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Book of Abstracts

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JAGIELLONIAN UNIVERSITY
IN KRAKOW

Institute of Environmental Sciences



POLISH ACADEMY of SCIENCES

Committee on Evolutionary and Theoretical Biology

Venue

Jagiellonian University, Natural Science Complex, Gronostajowa 7, Kraków

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Program

Thursday 19th September: registration and welcome reception in the evening

Friday, 20th September		Saturday, 21st September	
09:00-10:00	Plenary: Neil Metcalfe The origins and ecological consequences of variation in aggression and metabolic rate in fish	09:00-10:00	Plenary: Janusz Bujnicki RNA structure, function and evolution (a bioinformatician's view)
10:00-11:00	Plenary: Ewa Bartnik Evolution of mitochondria	10:00-10:30	coffe break
11:00-11:30	coffe break	10:30-10:50	Maciej Pabijan Body size and speciation rate in tropical frogs - a case study from Madagascar
11:30-11:50	Piotr Dawidowicz Climate change, costs of diel vertical migrations and size structure of lakes' zooplankton communities	10:50-11:10	Piotr Zieliński Nuclear genome integrity despite complete mtDNA replacement in newts.
11:50-12:10	Szymon Śniegula Variation in development rates in core and peripheral populations of <i>Lestes sponsa</i> - the importance of photoperiod	11:10-11:30	Krzysztof Spalik Is long-distance dispersal necessary to explain wide distribution of hydrophytes? Case study of hydrophytic umbellifers
12:10-12:30	Dawid Moroń Short-lived ants take greater risks during food collection	11:30-11:50	Jacek Radwan Evolution of polymorphism of MHC genes: simulation models
12:30-12:50	Paweł Koteja Multidirectional artificial selection experiment in a wild rodent, the bank vole: mimicking an adaptive radiation	12:00-13:20	lunch
13:00-14:20	lunch	13:30-13:50	Tereza Petruskova Ecological and evolutionary interactions of two closely related songbird species in their contact zone: the case of Nightingales (<i>Luscinia</i> spp.)
14:30-14:50	Grażyna Jasińska Trade-offs between reproduction and aging in women: biomarkers and confounders	13:50-14:10	Piotr Minias Habitat structure and evolution of distribution patterns in colonial birds
14:50-15:10	Łukasz Oldakowski Is the oxidative stress a proximate mechanism of reproductive costs?	14:10-14:30	Marta Szulkin RAD sequencing in a wild passerine bird: genetic structuring and signatures of selection in a phenotypic trait?
15:10-15:30	Barbara Pietrzak Evolutionary ecology of ageing in a clonal organism	14:30-15:00	coffe break
15:30-16:00	coffe break		
16:00-16:20	Eoin Duffy The role of sexual selection during adaptation to a novel, stressful environment	15:00-17:00	poster session
16:20-16:40	Magdalena Herdegen Strong association between heterozygosity and orange colouration in the guppy (<i>Poecilia reticulata</i>)		
16:40-17:00	Agata Plesnar-Bielak Sexual conflict explains the coexistence of alternative reproductive phenotypes in the bulb mite.	from 18:00	Collegium Maius guided tour and Conference Dinner

Evolution of mitochondria

Ewa Bartnik

Institute of Genetics and Biotechnology, Faculty of Biology, University of Warsaw
and Institute of Biochemistry and Biophysics, Polish Academy of Sciences

ebartnik@igib.uw.edu.pl

A long time ago a meeting of two organisms gave rise to the ancestral eukaryotic cell. One of the partners of the meeting, presumably a *Rickettsia*-like bacterium, had about 800 genes and was the ancestor of mitochondria. Originally the non-mitochondrial partner was presumed to have been a eukaryotic cell lacking mitochondria, but all known eukaryotes which lack mitochondria appear to have had them and lost them, so the other partner may have been an archaeobacterium. The result of this partnership was the progressive loss of genes from the mitochondrion to the nucleus and the reduction of the mitochondrial genome, as mitochondria increasingly became dependent on nuclear gene products for their function.

Both the size of the mitochondrial genome and the number of genes it contains encompass a wide range, from small mitochondrial DNAs in some yeasts to enormous ones in the cucumber family. The number of genes in the mitochondrial varies from several in some Protozoa to about 100 in the largest known genome in *Reclinomonas americana*.

The important question is why there still are mitochondria and why they have been retained in spite of losing most of their original genes. Several explanations have been proposed and will be discussed.

RNA structure, function and evolution (a bioinformatician's view)

Janusz Bujnicki

The International Institute of Molecular and Cell Biology, Warszawa

iamb@genesilico.pl

Ribonucleic acid (RNA) is a large group of biological macromolecules. Recently, numerous types of RNA molecules have been identified, beyond those involved in protein synthesis (i.e. mRNA, rRNA, and tRNA). It has been found that most of the human genome is transcribed into RNAs, of which only a small fraction is translated into proteins, and that non-coding RNA transcription is also pervasive in bacteria. These RNA molecules are involved in essential processes, in particular in regulation of gene expression at various levels, and they interact with coding RNAs, proteins, DNA, small molecules, and with each other, forming a very complex system of mutual dependencies. Not surprisingly, mutations in RNA molecules (beyond the protein-coding regions) have been implicated in various diseases.

The function of RNA and its ability to interact with other molecules depend on the RNA structure and dynamics, which in turn are encoded in the linear sequence of ribonucleotides. To understand the biology of a cell comprehensively, it will be necessary to learn the identity of all encoded RNAs and their molecular structures. Currently, various initiatives employ methods of high-throughput sequencing to obtain sequences of RNAs expressed in different organisms, different cell types and under different conditions. However, experimental information on structures of RNA molecules is currently very scarce, compared to e.g. proteins.

One of my goals is to understand how the sequences, structures, and functions of RNA molecules change in time. My research group works towards achieving this goal by developing new computational methods for relating RNA sequence and structure, and by performing a series of systematic comparative analyses of RNA molecules. Wherever possible, we verify the predictions experimentally for selected representative molecular systems. Based on these analyses, we intend to formulate general rules concerning RNA structure and evolution, and to relate these features to the corresponding features of proteins that are much better known.

In my presentation, I will describe results of one of such analyses, focused on *cis*-regulatory structural RNA motifs, an important class of prokaryotic RNA elements. They are often located in the 5' untranslated regions (UTR) of the mRNAs, and can sense or interact with cognate factors, including proteins, RNAs, small metabolites, or even temperature changes, to mediate transcription attenuation, translation initiation, or mRNA stability. A variety of *cis*-regulatory motifs have been identified and characterized, but many still await identification. This especially concerns RNA motifs, whose taxonomic distribution is limited or scattered, and those present in the context of evolutionary unrelated genes. We analyzed motifs present within the 5' UTRs of operons encoding ribosomal proteins and we identified a new regulatory system involving proteins S6 and S18. We also analyzed the patterns of *cis*-regulatory motifs in bacteria with reduced genomes

The origins and ecological consequences of variation in aggression and metabolic rate in fish

Neil B. Metcalfe

University of Glasgow

Neil.Metcalfe@glasgow.ac.uk

Why do some individuals have two to three times the ‘maintenance costs’ of conspecifics, how is this linked to behaviours such as aggression, and what are the consequences? In this talk I will consider the causes of these traits, the links between them, and their fitness consequences. Using evidence from my group’s work on salmonid fish, I hope to show that diverse factors (including maternal effects and early developmental conditions) contribute to variation in individual resting metabolic rate. I will also present evidence that an individual’s metabolic rate influences its fitness through various routes – e.g. through links with aggression (which influences its ability to obtain a territory), appetite, maximum rate of digestion and growth rate. However, these relationships are modulated by environmental conditions (e.g. food supply), suggesting that the fitness consequences of a given metabolic rate may be context-dependent. This may explain why variation in metabolic rate might persist in natural populations.

Climate change, costs of diel vertical migrations and size structure of lakes' zooplankton communities

Piotr Dawidowicz, Joanna Pijanowska

Department of Hydrobiology, University of Warsaw, Poland

p.dawidowicz@uw.edu.pl

Numerical simulation models predict that along climate change, the epilimnetic temperatures in temperate lakes will be higher than now, but will increase slower than air temperature, while hypolimnetic temperatures may even decrease, due to shortened duration of spring circulation. As a result, the surface-to-bottom thermal gradients will be steeper in those lakes. Using meta-analysis of the data published for *Daphnia*, we demonstrate that this change will strongly increase the costs of diel vertical migration (DVM), a behavioral antipredator defense that is shaped by the trade-off between higher predation risk at the surface and reduced growth in deeper waters. This, in turn, will elevate the threshold predation risk, below which the defenseless (i.e. nonmigrating) phenotypes, that do not pay the costs of predator avoidance, will be able to achieve higher fitness than the defended ones (i.e. vertically migrating). Ultimately, the large-bodied zooplankton species (such as *Daphnia*) that have to perform long-range DVM to avoid fish predation, will be replaced by short-distance (or non-) migrating, small-sized species.

The role of sexual selection during adaptation to a novel, stressful environment

Eoin Duffy

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

eoinduffy0000@googlemail.com

The interplay between natural and sexual selection has been widely studied, and although Darwin invoked sexual selection to explain traits that were clearly not naturally selected, it is unclear whether sexual selection facilitates adaptation to novel environments or not.

Here we examined whether sexual selection promotes adaptation to a novel environment using the powerful method of experimental evolution. Using a fully factorial design, we established replicate *Drosophila simulans* populations in both standard and novel temperature environments, both with and without sexual selection. We found that sexual selection did not promote adaptation to the novel environment and this does not appear to be due to intralocus conflict constraining the evolution of the sexes. These results therefore support the original view of sexual selection as a non-adaptive process. However after 30 generations of selection we did find significant differences in fecundity between mating regimes that demonstrate the same pattern in both standard and novel environments. We plan to further discuss these findings.

Evolution of polymorphism of MHC genes: simulation models

Maciej Ejsmond¹, Anthony Wilson², Jacek Radwan¹

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

² University of Zurich, Switzerland

jacek.radwan@uj.edu.pl

The extreme polymorphism that is observed in major histocompatibility complex (MHC) genes, which code for proteins involved in recognition of non-self oligopeptides, is thought to result from a selection pressure exerted by parasites (heterozygote advantage and/or frequency dependence), but mate choice for MHC-dissimilar males can also play a role. We investigated relative roles of these processes in maintaining MHC polymorphism in a series of computer simulations. We found that both heterozygote advantage and frequency dependence are capable to maintain polymorphism, but frequency-dependence retains new MHC variants more readily than heterozygote advantage. Mate choice for dissimilar mates generally increases the level of MHC polymorphism over that maintained by parasite-induced selection, but the effect depends on host population size. In small population, pressure from parasites tends to decrease, rather than increase MHC polymorphism, but mate choice may prevent the loss of genetic variation in bottlenecked populations.

