbes may colonize unrelated and physiologically distinct species from completely different environments, and highlight traits that may influence broad host range and infection effects.

P48. The role of thermo-oxygenic environmental conditions in shaping biodiversity patterns

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The effect of temperature on the local and global patterns of biodiversity is widely studied and discussed. Much less space is devoted to oxygenic conditions. Yet, oxygen availability to living organisms is strictly dependent on thermal conditions. There is a growing number of empirical evidence that some biogeographical rules, such as those focusing on body size response to temperature, are in fact driven by oxygenic conditions. The body size response to temperature-dependent oxygenic conditions are specifically apparent in small ectotherms living in aquatic systems, such as rotifers. The empirical evidence collected so far seems to be sufficient to infer that, at least in this groups of organisms, oxygen plays at least as important role in selection for body size, as temperature. There is a hot scientific debate, however, on how universal such responses are across different groups of organisms. The common suggestion is that environmental oxygen availability should be included in both, large scale experiments and theoretical modelling, if we are to understand the effect of global warming on organisms, communities, and ecosystems, and to possibly prevent some negative changes.

P49. Ecological and evolutionary implications of interspecific protective associations in birds

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Interspecific protective nesting associations in birds are one of the most fascinating examples of avoidance of predation pressure in nature. The literature is replete with papers describing this phenomenon, but our knowledge still contains gaps that make it difficult to thoroughly understand the mechanism by which such relationships are formed. In general, these positive biotic interactions imply the nesting of small, non-aggressive, cryptic bird species under the "protective umbrella" of larger, usually colony-breeding, and more aggressive species. Here, we verify the hypothesis that the probability of establishing this type of association is related to life history traits, population vital rates, and phylogeny. We performed a literature search to identify pairs of species involved in this type of interaction, then we used the AVONET database (Tobias et al., 2022) as a source of trait data, and the Polish Red List of Birds (Wilk et al., 2020) as a source of population vital rates data. Our preliminary analysis applies to a subset of species (breeding in Poland), but it can be extended to check if results represent a more general rule of thumb. The study was supported by the National Science Centre, Poland (grant no. 2018/29/B/NZ8/00066).

P50. The effects of hypoxia on threshold food concentrations in different Daphnia species

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Numerous studies have revealed an apparent decrease in individual body size among a variety of aquatic ectotherms as well as the mean body size of their populations and communities at elevated temperatures. This global temperature-size pattern is ubiquitous both spatially and temporally and is evidently due to the decrease of competitive abilities of larger- over smaller-bodied species. However, the mechanisms behind this decrease are still not fully explored - many studies suggest that, at least in case of zooplankton, the production (i.e. growth and reproduction) of individuals of larger species is more limited due to their increased oxygen demands and greater susceptibility to decreased oxygen concentrations at elevated temperatures. To test this, we performed

several experiments on the food thresholds (which is a proxy for competitive ability) of 6 zooplankton (Daphnia) species differing in body size: *D. magna, D. pulex, D. pulicaria, D. galeata, D. longispina* and *D. cucullata* at high and low oxygen concentrations (8.0 and 3.0 mg O2 L-1). Contrary to our hypothesis, oxygen deficits favoured larger-bodied species, which may be attributed to their better evolutionary adaptations to oxygen depleted environments. Our results suggest that hypoxic conditions at elevated temperature alone are not responsible for the temperature-size pattern observed in zooplankton (although we cannot exclude the possibility that it plays a significant role when combined with other size-selective factors such fish predation). The research was financed by the National Science Centre, projects no. 2016/23/D/NZ8/03532, 2019/35/B/NZ8/04523 and 2020/37/N/NZ8/04099.

P51. Density-dependent effect of introduced fallow deer (*Dama dama*) on the diet composition, prey preferences and spatial ecology of the grey wolf (*Canis lupus*)