Strong association between heterozygosity and orange colouration in the guppy (*Poecilia reticulata*)

Magdalena Herdegen, Katarzyna Dudka, Jacek Radwan

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

magherdegen@gmail.com

Good genes as heterozygosity hypothesis assumes that elaboration of male sexual ornaments is positively correlated with heterozygosity, and recent theoretical work indicates that such correlations are likely to arise in finite, structured populations. We investigated the correlation between multi-locus heterozygosity (MLH), estimated from 13 microsatellite loci, and male colouration in a natural population of the guppy *Poecilia reticulata*, a model species in sexual selection research. We found that MLH was a significant predictor of the relative area of orange colouration, a trait subject to strong female preferences in this species. The relative area of black, and the number of black and orange spots were not significantly correlated with MLH. We found no statistical support for so called local effects (i.e. strong effects of heterozygosity at specific markers on the traits measured), which suggests that orange colouration reveals genome-wide heterozygosity. The effect size of MLH-orange area association ($r=0.22$) exceeds those typically found for heterozygosity-fitness correlations, indicating that sexual ornaments may be reliable indicators of genome-wide heterozygosity under natural conditions.

Trade-offs between reproduction and aging in women: biomarkers and confounders

Grażyna Jasińska

Instytut Zdrowia Publicznego, Uniwersytet Jagielloński Collegium Medicum, Polska

jasienska@post.harvard.edu

Factors related to fertility play crucial, but often unappreciated, role in influencing health, aging and lifespan of modern women. Pregnancy, lactation and childcare are energetically expensive, especially in women with high lifetime reproductive effort and particularly those who are in poor nutritional status. Allocation of resources to support reproduction may cause their insufficient supply to other metabolic functions, resulting in compromised physiology, increased risks of diseases and, consequently, a reduced lifespan. Variation in health, aging and longevity among women may, therefore, be partially explained by differences in their lifetime reproductive effort.

I present an overview of a conceptual and methodological approach that could be used when studying tradeoffs between aging and reproduction. It is important to identify biomarkers of health and aging processes, account for polymorphism in genes having antagonistic pleiotropic effects and provide detailed description of confounding factors. Biomarkers of aging should include quantitative indices of inflammation, cognitive decline, and of muscle strength and risk factors of metabolic syndrome. Information about genotypic identity of participants (with respect to APOE, PPAR-gamma, and IL-10 loci) will allow controlling for pleiotropic relationships between reproductive effort and health status of women. Factors that may alleviate costs of reproduction (e.g. social status, nutritional status, help provided by neighbors and relatives) magnify physiological variation among subjects and should be explicitly controlled in statistical models. Preliminary results of the FEM-AGING study conducted in a rural population that utilizes this methodological approach will be presented.

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Multidirectional artificial selection experiment in a wild rodent, the bank vole: mimicking an adaptive radiation

Paweł Koteja, Katarzyna M. Chrząścik, Geoffrey Dheyongera, Agata Kołodziejczyk, Uttaran Maiti, Ewa Prawdzik, Agata Rudolf, Julia Wyszowska, Edyta T. Sadowska

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

pawel.koteja@uj.edu.pl

A central question in evolutionary physiology is how complex physiological adaptations evolve in response to natural selection operating on performance traits hypothetically associated with Darwinian fitness. Experimental evolution offers a powerful yet underutilized approach to test hypotheses concerning the correlated evolution of animal behavioural and physiological traits, which can underlie evolution of the complex adaptations. We established a selection experiment with lines of bank voles *Myodes* (= *Clethrionomys*) *glareolus* selected in three distinct directions: high swim-induced aerobic metabolism (A), the ability to cope with a low-quality herbivorous diet (H), and intensity of predatory behaviour towards crickets (P). Four replicate lines are maintained in each of the selection directions and unselected control (C). Significant differences between the selected and control lines appeared already after three generations of the selection. In generation 13, voles from the selected lines achieved 48% higher maximum rate of metabolism (A lines), lost 38% less mass in the 3-day test with low-quality diet (H lines), and attacked crickets 5 times more frequently (P lines), than voles from the unselected C lines. We observed several correlated responses to the selection in behavioral, morphological, physiological and life history traits. The selected lines provide a unique model to study genetic correlations between the physiological and behavioural traits, as well as cellular, biochemical and molecular factors underlining changes of the traits observed at phenotypic organismal level.

Habitat structure and evolution of distribution patterns in colonial birds

Piotr Minias

Zakład Dydaktyki Biologii i Badania Różnorodności Biologicznej, Uniwersytet Łódzki, Polska

pminias@op.pl

According to the classic theoretical predictions on resource acquisition in animals, individuals should be distributed in the environments so as to maximize their fitness. In colonial species there are two major components of nesting site attractiveness that may have important fitness consequences: central location within a colony and favourable physical characteristics. Consistently with the relative importance of these two components, distribution of birds within colonies should follow one of two theoretical patterns: central-periphery (high quality pairs nesting in the colony centre) or random (high quality pairs occupying sites of good physical quality independently of their location within a colony). It has been suggested that evolution of these spatial patterns in colonial birds was linked to heterogeneity of habitat, with central-periphery patterns prevalent in homogeneous habitats, and random patterns prevalent in heterogeneous habitats. To test for the correlated evolution of breeding habitat structure and within-colony distribution patterns I used continuous-time Markov model, which characterizes evolutionary changes in the selected pair of variables along each branch of the phylogenetic tree. The results support the hypothesis of a correlated evolution between the preferences for heterogeneous breeding habitats and random patterns of within-colony distribution. Breeding in homogeneous habitats and random distribution of pairs within the colony were identified as ancestral states in birds.

Short-lived ants take greater risks during food collection

Dawid Moroń

Instytut Systematyki i Ewolucji Zwierząt PAN, Polska

dawidmoron@poczta.onet.pl

Life-history theory predicts that organisms should alter their behavior if life expectancy declines. Recent theoretical work has focused on worker life expectancy as an ultimate factor in allocating risk-related tasks among the workforce in social insects. A key prediction of this evolutionary model is that workers with shorter life expectancy should perform riskier tasks. We tested this hypothesis, using laboratory colonies of the ant *Myrmica scabrinodis*. We modified foraging so that it differed in level of risk by manipulating distances, temperatures, and the presence of competitors on foraging patches. The life expectancies of foragers were shortened by poisoning with carbon dioxide or by injury through removal of their propodeal spines. Both treatments significantly shortened worker life expectancy in comparison with untreated ants. We show, for the first time, that foragers with a shorter life expectancy foraged under risk more often than foragers in the control group. Thus, a worker's strategy of foraging under risky circumstances appears to be fine-tuned to its life expectancy.

Is the oxidative stress a proximate mechanism of reproductive costs?

Łukasz Ołdakowski¹, Edyta T. Sadowska², Paweł Koteja², Jan R. E. Taylor¹

¹ Institute of Biology, University of Białystok, Poland

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

lukasold@uwb.edu.pl

According to life-history theory, investment in reproduction is associated with costs, which should appear as decreased survival to the next reproduction or lower future reproductive success. It has been suggested that oxidative stress may be a proximate mechanism of these trade-offs. We measured oxidative damage (OD) to lipids and proteins in breeding bank vole females from lines selected for high maximum aerobic metabolic rates (which also had high resting metabolic rates and food intake) and non-selected control lines in two experiments. In the first experiment OD was measured in females after rearing one and two litters, and in non-breeding females. Surprisingly, we found that OD to lipids in kidneys and muscles was actually lower in breeding than in non-breeding voles, and it did not differ between animals from the selected and control lines. Thus, contrary to our predictions, females that bred, suffered lower levels of oxidative stress than those that did not reproduce. We got similar preliminary results from the second experiment in which we manipulated number of offspring in 4 consecutive litters of each female. In one group of females, each litter was enlarged with 2 pups, and reduced to 2 pups in the other group. After weaning 4 litters, females with enlarged litters had lower OD than females with reduced litters and non-breeding females. The OD did not differ between animals from the selected and control lines. Our results do not support the hypothesis that oxidative damage to tissues is the proximate mechanism of reproduction costs.

Body size and speciation rate in tropical frogs - a case study from Madagascar

Maciej Pabijan¹, Katharina Wollenberg², Miguel Vences³

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

² Department of Biogeography, Trier University, Germany

³ Zoological Institute, Technical University Braunschweig, Germany

maciej.pabijan@uj.edu.pl

Speciation rate is potentially influenced by a multitude of intrinsic and extrinsic factors, however, it is ultimately a process occurring at the population level. We evaluated the contributions of five variables thought to influence speciation in frogs (body size, range size, reproductive mode, adult microhabitat and skin texture) on mitochondrial sequence variation in 40 species of rainforest frogs (Mantellidae) from Madagascar. Contrary to expectations, four out of five variables (range size, adult habitat preference, skin texture or reproductive mode) showed no relationship to regional differentiation or levels of genetic variation within populations of mantellid frogs. However, body size was inversely correlated with nucleotide divergence between populations and was coupled with high F_{ST} levels and an absence of haplotype sharing in small-bodied and medium-sized frogs. This implies substantial population subdivision and low levels of gene flow in small-bodied mantellids and is corroborated by a lack of haplotype sharing in nuclear genes at least in some species. In contrast, most large species exhibited low genetic differentiation among populations and evidence of haplotype sharing. We suggest that low dispersal ability most likely caused higher population differentiation in small-bodied mantellids and has the potential to accelerate rates of allopatric speciation in small frogs relative to large species. A consequence of higher regional genetic differentiation in small-bodied frogs may include increased speciation rates in clades containing small species. However, in mantellids, small body size correlates with small range sizes and higher rates of nucleotide substitution, but not increased rates of cladogenesis. We argue that this apparent inconsistency between macroevolutionary pattern and microevolutionary process may stem from the cumulative influence that dispersal has on diversification at short and long temporal scales.

Ecological and evolutionary interactions of two closely related songbird species in their contact zone: the case of Nightingales (*Luscinia* spp.)