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The gray wolf (*Canis lupus*) was extirpated from western Poland, but since enforcement of strict protection in 1998 recolonized most of the suitable habitats. One of such recently recolonized areas is Tuchola Forest, a large forest complex in north-western Poland, characterized by a very high density of introduced for hunting purposes, allien medium-sized ungulate species, fallow deer (*Dama dama*). We investigated how the fallow deer density affects wolf diet composition, prey preferences patterns as well as dynamics and spatial organization of the local wolf population. We found that fallow deer was the preferred wolf prey. In regions of its highest density, fallow deer constituted ca. 35-40% of ungulate biomass consumed by wolves. Unsurprisingly, the share of other ungulates in the wolf diet decreased with the increase of fallow deer share in the ungulates community. However, the size of this effect differed between the prey species: while the biomass of consumed roe deer (*Capreolus capreolus*) decreased only slightly, the decrease of red deer (*Cervus elaphus*) consumption was significant. Concordantly, the Jacobs' D selectivity index indicated that red deer was avoided by wolves in areas characterized by high fallow deer density, while when fallow deer was absent or present at very low densities, red deer was the preferred prey species, similarly as in other wolf diet studies from central Europe. Thus, it indicates that the introduction of fallow deer significantly alters the grey wolf dietary preferences and may affect grey wolf – red deer ecological relationship. Interestingly, we have found that the fallow deer introduction affects also wolf spatial ecology. The nearest neighbor distance between the core areas of wolf territories was the lowest (10,1 km) in the region where fallow deer density was the highest. Moreover, the rate of spatial overlap between adjacent wolf territories was positively correlated with fallow deer density.

P52. Does personality affect host's resistance to parasites and the cost of infestation?

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Hosts exploited by parasites need to defend themselves from energy loss. The first line of anti-parasitic defence against ectoparasites is behavior, such as self-grooming, that represents a crucial component of host's resistance because its cost is lower, it is faster and often more effective than immune defences. However, the plasticity of behavior is limited and shaped by animal's personality type: animals with different personalities may adopt different strategies to allocate energy and to fight parasites depending on their energetic budget and activity levels. For instance, for proactive, bold animal with high energy budget, the cost of infestation can be low enough to not invest in behavioral defences, meanwhile the shy reactive individuals may have to save energy from their overall lower energy reserves. Therefore, host's ability to kill parasites and impede their reproduction (measured as survival and egg production) can be also shaped by personality types. Moreover, the level of activity and tendency to explore the environment can affect how many parasites the animal harbors in its natural environment. I will present the results of laboratory experiments and field data on the possible link between host's personality and ectoparasite survival and reproduction using the model of 4 species of desert rodents parasitized by fleas and one forest species and its natural tick burdens.

P53. The effect of microplastics on the interspecific competition of Daphnia

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Microplastic pollution is currently one of the most intensely studied ecological issues. Numerous studies have estimated the distribution and concentration of microplastics in various environments and determine how they affect their inhabitants. Much less effort has been place toward assessing the possible effects of microplastics on the interactions between organisms, including interspecific competition. Our aim was to test the hypothesis that the presence of microplastics affects the proportions of individuals of coexisting species and the elimination rate of an inferior competitor. The hypothesis was tested in competitive experiments done in the absence and presence of spherical non-biodegradable polystyrene and polyethylene and biodegradable polyhydroxybutyrate in environmentally relevant densities. In each of the experiments, we used three different pairs of closely related planktonic species of the genus Daphnia composed of the superior and inferior competitor: *D. pulex* and *D. magna*, *D. magna* and *D. galeata*, *D. pulex* and *D. galeata.* The results support our hypothesis and demonstrate each microplastic type had a different effect on the density of the competing species. The presence of polystyrene and polyethylene lowered the density of the superior competitor in each of the three pairs, at least partially due to decreasing the number of adults with eggs but not their fecundity. The presence of the polyhydroxybutyrate, in turn, increased the population density of *D. magna* in the treatments with each of the two remaining species. Moreover, the presence of microplastics affected the elimination rate of the inferior competitor, i.e. polystyrene expedited the exclusion of *D. magna* by *D. pulex*, and polyhydroxybutyrate hampered the exclusion of *D. magna* by *D. pulex*. The results of our study suggest that long-term exposure to environmentally relevant densities of both non-biodegradable and biodegradable microplastics may affect the relative abundance of co-occurring species in zooplankton communities, and thus the functioning of aquatic ecosystems. The research was financed by the National Science Centre, project no. 2019/35/B/NZ8/04523.

P54. Preferences for the colour of artificial nest material in a Great Tit (*Parus major*)

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Tits (*Paridae*) are known to use anthropogenic materials for nest building. Mechanisms governing such behavior remain unclear. In this study we performed an experiment in which Great Tit females could choose between four colours of artificial nest material to use it as a nest lining. The study was performed in a woodland population of Great Tits nesting in nest boxes (n = 37). Equal amounts of red, yellow, blue and white samples of acrylic fibers ("artificial fur"), were evenly distributed in the study area prior to the nest building period. The use of each colour was assessed from photographs taken during egg laying period and expressed as a percentage of the nest area covered with a given colour. Acrylic fibers were found in 89% of nests (n = 33). We found significant differences in amounts of fibers of different colors used to build the nest lining. Females preferred red fiber more than yellow and blue ones. We discussed possible reasons and consequences of the pattern found.