Tereza Petruskova¹, Jiri Reif², Jana Vokurkova¹, Martin Jiran¹, Silke Kipper³, Adam Petrussek¹, Radka Reifova⁴

¹ Department of Ecology, Charles University in Prague, Czech Republic

² Institute for Environmental Studies, Charles University in Prague, Czech Republic

³ Institute of Biology, Free University Berlin, Germany

⁴ Department of Zoology, Charles University in Prague, Czech Republic

kumstatova@post.cz

Understanding mechanisms causing reproductive isolation between incipient bird species can provide important insights into the speciation process. We study these mechanisms in closely related species pair of songbirds with similar ecological requirements, Common Nightingale (*Luscinia megarhynchos*) and Thrush Nightingale (*L. luscinia*), combining multiple approaches ranging from ecology and genetics to bioacoustics and behavioural experiments. Populations of these two species, which diverged about 1.8 My ago, came recently into secondary contact in Northern and Eastern Europe, where they occasionally hybridize. In sympatry, they asymmetrically diverge in relative bill size (with only Common Nightingale differing in comparison with allopatry). In contrast, the species show asymmetric convergence in song, an important component of territorial defence and courtship behaviour: a substantial proportion of Thrush Nightingale males include in their repertoires song types copied from Common Nightingale but not vice versa. This convergence apparently does not increase hybridization, as hybrids are relatively rare in sympatry (ca 3-5%), and most of them are apparently formed by mating of Thrush Nightingale females with Common Nightingale males. Possibly, song convergence increasing the complexity of Thrush Nightingale repertoires might be driven by female preference for richer song. Playback experiments proved that both species show interspecific territoriality. Although the directionality of morphological trait displacement in sympatry, and larger body mass of Thrush Nightingales suggest that it is a better competitor, Common Nightingale males generally responded to playback by more aggressive reactions. Our future research will shed more light on female behaviour and its role in interactions between the two species.

Evolutionary ecology of ageing in a clonal organism

Barbara Pietrzak¹, Piotr Dawidowicz¹, Mirosław Ślusarczyk¹, Anna Bednarska¹, Maciej Dańko², Małgorzata Grzesiuk³, Piotr Prędko¹, Maciej Rojek¹, Ewa Szymańska¹, Magdalena Markowska¹, Joanna Pijanowska¹

¹ Department of Hydrobiology, University of Warsaw, Poland

² Max Planck Institute for Demographic Research, Germany

³ Department of Animal Physiology, University of Warsaw, Poland

b.pietrzak@uw.edu.pl

Senescence is widely believed to be rare in the wild, and aged individuals contribute little to fitness. Yet, lifespan and aging patterns can be good indicators of selective pressures acting on natural populations. The freshwater crustacean *Daphnia*, being both a clonal organism and an indeterminate grower, could be expected to show ‘little’ aging. Yet, this is fish predation that plays major role in shaping its aging patterns. Here we both review our recent and present new results from our studies on longevity and ageing in *Daphnia*. First, we propose mechanisms behind over twofold differences in lifespan within a single *Daphnia* clade and a single habitat, Czarny Staw pod Rysami. In such a cold oligotrophic fishless habitat individual *Daphnia* can live for over a year, several times the usual *Daphnia* lifespan. This extreme lifespan is in part a consequence of the overwintering strategy which includes storing resources and delaying reproduction until another spring. Here we propose physiological and behavioural mechanisms behind this adaptive difference. Second, we show over 20% difference in lifespan between *Daphnia* from microhabitats differing in fish predation pressure, as well as differences between individuals within a single genotype expressed upon perceiving a threat of fish predation. The shorter lifespan is associated with higher early reproductive output and we propose it shall be viewed as the cost of predation avoidance. The change in aging pattern appears to be similar, whether it is realized within phenotypic plasticity of a genotype or as a result of different selective pressures among populations.

Sexual conflict explains the coexistence of alternative reproductive phenotypes in the bulb mite

Agata Plesnar-Bielak, Anna Skrzynecka, Krzysztof Miler, Jacek Radwan

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

agata.plesnar@gmail.com

Alternative reproductive phenotypes are one of the most interesting examples of discontinuous phenotypic variation in nature. In the bulb mite *Rhizoglyphus robini* aggressive fighters, possessing sharply terminated thickened third pair of legs used to combat other males coexist with benign scramblers unable to kill rivals. As fighters achieve higher reproductive success (and hence probably higher fitness) than scramblers, the coexistence of the two morphs is an interesting question. We hypothesized that although genes affecting the expression of fighter morph increase fitness in males, they might reduce female reproductive success at the same time, revealing intra-locus sexual conflict. To test this, we established replicated lines which we selected for increased proportion of one of the alternative male morphs and measured fecundity of females originated from those lines. As predicted by the sexual conflict scenario, selection for increased frequency of fighters was associated with lower female fecundity in comparison to lines with increased scambler proportion. This shows that intra-locus sexual conflict may be a mechanism explaining the coexistence of alternative reproductive phenotypes.

Is long-distance dispersal necessary to explain wide distribution of hydrophytes? Case study of hydrophytic umbellifers

Krzysztof Spalik¹, Łukasz Banasiak¹, Mary Ann E. Feist², Stephen R. Downie²

¹ Wydział Biologii, Uniwersytet Warszawski, Polska

² Department of Plant Biology, University of Illinois at Urbana-Champaign, United States

spalik@biol.uw.edu.pl

Long-distance dispersal (LDD) by migratory birds is often invoked to explain the broad distribution of aquatic plants. Such a distribution may also be achieved by recurrent short-distance dispersal (SDD) to adjacent areas. To test the relative importance of LDD and SDD in shaping the distribution of hydrophytes, we examined different dispersal models for a clade of hydrophytic umbellifers (Apiaceae tribe Oenantheae). A dated phylogeny of the group was obtained with Bayesian methods using nrDNA ITS and cpDNA *rps16-trnK* sequences from 100 species and infraspecific taxa of Oenantheae and two outgroups. Ancestral habits were inferred using maximum likelihood. Six connectivity models were compared using a maximum likelihood-based method (*lagrange*), four with symmetrical dispersal rate matrices and two assuming asymmetrical exchanges between Eurasia and North America, with or without spatial and temporal constraints on LDD. The results suggest that throughout the phylogeny of Oenantheae, the hydrophytic habit (including helophytes and amphiphytes) dominated. Western Eurasia was reconstructed as its most likely ancestral area. Of the six connectivity models considered, the model restricting all intracontinental and transoceanic LDDs and assuming an almost unidirectional dispersal from Eurasia to North America received the highest likelihood score. This model was also characterized by the highest dispersal rate. The results suggest that the broad distribution of hydrophytic Oenantheae has been achieved through an increased dispersal rate and recurrent SDD rather than frequent LDD.

RAD sequencing in a wild passerine bird: genetic structuring and signatures of selection in a phenotypic trait?

Marta Szulkin

Centre d'Ecologie Fonctionnelle et Evolutive, CEFE CNRS Montpellier , France

marta.szulkin@zoo.ox.ac.uk

Large panels of SNP markers allowing for detailed insight into footprints of selection and genotype-phenotype associations in natural populations are becoming increasingly accessible to field evolutionary biologists. In particular, the growing use of RAD sequencing is undeniably boosting the development of polymorphic markers among species with no reference genome. We used RAD-sequencing to infer the genetic structuring of 4 populations of wild blue tits (*Cyanistes caeruleus*) living in a highly heterogeneous environment in the South of France and in Corsica. We present preliminary findings summarising RAD sequencing outputs, discuss sequencing repeatability statistics and the necessity of including control samples in genomic studies of natural populations. Finally, we examine the genetic structuring of these populations and discuss some intriguing genotype-phenotype associations detected in the study.

Variation in development rates in core and peripheral populations of *Lestes sponsa* - the importance of photoperiod

Szymon Śniegula

Instytut Ochrony Przyrody PAN, Polska

szymon.sniegula@gmail.com

Genetic and phenotypic variation in developmental and growth rates along latitudinal gradients may benefit our understanding of the evolution of latitudinal compensating mechanisms. I explored compensatory developmental mechanisms with respect to photoperiod in central, northern and the northernmost peripheral populations of a damselfly *Lestes sponsa*. In addition, genetic variances in development and growth rate were evaluated across the populations.

L. sponsa is strictly univoltine with egg overwintering throughout its geographic distribution. The role of photoperiod on the expression of larval development was evaluated under controlled laboratory conditions. Larvae from each region were grown in both high and low latitude photoperiod.

All three populations shortened development time and accelerated growth as a response to high latitude photoperiod (phenotypic plasticity present). The slopes of reaction norms differed between populations. There was a genetic differentiation between populations and this resulted in a genotype-by-environment interaction in development time and growth rate.

Genetic variance (V_g) in development time was significant, however it did not differ across populations. V_g in growth rate was non-significant. Reaction norms in development time and growth rate also showed non-significant V_g .

Results supported the presence of countergradient variation in development time and growth rate as seasonally more time stressed populations took shorter time for development and grew faster than less time stressed populations. Slopes of reaction norms indicated that the latitude compensating mechanism was mediated by photoperiod.

Development time has a potential to evolve, though, at a similar rate across study regions. Growth rate seems to be genetically constrained for further evolution. Reaction norms seem to be canalized with respect to photoperiod. The later could be an effect of strong selection for optimal reaction norms in development and growth – traits important for seasonally time constrained species.

Nuclear genome integrity despite complete mtDNA replacement in newts.

Piotr Zieliński¹, Krystyna Nadachowska-Brzyska², Wiesław Babik¹

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

² Department of Evolutionary Biology, Uppsala University, Sweden

piotr.zielinski@uj.edu.pl

The discovery of patterns of introgression can provide an important insight into the history and dynamics of genetic interactions between hybridizing species. The Carpathian (*Lissotriton montandoni*) and smooth (*Lissotriton vulgaris*) newt are sister species which hybridize, wherever their ranges overlap. Previous analyses have shown that both species share several mtDNA lineages, and multiple introgressions of *L. vulgaris* mtDNA into *L. montandoni* have been inferred. Understanding the hybridization in this system requires assessing to what extent the extensive introgression of mtDNA from the smooth newt into the Carpathian newt is mirrored by nuclear genes. We did an extensive survey of the mitochondrial and nuclear (15 microsatellites and 139 SNP's) markers to assess the genetic structure and estimate the gene flow rates between the smooth and Carpathian newts. The extent of introgression differs dramatically between the mitochondrial and nuclear genome. Mitochondrial DNA shows evidence for multiple introgression events from the smooth newt to the Carpathian newt and complete haplotype replacement in the Carpathian newt, while there is only little evidence for recent interspecific nuclear gene flow in the assayed markers. Moreover, the patterns of genetic structuring within the Carpathian newt differ between nuclear loci. Microsatellite differentiation within the Carpathian newt defines three groups, while the SNP's only two. Separate groups might come from separate glacial refugia, located in distinct parts of the Carpathians. Range fragmentation into multiple glacial refugia would facilitate local mtDNA haplotype introgression and fixation in different parts of species range. These distinct events of mtDNA haplotype introgression in the Carpathian newt accompanied by the limited signal of gene flow in the nuclear genome and strong intraspecific structuring point to a complex history of interactions between those two species of newts.

Dating phylogeny of Apiaceae (Magnoliophyta, Apiales) revisited: evidence from the analyses of pollen evolution

Łukasz Banasiak, Krzysztof Spalik

Wydział Biologii Instytut Botaniki Zakład Systematyki i Geografii Roślin, Uniwersytet Warszawski,
Polska

banasiak@biol.uw.edu.pl

Fossil data are indispensable for a proper calibration of molecular trees. However, fossil records for many groups of plants, particularly for herbaceous taxa like Apiaceae, are rare and usually only pollen grains can be found. Moreover, their identification is often arbitrary and based on idiosyncratic decisions rather than proper analyses. This can lead to highly inconsistent results and the estimated age of the group may differ by tens million years. We provide a review of fossil pollen records provisionally identified as Apiaceae and using formal methods of phylogenetic reconstruction assign them if possible to particular clades. Most reported palynomorphs have not been included in the analyses due to insufficient degree of preservation. Seven best preserved fossil pollens were compared to the reconstructed ancestral morphologies based on a phylogeny of 59 extant representatives of the family and two outgroup taxa. Using maximum parsimony we identified four reliable calibration points that were subsequently used to calibrate phylogeny of Apiaceae and outgroups based of 654 sequences of chloroplast *rps16* intron. Estimated divergence age of Apiaceae and its sister group Araliaceae is 68.9 Ma (late Cretaceous) and the most recent common ancestor of Apiaceae lived 64.8 Ma (K/T boundary).

The effect of cyanobacteria and raised temperature on reproductive success of *Daphnia*

Anna Bednarska, Małgorzata Grzesiuk

Wydział Biologii, Uniwersytet Warszawski, Polska

a.bednarska@uw.edu.pl

Planktonic cladocerans of genus *Daphnia* usually are one of the most efficient grazers of phytoplankton but they fail to control cyanobacteria biomass. Cyanobacteria were proven to be an inadequate food source for herbivorous planktonic animals due to their toxicity, poor nutritional value and poor manageability. In the presence of cyanobacteria, *Daphnia* fitness is severely reduced. The aim of the study was to determine mechanisms responsible for suppressing *Daphnia* fitness in the presence of non-toxic cyanobacteria. Three clones of *Daphnia magna* were exposed to the presence of cyanobacteria for five generations under two temperature regimes. *Daphnia* were cultivated until the third reproduction and the key life history parameters were monitored. Results show that cyanobacteria presence caused profound changes in *Daphnia* phenotype and that the reproduction-related traits were more affected than growth-related traits. Thus, it appears that *Daphnia* can grow but not effectively reproduce in the presence of cyanobacteria. The negative effect of cyanobacteria on *Daphnia* fitness was enhanced by increased temperature. The reduced reproductive success of *Daphnia* was related to three phenomena: decreased fecundity, occurrence of non-reproductive instars and egg abortion. The presence of cyanobacteria also triggered the change of reproductive mode in *Daphnia*, i.e. change from parthenogenesis to sexual reproduction resulting in formation of resting eggs. Moreover, there were interclonal differences in the degree of suppression of the reproductive success caused by cyanobacteria presence. This may lead to the changes in frequency of genotypes and thus may trigger the microevolutionary changes in cladoceran populations in cyanobacteria dominated lakes.

High basal metabolic rate in laboratory mice does not elevate oxidative stress during lactation

Paweł Brzek, Aneta Książek, Łukasz Oldakowski, Marek Konarzewski

Institute of Biology, University of Białystok, Poland

brzek@uwb.edu.pl

Evolution of high level of basal metabolic rate (BMR) and endothermy are hypothesized to be related to selection for better parental capacities. However, it is not known if elevated BMR incurs also increased costs of reproduction, in particular increased oxidative stress (OS). Previous studies of the effect of reproduction on OS reported ambiguous results, with some even showing a reduction of oxidative damage during reproduction. We propose that the link between reproduction and OS may be mediated by BMR, which can affect both the rate of radical oxygen species production and anti-oxidative capacity. We studied oxidative damage to protein, lipids, and DNA, and the magnitude of anti-oxidative defence in lactating females of laboratory mice, divergently selected for high (H-BMR) and low (L-BMR) BMR. In non-lactating females, markers of oxidative damage were similar in both lines or higher in L-BMR line type. The magnitude of oxidative damage did not change or was reduced during lactation. Changes in oxidative damage were not related to anti-oxidative capacity; however, we found evidence that oxidative damage might be modulated by interaction between anti-oxidative capacity and line-type-specific susceptibility to ROS. We conclude that magnitude of OS may depend on intra-specific variation in BMR; however, high BMR (previously shown to correlate with effective parental care in H-BMR line type) does not increase oxidative damage both in non-lactating and lactating females.

Antler quality in red deer: a test of Hamilton and Zuk hypothesis

Mateusz Buczek¹, Jacek Radwan², Henryk Okarma³

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

² Faculty of Biology, Adam Mickiewicz University, Poland

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

mateusz.buczek@uj.edu.pl

The evolution and maintenance of elaborate secondary sexual traits in males has been the subject of intense interest since Darwin. Hamilton and Zuk (1982) hypothesis of parasite-mediated sexual selection suggests that genetically resistant males can afford to invest more in costly ornaments. Therefore elaborated sexual traits can serve as honest indicators of male health and parasite load. We study the association between the MHC (Major Histocompatibility Complex) class II genes, gastro-intestinal and lung parasite burden and the development of antler (sexual ornament) in red deer (*Cervus elaphus*). We analyzed associations between antler elaboration (mass and 8 other measurements) and parasite burden (lung nematode larva, abomasum nematodes and fecal egg counts). We found a very complex pattern of relationships. The mass of antler was significantly affected by the lung nematode larva burden. We used 8 antler measurements to describe antler size using principal component analysis (PCA). PC1 (explaining 80% of variance in antler size) was significantly affected by lung nematodes burden and PC3 (explaining 5% of variance) by abomasum nematode burden. We will additionally present results of analyses investigating the effect of MHC genotype on parasite load.

Evolutionary definition of individual as a step toward the biological system of concepts more general than the one from the population genetics

Krzysztof Chodasewicz

College of Physiotherapy in Wrocław, Poland

kchodasewicz@o2.pl

However, this approach is problematic in the context of modular organisms (some plants and coelenterates, for example) or the sets of the genetically identical organisms which are considered as single organism (clonal plants, for example). Although the selection can operate on each of individuals, if there is no mutation, there is no evolutionary change from the point of view of population genetics. However, the inheritance can take place in other Jablonka's "evolutionary dimensions". Another issue is generated by the colonies of eusocial insects, which may undergo of selection as a whole.

This lecture aims to outline the concept of the individual as a subject of selection. Similar, but narrower approach is proposed by Folse III. The point of departure is an abstract reconstruction of requirements for Darwinian evolution. The reconstruction shows that the natural selection does not require to distinguish the specific unit of inheritance (the gene). The Darwinian mechanism requires only the entities, which are able to reproduce, exhibit the hereditary variability and undergo selection due to certain features – these are the individuals. For this reason, the population genetics can be considered as a special case, which is related with one of the channels of heredity. If we consequently consider the individual as the subject of selection, the concept of individual is less problematic than genetic-structural approach.

Learning and memory in bank voles from a multidirectional artificial selection experiment

Katarzyna Chrzęścik, Edyta T. Sadowska, Paweł Koteja

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

katarzyna.chrzascik@uj.edu.pl

Evolution of cognitive abilities could play an important part in evolution of predatory or herbivorous lifestyle but this relation is still not clear and difficult to investigate. To test hypotheses concerning evolutionary changes in learning and memory we used replicated lines of bank voles *Myodes* (= *Clethrionomys*) *glareolus* selected for intensity of predatory behavior towards crickets (P), high aerobic capacity during swimming (A), ability to grow on a herbivorous diet (H) and unselected control lines (C). We expected that voles from P lines, inversely to voles from A lines, should have better memory and learn faster than those from C lines. Learning and memory of 350 voles from generation 13 of the selection experiment were examined in Morris Water Maze test. During the 6-day test comprising of 18 observations, the animal have learned how to find the hidden platform in a circular water pool. All trials were recorded and analyzed with the using video tracking software (EthoVision XT). Mean time to find the platform was more than 50% shorter in the last day compared to the first day of test (first day P:47s, A:49s, H:48s, C:45s; last day P:21s, A:25s, H:17s, C:18s), similarly like total distance traveled before finding the platform (first day P:11.2m, A:11.7m, H:10.9m, C:10.8m; last day P:5.4m, A:5.8m, H:4.2m, C:4.7m). Voles from different types of selection did not differ in any index of learning and memory ($p > 0.05$). Thus, surprisingly, selection appeared to not affect learning and memory in any way - positively or negatively.

Phylogeography of a widespread amphipod species complex in the Carpathian Arc suggests persistent effects of Tertiary sea level changes

Denis Copilaş-Ciocianu¹, Lucian Pârvulescu¹, Adam Petrusek²

¹ Department of Biology and Chemistry, West University of Timișoara, Romania

² Department of Ecology, Charles University in Prague, Czech Republic

petrusek@cesnet.cz

South-east Europe is an important area for biodiversity and phylogeography studies of both terrestrial and freshwater organisms, thanks to its complex palaeogeography and refugial role during the Pleistocene glaciations. Despite their low dispersal abilities and vicariant distributions that seem to reflect past geological events, freshwater amphipods from this region nevertheless received relatively little attention. We chose the widely distributed *Gammarus balcanicus* species complex to evaluate the role of geological vicariance in its present distribution in the Carpathian Arc. We sequenced four genes (one mitochondrial and three nuclear) of individuals from 49 localities, and populations from additional 270 sites were morphologically analysed. Morphological and molecular data revealed the existence of two main clades with distinct geographical ranges. A widespread clade originating at ~20 MA, comprised of several highly divergent, morphologically cryptic lineages, inhabits the older landmasses, suggesting multiple freshwater colonization events. Across the more recent landmasses and former Miocene lakes, a genetically and morphologically distinct lineage is present that fits the description of a previously discarded endemic subspecies. According to its distribution pattern and molecular dating, this lineage seems to have radiated into freshwater more recently, at ~8 MA, although it appears to have an ancient Oligocene origin. The current distribution of distinct lineages and estimation of their divergence times suggest that Miocene geological events such as different timings of landmass uplift and sea level fluctuations are still reflected in the *Gammarus balcanicus* phylogeography in the Carpathians.

Small cells with large fitness consequences: how and why thermal environment shapes cell size in ectotherms?

Marcin Czarnołęski

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

marcin.czarnoleski@uj.edu.pl

Body size and cell size of ectotherms often increase in cold environments. Evolutionary significance of this pattern remains unclear. Larger body size in cold may reflect adaptive responses in resource allocation to decreased mortality and changes in mass-scaling of physiological rates. Physiological properties depend on the amount of plasma membranes, which in turn depends on cell size. Plasma membranes benefit cells by regulating transport, but they cost energy to maintain. Recent experiments on thermal fluctuations in *Drosophila melanogaster* show that not only average temperature but also variance in temperature affect body size and cell size of ectotherms. These findings help to understand a potential adaptive value of cell size in ectotherms challenged by thermal environments.

Is temperature-cell size-rule stronger than temperature-body size-rule?

Marcin Czarnołęski, Anna Łabecka, Ulf Bauchinger, Jan Kozłowski

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

anna.labecka@uj.edu.pl

Temperature-size rule predicts slower growth, delayed maturation and larger body at maturity under colder ambient temperature. Under laboratory conditions more than 4/5 of the ectotherms examined confirm this prediction. We tested temperature-size-rule predictions for growth for two subspecies of the garden snail, *Helix aspersa* (*Cornu aspersum*) raised at either 15° or 20°C in our laboratory until day 400. We predicted that ambient temperature during development not only affects growth rate and body mass at maturity (classical temperature-body size rule), but also affects cell size (temperature-cell size rule): ectotherms will develop larger cells under colder temperature.

Compared to *Helix aspersa aspersa* (HAA), *H. aspersa maxima* (HAM) grew faster and to a larger adult body mass. Both subspecies grow slower at 15°C compared to 20°C, but did not reach a higher adult body mass, against predictions of temperature-body size rule. Cell size measurements for three tissues reveal a differential pattern: cells of foot muscle and epithelium were larger in HAA, the subspecies with a more northern distribution, but were not different between subspecies in the case of hepatopancreas cells. Temperature treatment resulted in larger cell size for muscle and epithelium, but smaller cell size for hepatopancreas at 15°C, compared to 20°C.

Temperature-body size-rule could not be confirmed for garden snail and temperature-cell size-rule applies to some, but not all tissues. Tissue specific or function specific reasons may be put forward to explain this result, but remain to be explored.

Body size, reproduction and mortality of entomopathogenic nematode, *Steinernema feltiae* (Nematode: Rhabdidae) in constant and fluctuating thermal conditions

Jaśmina Czech, Katarzyna Pawlik, Daniel Kübler, Paulina Kramarz

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

jasmina.czech@gmail.com

Environmental temperature has a strong influence on the life-history traits such as growth and reproduction, development time, body size, mortality and eventually fitness. Relation between phenotype and temperature describes function, usually curved – thermal reaction norm. Despite of high temperature variability (daily and/or annual), prevailing number of studies on thermal reaction norms are performed in constant conditions.

Here we investigated differences in reaction norms of *Steinernema feltiae* between constant and fluctuating temperature. This entomopathogenic nematode has one free-living and infectious stage (Dauer larvae, DJ) searching for a host in a soil. After infection DJs release symbiotic bacteria which proliferate in the host and are main food source for the nematodes. Then the nematodes mature, reproduce and their progeny develops into DJs which leave the cadaver to infect a new host. At the same time, *Steinernema feltiae* can be successfully cultured on artificial diet containing their symbiotic bacteria.

We subjected populations of laboratory strain to three constant temperature treatments of 15, 20 and 25°C and three fluctuating (daily) temperatures with means of 15, 20 and 25°C respectively. Measured traits were: survival of DJs without food resources (conditions similar to free-living stage while searching for insect host), survival of DJs on diet with bacteria (favorable conditions) as well as a number and size of produced DJs. We found different plasticity of studied traits depending on both value and variation of the temperature. In general, constant thermal conditions caused bigger differences between values of the traits in comparison to fluctuating ones.

Food plasticity of moose, *Alces alces* in Poland

Marta Czernik, Magdalena Świsłocka, Magdalena Czajkowska, Mirosław Ratkiewicz

Institute of Biology, University of Białystok, Poland

czernik.marta@gmail.com

The moose *Alces alces*, as a large herbivore, has a significant impact on ecosystems. However, knowledge about the food plasticity and food resources usage by this species is incomplete. Prevailing view is that in winter moose feed mainly on pine. We developed a PCR-based method of qualitative winter diet analysis of cervid's diet. Amplifying a P6 loop of chloroplast intron *trnL* (UAA) of plant DNA from feces allowed the identification of different coniferous and deciduous plant species. We used our method for moose diet analysis in three areas in Poland: the Biebrza valley, Kampinos Biosphere Reserve and West Polesie Biosphere Reserve. We showed significant differences between studied areas, mainly in the consumption of juniper, pine, willow and spruce. These differences could indicate a food plasticity. These differences are probably due to the different plant communities and/or forms of active protection.

Can potentially non-senescent hydra unravel the mystery of aging?

Maciej Dańko

Max Planck Institute for Demographic Research, Rostock, Germany

danko@demogr.mpg.de

Unlike other metazoans, *Hydra* do not undergo the distinctive rise in mortality with age known as senescence, resulting from an increasing imbalance between damage and repair. We propose that *Hydra* control their damage accumulation mainly by damage-dependent cell death and cell sloughing. We examine our hypothesis with a model that combines cellular damage with stem cell renewal, differentiation and elimination. *Hydra* individual can be considered as a large single pool of three types of stem cells with some features of differentiated cells. This large stem cells community prevents “cellular damage drift”, which is inevitable in complex conglomerate (differentiated) metazoans with numerous and generally isolated pools of stem cells. The process of cellular damage drift, similarly to the process of genetic drift, is based on changes in distribution of damage among cells due to random events. In the model events that are sources of randomness include: budding, damage caused by cellular death, and undergoing and repairing cellular damage. Results favor the view that non-senescence is possible only in simple *Hydra*-like organisms characterized by high proportion and number of stem cells, high cell division rate, an effective cell selection mechanism, and having stem cells with the ability to take some roles of differentiated cells.

**Cellular bases of body size variance in the fence lizard
Sceloporus undulatus (Phrynosomatidae) from different latitudes**

Natalia Derus, Marcin Czarnołęski

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

natalia.derus@uj.edu.pl

No one knows why many species of ectotherms and endotherms attain larger body size at higher latitudes. Mammals, birds and turtles usually follow this so-called Bergmann's rule, but not lizards and snakes. In contrast to general tendencies of lizards, in the North American lizard *Sceloporus undulatus* individuals from northern populations are typically larger than individuals from phylogenetically related populations from the south. Our study evaluates how differences in body size between four geographically distant populations of *Sceloporus undulatus* (from Nebraska, Florida, Indiana and Texas) link to changes in the size of cells in two tissue types - red blood cells and skeletal muscles. We discuss results in the context of emerging theory on changes in the adaptive value of cell size across thermal environments. Understanding how and why cell size changes with latitude in *Sceloporus undulatus* can help future work that aims at finding ultimate explanations of Bergmann's clines in ectotherms.

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The effect of malaria parasites on reproductive success in the great tit – the medication experiment

Anna Dubiec¹, Edyta Podmokła², Magdalena Zagalska-Neubauer³, Lars Gustafsson⁴

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

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

³Ornithological Station, Museum and Institute of Zoology,
Polish Academy of Sciences, Gdańsk, Poland

⁴Department of Animal Ecology, Uppsala University, Uppsala, Sweden

adubiec@miiz.waw.pl

Haemosporidians causing avian malaria are one of the most common and widespread parasites among bird species. In wild populations, effects of malaria parasites on host fitness are generally difficult to detect, because the majority of individuals hold chronic infections. One way of overcoming this obstacle is experimental eradication or decrease of intensity of parasitic infection. To investigate the consequences of infection with malaria parasites for the parameters of reproductive success in the small hole-nesting passerine – the great tit (*Parus major*), the group of females was medicated at the early stage of the nesting cycle. During two breeding seasons females caught at the nest building stage were injected intraperitoneally either with an antimalarial drug - primaquine, or with a physiological salt. Reproductive performance of treated birds was assessed with clutch initiation date, clutch size, nestling body mass 2 days post-hatching, fledgling body mass and tarsus length. During the nest building stage 86.9% of females were infected with at least one parasite lineage (genera *Haemoproteus* and *Plasmodium*), while at the end of the nestling stage – 96.4%. Clutches laid by females from both groups did not differ in clutch initiation dates or size, however, nestlings produced by medicated females were larger than nestlings produced by non-medicated females. This data suggests that malaria parasites affect reproductive success in the great tit via reduced body size of the offspring, which is a reliable predictor of the survival probability.

Patterns of genome divergence in hybridizing *Bombina* species

Anna Fijarczyk, Jacek M. Szymura

Institute of Zoology, Jagiellonian University, Kraków, Poland

ania.fijarczyk@uj.edu.pl

Divergence between hybridizing sister species is shaped by functional constraints, divergent selection, gene flow, but also neutral divergence. We have analyzed transcriptomes of two amphibians with incomplete reproductive barriers that are in the final stage of speciation: *Bombina bombina* and *Bombina variegata*. In the first attempt to characterize genome-wide divergence of these non-model organisms we focused on the possible role of positive selection, gene flow and differences in gene expression. General study including single transcriptomes of each species enabled us to draw general conclusions and raise several interesting hypotheses on sources of functional divergence and role of geographical history. The average divergence of transcripts is 1.1% with over 90% of 1 594 sequences differing by at least one substitution. In spite of clear genetic distinctness but in concordance with low nonsynonymous substitution rate we found no significant signatures of positive selection. However a few nuclear loci engaged in the oxidative phosphorylation pathway and functioning of mitochondria show increased levels of nonsynonymous substitution rate suggesting their role in generating cyto-nuclear conflicts and reproductive isolation. We hypothesize that gene expression can be important in shaping adaptive divergence of species as revealed by significant positive correlation between nonsynonymous substitution rate and differential expression. Although we could not reject the hypothesis of gene flow between *B. bombina* and *B. variegata*, analysis of transcriptomes showed that two species represent two genetically distinct gene pools.

Multielemental stoichiometry of wood eaters and deadwood: nutritional determinants of the life histories of xylophages

Michał Filipiak, January Weiner

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

michal.filipiak@uj.edu.pl

The stoichiometric transition between producers and herbivores is a challenge because of the mismatch between nutritional supply and demand. To find out how xylophagous insects manage drastic stoichiometric imbalance we compared element contents in the bodies of three species of wood-boring beetles: *Stictoleptura rubra*, *Arhopalus rusticus* (Coleoptera, Cerambycidae), *Chalcophora mariana* (Coleoptera, Buprestidae), with those of woody tissues, from a life history perspective. Simultaneously we measured selected PLFAs content as a proxy for fungal tissue content in the wood in order to examine if fungi may contribute to enrich dead plant matter in nutrients other than carbon. The ratios C:N, C:P, C:Cu, C:K and C:Na in the beetles are approximately $\times 10^3$ (N), $\times 10^2$ (P, Cu), and $\times 10$ (K, Na) lower than in dead but undecayed pine wood, causing severe nutritional imbalance. Carbon loss from wood cannot explain the increase in the percentage of other elements, because their absolute content is increasing in dead wood during decomposition. Simultaneously increases the amount of fungal tissue presented in dead wood. Simulation of the life history of *S. rubra* shows that the beetle could not complete its life cycle depending on wood as the only source of nutrients. Fungal mycelium, covering large area of the forest, can transfer nutrients between soil and carbon-rich niches such as deadwood. Fungi play a pivotal role in nutrient cycling in the deadwood carbon-rich ecosystem and serve as nutrient delivers. This is the first attempt to study the essential macro- and microelement stoichiometric relations in a fundamental terrestrial trophic link.

Duration of breastfeeding is differentially influenced by paternal or maternal grandparents

Andrzej Galbarczyk, Magdalena Walas, Ilona Nenko, Grażyna Jasiońska

Department of Environmental Health, Jagiellonian University Medical College, Poland

agalbarczyk@gmail.com

Several studies have shown that grandparents have a significant impact on the initiation and duration of their grandchildren's breastfeeding. Maternal grandparents (MGPs) should affect breastfeeding duration differently than parental grandparents (PGPs), due to difference in sex-specific reproductive strategies of their children.

Data were collected as part of an ongoing longitudinal study conducted since 2003 at the Mogielica Human Ecology Study Site. A questionnaire was used to collect information on women's reproductive history and on household composition after their marriage. In order to compare the impact of grandparents, for the analysis we selected women who lived after marriage in a household with at least one of their own parents (N=148) or with at least one of their husband's parents (N=245).

The average duration of breastfeeding differed depending on which grandparents were present in a household. Mothers who raised children in the presence of co-residing MGPs breastfed their children longer than did mothers co-residing with PGPs (8.5 vs. 7.0 months, $P < 0.001$). The observed difference did not depend on the sex of children.

Our findings support the hypothesis that paternity uncertainty may differentiate grandparents' offspring investment strategies. These results may indicate that MGPs, whose interest lies in improving the 'quality' of grandchildren, support their daughters during breastfeeding. In natural fertility populations variation in breastfeeding duration may affect average inter-birth intervals, therefore a presence of PGPs could have resulted in a greater number of children.

**From a theory of purposefulness and biological information,
through Darwinian mechanism and chaos in the complex
networks, to structural tendencies**

Andrzej Gecow

Centrum Badań Ekologicznych, Polska

gecow@op.pl

The evolution and its Darwinian mechanism are the base of understanding of observed structures in organisms or in processes such as an ontogeny. The development of complex network science, particularly the theme of a place for the life in the aspect of deterministic chaos in these complex systems, in the main part result from attempts of their application to description of living objects and their evolution. Unfortunately, such attempts are made outside of the biology, what have negative impact on the depth and correctness of biological aspects. It is currently known, that some problems of evolution cannot be taken by population genetics. But reaching for such dissimilar tools, as complex networks or theoretical description of information and purposefulness, are still an exception in the biology. I signalise an arising of coherent theoretical depiction, which starts from notions of information and coding applied not into technology, but for phenomena description. It gives modern depiction of the purposefulness problem and the clear definition of purposeful information, which replaces unclear notion of biological information. Next, the basic Darwinian mechanism is derived from certain definition of process based on such notions. This process seems to be a life process. A hereditary information and model of living object as functioning complex network formed by Darwinian mechanism are next stages. Here a dispute on a shift of the life from edge of chaos deeper into chaos occurs. On the end, an expectation of structural tendencies is obtained using simulation of such model of living object. Structural tendencies can be considered as nonadaptive mechanisms of evolution in the Lynch sense.

Longer development can lead to smaller body mass - response of *Tribolium castaneum* to constant and fluctuating thermal environment

Agnieszka Gozdek, Katarzyna Pawlik, Paulina Kramarz

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

aga.gozdek@uj.edu.pl

Temperature Size Rule (TSR) states that body size of ectotherms is negatively correlated with temperature. At the same time, growing number of studies indicates on great importance of temperature fluctuation on life history traits. Our study aimed to investigate the effect of novel temperature (including fluctuating thermal conditions) on body mass and development time as well as whether there are differences between sexes in studied traits.

We subjected a progeny of half-sib families of laboratory strain of *Tribolium castaneum* to four thermal treatments: ancestral, that is constant 30°C; novel constant 25°C and novel fluctuating (daily) with mean either 25°C or 30°C. Every 24h, eggs freshly laid by a single female, were split into four and then placed in each of thermal treatment. The development time and body mass at adult emergence were measured for both sexes.

The beetles developed the fastest and emerged the heaviest at the constant high temperature (30°C). In low constant temperature (25°C) the pattern was reverse– the beetles developed the longest and had the smallest body mass. At the same time, differences between fluctuating thermal conditions were not so distinct in case of body mass but the development time was longer in 25°C then in 30°C. These findings do not support TSR. Furthermore, despite of thermal treatment, females were heavier but developed faster than males. It is in contrast to one of the explanation of smaller size of males: selection favours early emergence of males. We discuss possible explanation of our outcomes.

Nest building costs in the females of Great Tit

Iga Gózdź, Tomasz Mazgajski

Muzeum i Instytut Zoologii PAN, Polska

iga@miiz.waw.pl

Reproduction may lead to high costs - suffered by one or both parents. Breeding costs in birds are investigated mostly for incubation and nestling feeding stages by manipulation of parental investment. Such research are based on the assumption, that each of the breeding stages is associated with some costs and larger investments in one of the stages lead to decreasing expenditures in subsequent reproductive phases. The increase of investment in reproduction may also reduced parents ability to self-maintenance, what is often reflected in the reduced ability to cope with pathogens.

In our study on the Great Tit *Parus major*, a species in which only females build the nest, we would like to verify whether the experimental increase of expenditures (costs) on nest building affects the course of the following breeding stages (e.g. the number and mass of eggs laid; incubation and feeding patterns) and females condition (e.g. the degree of investment in body self-maintenance), expressed in degree of blood parasitic infestation, white blood cell profile (including heterophil to lymphocyte ratio), body mass and hemoglobin concentration. The experiment was based on the manipulation of the area that can be used by birds for the nest construction. We assumed that the construction of larger nest translates into greater physical activity, which in turn, should worsen condition parameters of the builders.

The preliminary data shows that experimental nests were significantly heavier than nests from control group, suggesting, that birds from experimental group had increased their expenditures on nest building. However the experiment did not influence the eggs number or their mass and we didn't find any relationship between females condition and clutch size. In our study population females of great tit were infected with blood parasites from the genera of *Haemoproteus* and *Plasmodium*. There were no differences in the intensity of infection with parasites in both studied groups of females. Surprisingly females were less heavily parasitised than males. Hemoglobin level significantly differed between males and females (with higher in females).

The year-to-year survival rate in our Great Tit population is very low (ca. 18%). We hope that the study in next breeding season and analysing of physiological parameters, allow as to estimate how costly is the process of nest building.

Will global warming change the future of birds? Influence of weather disturbance for the immune condition and reproductive success of tits.

Emilia Grzędzicka

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

emilia.grzedzicka@uj.edu.pl

Global warming causes higher temperature, faster trees' vegetation or weather disturbances that influence breeding phenology and birds could not react fast enough to be synchronous with peak of food availability. Since climate change has affected bird behavior, they may no longer be in synchrony with their food sources and other habitat needs. When the temperatures during the period after birds have laid their eggs are extremely high or intensive raining causes longer incubation, the mismatch between predators and their prey is larger. In the past, species and ecosystems were able to respond to the global temperature shifts because average temperatures changed slowly and weather disturbances did not happened so often. The consequences of forced responses for survival and immune condition is still an area requiring in-depth research. Research included two species of hole-nesting birds: Great Tits *Parus major* and Blue Tits *Cyanistes caeruleus* breeding in Niepołomice Forest. In the season 2010 with intensive raining from the beginning of May which was caused by global weather disturbance, I could find out what is happening with young tits' immune condition and compare these data with season 2009 and 2011 – both with good weather and peak of caterpillars. The hypotheses is that immunocompetence level of birds depends on the weather condition and the match between breeding and peak of caterpillar abundance: only birds which have the possibility to "hit" the caterpillar abundance achieve good breeding success.

Do symbiotic bacteria enable terrestrial isopods to cope with minimum diets?

Terézia Horváthová, Marcin Czarnołęski, Ulf Bauchinger

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

tereza.horvathova@gmail.com

The evolutionary milestone of land invasion required many fundamental adaptations. Here we present research on one of them, the acquisition and maintenance of symbiotic bacteria allowing their hosts to dwell on low-quality food sources in terrestrial habitat. Not only do endosymbionts increase digestive efficiency of the host by hydrolysis of cellulose and oxidation of phenolics and lignins, but additionally they may act as source for food-limited components like for example vitamins and fatty acids.

Mechanism and time course of endosymbiont transmission into digestive tract have not been confirmed in detail however three mechanisms have been suggested. Symbionts may be acquired through vertical, horizontal and/or environmental transfer. The vertical (mother-offspring) transfer can be mediated through marsupial fluid or oocytes. Horizontal transfer may be facilitated through feeding on conspecifics and environmental transfer through ingestion of faeces (coprophagy), leaves and other food sources.

Here we present experimental results of an in-vitro approach that allow us to differentiate between the three principal modes of bacteria transfer. Early embryonic stages of *Porcellio scaber* are removed from the female brood pouch and subsequent in-vitro ontogenetic development is quantified under manipulated conditions. These manipulations simulate environmental and horizontal transfer, allowing us to determine single or multiple modes of bacterial transfer. Additionally, analysis of marsupial fluid and oocytes will be performed to test for endosymbiont inoculation during early life stage in the motherly brood pouch.

Transcriptomics of male reproductive proteins in *Drosophila melanogaster* populations in absence of sex peptide receptor

Richa Joag

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

richajoag@gmail.com

Accessory gland proteins (Acps) are male reproductive tract proteins transferred to females during copulation, which alter their reproductive physiology and behaviour. One of the Acps in *Drosophila melanogaster*, sex peptide (SP) not only alters fecundity and sexual receptivity of females, but also affects their immune system, feeding, and longevity. It is thus sexually antagonistic and costly to females. We want to examine whether production of SP is costly to males. SP acts through binding to specific sex peptide receptors (SPR) in the female reproductive tract and the central nervous system. The benefit of producing SP is removed if females do not express the receptor. We hypothesize that, if the production of SP is costly to males, this should lead to decreased gene expression. We are studying gene expression levels of SP in selection populations of *D. melanogaster*, with a deletion mutation that leads to lack of expression of SPR. We also intend to test whether the males compensate by increasing production of other Acps/seminal proteins such as Ovulin and DUP99B (Ductus ejaculatorius peptide 99B) since these proteins have some overlapping functions with SP. RT-qPCR will be used to quantify the expression of SP, Ovulin and DUP99B in the males. ELISA of female reproductive tract will be used to quantify the Acps transferred to the females during mating. This will indicate whether or not there is a correlation between gene expression levels and the amount of protein retained in the female an hour after mating.

The private life of malaria parasites

Szymon Kaczanowski

Instytut Biochemii i Biofizyki PAN, Polska

szymon@ibb.waw.pl

The malaria parasite *Plasmodium* is still the cause of one of the most important health problems of the current world. *Plasmodium* developed some complex adaptations for parasitic life. One example of such an adaptation is an apoptotic like suicidal cell death used for population control. We showed that the main pro-apoptotic factors are conserved between animals, plants and protists. This observation enabled us to suggest a putative mechanism of apoptotic like cell death of parasitic protists. Recently we have described a fast male evolution phenomenon, which is a hypothetical mechanism involved in an immune escape of antigens that are expressed by the male gametes. In a host, the male and female gametocytes reside inside the red blood cells, therefore they are “hidden” and the immune response against gametocytes is weak. During gametogenesis which takes place in the swallowed blood in the mosquito’s stomach, the gametocytes expose the epitopes which are otherwise hidden in the human blood stream and become more vulnerable to the host (human) immune factors. Particularly strong immune response is targeted against male gametes. Due to a rapid evolution of the antigens expressed only in the male cells, parasites avoid host immune response.

Correlation between genetic and ecological differences in bank vole populations in the contact zone of two phylogenetic lineages in NE Poland

Ewa Kaczyńska¹, Magdalena Niedziałkowska¹, Bogumiła Jędrzejewska¹, Joanna Gerc², Zofia Korbut³, Wiesław Babik⁴, Jacek Radwan⁴, Mateusz Konczal⁴

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

² Nicolaus Copernicus University, Ludwik Rydygier Collegium Medicum, Bydgoszcz, Poland

³ University of Białystok, Institute of Biology, Białystok, Poland

⁴ Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

ekaczynska@ibs.bialowieza.pl

Mitochondrial DNA and nuclear DNA co-evolve together because both encode proteins involved in many cellular processes, for instance in respiration. There might be some incompatibility between mtDNA and nuclear DNA when mtDNA comes from different species or populations than nuclear DNA e.g. in hybrids of two genetically different populations or subspecies. Such incompatibility may keep contact zones of different genetic lineages relatively narrow. We analysed partial cytochrome b sequences (424 bp) of 983 bank vole (*Myodes glareolus*) samples collected in years 2004-2012 in 7 large forests and on two 350 km transects in NE Poland in the contact zone of Eastern and Carpathian mtDNA lineages of this species. The share of specimens from the Carpathian clade has been decreasing from west to east and from north to south. Among all 983 samples analyzed we found 86 haplotypes with 77 polymorphic sites. Haplotype diversity was 0.72 and nucleotide diversity was 0.007 for all analyzed samples. The parameters of genetic diversity were decreasing from west to east. According to our study, the contact zone of Eastern and Carpathian clades was 254 – 307 km wide and was wider than previously thought. The mismatch distribution analysis showed that Eastern lineage has been under demographic and spatial expansion. Analyses of SNP show no evidence of fixations in mtDNA lineages of alternative variants in any of the nuclear genes encoding proteins that interact with proteins encoded in mtDNA. Some ecological and climatic factors are correlated with observed pattern of phylogenetic lineages distribution.

Mobility of the dryad butterfly in old and newly established populations: the effect of evolutionary history or environmental conditions?

Konrad Kalarus¹, Piotr Skórka², Wiktor Halecki¹, Agata Jirak¹, Joanna Kajzer-Bonk¹, Piotr Nowicki¹

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

² Instytut Zoologii, Uniwersytet Przyrodniczy w Poznaniu, Polska

klaus.vk5@gmail.com

Knowledge of mobility is essential for understanding animal habitat use and dispersal potential, especially in the case of species occurring in fragmented habitats. We compared within-patch movement distances and flight-related morphological traits in the locally endangered butterfly, the dryad (*Minois dryas*), between its old populations occupying xerothermic grasslands and newly established ones in wet meadows. Since the individuals of the latter populations are descendants of dispersers from the former ones, it could be predicted that they are more mobile, which should also be reflected in their morphology. Against the above expectations, we found no direct effect of habitat type on movement distances covered by the butterflies. Moreover, while individuals living in both habitat types did not differ in their body mass and size, those from xerothermic grasslands had wider thoraxes and longer wings. Consequently, they had greater wing loadings (defined as wing length to body mass ratio), which in butterflies is typically a good proxy of mobility. Such results suggest that the dryads from xerothermic grasslands have better flight capabilities, whereas those from wet meadows are likely to invest more in reproduction. Better flight capabilities within xerothermic grasslands are beneficial due to lower availability of larval foodplants, which thus have to be actively searched for, but considerably higher abundance of nectar sources, which provide energy utilised for flight by butterflies. Our findings imply that mobility in the investigated species is determined by environmental characteristics rather than by its recent evolutionary history.

Reconstructing the mating and social system of an extinct hominid species

Katarzyna A. Kaszycka

Department of Human Evolutionary Ecology, Institute of Anthropology,
Adam Mickiewicz University, Poznań, Poland

kaszycka@amu.edu.pl

Sexual dimorphism is used as a basis for reconstructing the social structure and mating systems of extinct hominid species. In 2007, an article published in *Science* by Lockwood et al. claimed evidence of an extended period of growth for males in a South African ‘robust’ australopithecines (*Australopithecus robustus*) sample from approximately 1.5 million years ago. It was argued there that this finding, combined with estimates of sexual size dimorphism, suggests a polygynous mating system similar to that of silverback gorillas today (i.e., one-male harems). On re-examination of this claim, and based on further analysis, I argue that some of the conclusions of the Lockwood’s paper can be questioned. Although morphologically *Australopithecus robustus* exhibits a marked – almost gorilla-like – level of facial dimorphism (implying a polygynous mating system), the one-male harem social structure of forest gorillas is not a particularly good model for interpreting the ecology and social behaviour of the savanna-dwelling ‘robust’ australopithecines. Instead, a multimale–mulifemale social system is suggested.

Life expectancy and offspring sex ratio in the red mason bee (*Osmia rufa* L.)

Justyna Kierat, Hajnalka Szentgyörgyi, Michał Woyciechowski

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

justyna.kierat@uj.edu.pl

Fisher's (1930) equal allocation theory states that parents on average in a population should invest equally in offspring of both sexes. In the Hymenoptera (ants, bees, wasps) maternal control of haplodiploid sex determination gives the ability to determine sex ratio of their offspring. The aim of the present study was to investigate the impact of different life expectancy of red mason bee females on their lifetime offspring sex ratio. Such an impact is probable because in red mason bee daughters are mostly produced at the beginning of the season, while sons mostly towards the end of it. Thus, if a short-living female did not begin laying male eggs earlier in life than long-living female, the former would have lifetime offspring sex ratio shifted towards daughters. But if a female with shorter life expectancy switches from producing daughters to sons earlier, it can be expected that offspring sex ratio will not depend on the longevity of the mother. In our experiment, the bees released earlier in the season, lived longer than those released about three weeks later. As expected, shorter-lived females (released later) produced fewer offspring than those longer-lived (released earlier). Interestingly, proportion of offspring was the same in both groups, what may suggest an adjustment depending on their life expectancy.

Local mate competition in a red mason bee (*Osmia rufa* L.)

Justyna Kierat¹, Hajnalka Szentgyörgyi², Michał Woyciechowski²

¹ Jagiellonian University, Kraków, Poland

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

justyna.kierat@uj.edu.pl

According to the theory of local mate competition (LMC), if siblings of one sex (e.g. brothers) compete, sex ratio in brood should be biased toward the opposite sex (females). Such a situation can take place when one or two females nest in one place, and there is a high site fidelity among their offspring. In the red mason bee individuals often remain nearby their natal nests and create aggregations of nesting females. Number of females nesting in one place can vary according to suitable nests availability. The aim of the experiment was to investigate if females adjust their offspring sex ratio according to the number of females nesting nearby. Red mason bee females due to their haplodiploid sex determination system have the ability to determine sex of each single offspring produced. We created aggregations of bees consisting of low or high number of individuals in their natural environment, and checked if the number of females nesting together influenced aggregation-wide progeny sex ratio. Results suggest that in the smallest aggregations females might bias offspring sex ratio toward females, in accordance with LMC theory predictions.

Digit ratio (2D:4D) as indicator of body size, testosterone concentration and number of children in human males

Magdalena Klimek, Andrzej Galbarczyk, Ilona Nenko, Ludwik Odrzywołek, Grażyna Jasińska

Department of Environmental Health, Jagiellonian University Medical College, Poland

magdalenaannaklimek@gmail.com

Prenatal exposure to sex hormones may play a significant role in programming male's future biological condition and, in consequence, his reproductive success. This study examined the relationship between 2D:4D (biomarker of fetal programming, related to prenatal hormone concentrations) and body size at different life stages, adult's testosterone levels, and number of children among males.

Methods: 688 men from rural Poland at the Mogielica Human Ecology Study Site participated in this study. Life history data, anthropometric measurements, and morning and evening saliva samples were collected.

Results: More masculine 2D:4D (higher prenatal testosterone concentration) was related to higher birth weight ($P = 0.04$), higher birth length ($P = 0.01$), higher body mass during childhood and adolescence ($P = 0.02$), higher number of children among fathers ($P = 0.04$) and higher testosterone levels during adulthood ($P = 0.04$).

Conclusions: We show, for the first time in a single population, that digit ratio is related to body size at different stages of life course, adult testosterone levels and number of children. These results confirm a hypothesis which suggests that a higher prenatal testosterone concentration (as indicated by more masculine 2D:4D) may be related to larger body size in males during prenatal period (positive role of testosterone in determining body dimensions), and adolescence (better ability to store metabolic energy). Higher prenatal testosterone concentration and better biological condition afterwards, may increase male attractiveness and influence their reproductive strategies. Summarizing, 2D:4D should be further tested as an prenatal indicator of subsequent male condition and reproductive success.

The contact zone of phylogenetic lineages of the spittlebug *Philaenus spumarius*: an example of parapatric speciation in progress?

Agata Lis¹, Anna Maryńska-Nadachowska¹, Dorota Lachowska-Cierlik², Łukasz Kajtoch¹

¹ Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Polska

² Institute of Zoology, Jagiellonian University, Kraków, Poland

lukaszkaajtoch@poczta.fm

Previous studies on the phylogeography of the meadow spittlebug *Philaenus spumarius* suggest the existence of a contact zone of its main phylogenetic lineages along mountain chains in Europe and western Asia. This study presents a detailed examination of the population genetics of *P. spumarius* within the Carpathians. The main objective was to determine whether the populations inhabiting that area consist of individuals belonging to different genetic units and whether the observed pattern could be an example of parapatric speciation in progress. Specimens from six transects across the Carpathian arc were examined. The mitochondrial phylogeography of the meadow spittlebug in the examined area clearly shows that individuals from both main clades meet and mix there. Representatives of all three main EF1- α clades were also found. The present distribution of the main clades with a narrow zone of overlap along the mountain ranges may suggest that these phylogenetic lineages form a young hybrid zone with parapatric speciation in progress. Moreover, a limited number of individuals was shown to possess heteroplasmic mtDNA, which gives additional support to intraspecific hybridization. *P. spumarius* could be used in future work as an excellent model species in investigating population genetics, intraspecific hybridization, and parapatric speciation in progress.

Incongruence between morphology and phylogeny among eukaryotic microorganisms - a case study of autotrophic euglenids.

Maja Łukomska-Kowalczyk, Anna Karnkowska, Bożena Zakryś

Zakład Systematyki i Geografii Roślin, Uniwersytet Warszawski, Polska

majalukomska@gmail.com

Identification and description of species of eukaryotic microorganisms is still challenging even though nowadays both morphological and molecular characters are used for delimitation of species boundaries. In most cases combination of those two kinds of features is used for species identification, therefore understanding of relation between those characters is crucial. Autotrophic euglenids are very common freshwater unicellular algae and could be a good model for tracking the correlation between phylogeny and morphological diversity. Moreover they lack any sexual processes and have limited number of morphological features. Among autotrophic euglenids there were identified examples of morphologically different species with very similar molecular features, as well as cryptic species, described according to genetic features only. In this work morphological and molecular diversity of 19 strains representing two closely related euglenoid species, *Phacus longicauda* and *Phacus helikoides*, have been studied. They were chosen because they possess two features with large variability (cell size and torsion). We found that all analyzed strains form one well-established clade and *Phacus longicauda* is a paraphyletic species, with *Phacus helikoides* clade within it. Both molecular and morphological diversity is relatively high in analyzed group and seven subclades could be recognized. However, due to complicated pattern of changes in size and appearance of torsion it's difficult to associate morphological features with phylogeny. Torsion appears at least twice independently in the evolution of this group and cell size changed several times. Because of the incongruence between morphology and phylogeny, morphological features appeared to be misleading in delimitation of species boundaries.

Exploratory performance in an open field test of bank voles from multidirectional artificial selection experiment

Uttaran Maiti, Katarzyna M. Chrzęścik, Agata Rudolf, Edyta T. Sadowska, Paweł Koteja

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

uttaranmaiti@gmail.com

It has been proposed that evolution of complex physiological adaptations, such as endothermy or capability to utilize a specific diet, could be driven by natural selection acting primarily on behaviour. Personality, defined as a suite of correlated behavioural traits that varies consistently among individuals in a population, influences habitat preference, reaction to risky but non-novel situation (evading predators), exploration of novel environment (foraging and dispersal). This is complemented by an individual's dynamic performance (e.g., sprint speed) and regulatory performance (e.g. physiological traits such as aerobic capacity, thermoregulation etc.). It can be hypothesized that proactive individuals are fast runners and would have high metabolic rate to meet their high energy demand. However, empirical evidence for this hypothesis remains ambiguous. To test the hypothesis we observed open-field exploratory behaviour in bank voles, *Myodes* (= *Clethrionomys*) *glareolus*, from lines selected for high aerobic capacity (A), predatory aggression (P), ability to grow on low quality herbivorous diet (H), and unselected control (C) (generation 13: N = 128, 14: N= 192). By measuring exploratory performance in an open field environment, which is novel and stressful to these semi-fossorial rodents, we can quantify personality on the "proactive – reactive" axis. The results will allow testing the hypotheses that voles from A and P lines have "proactive", whereas those from H lines "reactive" personality, compared to voles from unselected C lines. It will also allow investigating individual variation in personality traits and estimating their heritability and genetic correlations with other traits.

Restricted pleiotropy facilitates mutational erosion of major life-history traits

Agnieszka Marek

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

aga.marek@onet.eu

Radical shifts to new natural and human made niches can make some functions unneeded and thus exposed to genetic degeneration. This prediction is both intuitively appealing and confirmed for highly specialized and rarely used functions. Here we ask about major life history traits, rate of growth and resistance to prolonged starvation, and consider environmental conditions that are unlikely to require much more than a basic set of functions. We found that in yeast each of the two traits was visibly harmed by at least several hundred individual gene deletions. There were relatively few deletions with negative synergistic and probably none with positive synergistic or antagonistic affects. Functional profiles of genes affecting either growth or survival were strikingly different: the first related chiefly to synthesis of macromolecules while the second to maintenance and recycling of cellular structures. We conclude that transitions to new environments in which the ability to grow at possibly fastest rate or survive under very long starvation become practically unnecessary can results in rapid erosion of these vital functions because they are coded by many genes constituting large mutational targets and because synergistic pleiotropy is unlikely to constrain this process.

Selectivity by planktivorous fish at different prey densities, heterogeneities and spatial scales

Piotr Maszczyk, Z. Maciej Gliwicz

Uniwersytet Warszawski Wydział Biologii Zakład Hydrobiologii, Polska

p.maszczyk@uw.edu.pl

The results of studies performed in artificially confined, small-scale experimental systems with a homogeneous prey distribution, suggest that selectivity in planktivorous fish for more conspicuous and rewarding prey (such as adult *Daphnia* with eggs in the brood cavities) is stronger at high than at low prey population density. Here we examined whether prey selectivity is altered when fish are allowed to feed (1) in larger-scale systems and (2) on more heterogeneously distributed prey. The experimental system was comprised of 1000-liter tanks (1, 4 or 8), interconnected to allow free movement of roach (*Rutilus rutilus*, 8 per tank), with different densities of *Daphnia* prey, distributed with varying levels of homogeneity. As reported previously, the selectivity of roach was found to be increased at higher *Daphnia* densities, but only in small-scale systems where prey distribution was homogeneous. However, the opposite was found in large-scale systems with heterogeneous prey distribution, i.e. greater selectivity at lower prey densities. The reversed slope of the selectivity-on-prey-density regression was linked to increased swimming velocity at low prey density, where the fish, less constrained by the limited size of the experimental system, accelerate, possibly in an effort to compensate for low encounter rate and to more rapidly locate patches of prey. These findings suggest that more selective feeding on scarce and patchy prey may result from the decreased relative visibility of smaller prey, and from the increased capture costs due to the need to expend more energy for post-capture accelerations to regain a higher speed.

Evolution of cis-regulatory non-coding RNAs in reduced bacterial genomes

Dorota Matelska, Janusz Bujnicki, Stanisław Dunin-Horkawicz

Laboratory of Bioinformatics and Protein Engineering, International Institute of Molecular and Cell
Biology, Poland

sdh@genesilico.pl

The proteome size and complexity is frequently reduced in endosymbiotic and pathogenic bacteria such as *Buchnera*, *Mycoplasma* or *Mycobacteria*. Here we present results of a comparative genomics study indicating that the reduction of proteome is accompanied by a loss of cis-regulatory RNA structural motifs. These non-coding RNA motifs are usually localized in 5' untranslated regions (5'UTRs) of transcripts and regulate expression of cognate genes either at the level of transcription or translation. Frequently, despite of the RNA motifs loss, the associated genes (usually encoding housekeeping proteins) are preserved. Comparison of the 5'UTR sequences of these "survivors" genes to their counterparts in non-reduced genomes revealed that they are shorter, have considerably lower GC-content and lower propensity for RNA structure formation. Moreover, RNA motifs that regulate genes involved in the response to the environmental changes were found to be more prone to undergo such a decay process.

Nearly neutral evolution of mitogenomes in genus *Capreolus*

Maciej Matosiuk, Anetta Borkowska

Institute of Biology, University of Bialystok, Poland

maciej.matosiuk@gmail.com

Introgressive hybridization of the mtDNA genome between closely related mammal species, the European and the Siberian roe deer is widespread in Poland. However, there is no empirical evidence whether maintenance of Siberian roe deer genetic variants is a result of adaptive mtDNA introgression. Multivariate multiple regression analysis indicated that some environmental factors may have an effect on distribution of introgressed individuals. To test whether Siberian roe deer mtDNA show signs of adaptive evolution we sequenced and compared 16 complete mitogenomes of both *Capreolus* species and introgressed individuals. Average net divergence of species-specific lineages was estimated at 2,8%, however it varied across different gene classes. Despite of large interspecific differences, merely 21 out of 315 fixed differences identified in protein coding genes represented nonsynonymous changes. Most of the studied genes evolved neutrally since tMRCA of *Capreolus* species. Results of McDonald-Kreitman test reveal that three adjacent genes (ND4, ND5 and ND6) have signs of purifying selection. Nearly neutral evolution of mitogenomes in genus *Capreolus* supports hypothesis that maintenance of foreign genetic variants is a by-product of demographic changes and genetic drift during range expansion of European roe deer after LGM.

Origin of avian flight - problems solved and unsolved

Dawid Mika

High School nr 3 of Stanisław Wyspiański in Jastrzębie-Zdrój, Poland

hesperonychus@interia.pl

Theory BAD (Birds are Dinosaurs) is generally accepted, but beginnings of avian flight are still very controversial. There are two main questions: when and in what way flight arised? Answer to first with above mentioned doubts (was coelurosaurian flight arised one times or more independently?) depend in large degree on phylogenetics Maniraptora, particularly such taxons as *Archaeopteryx lithographica* (Meyer, 1861), *Pedopenna daohugouensis* (Xu & Wang, 2005), *Microraptor gui* (Xu et al., 2003), *Anchiornis huxleyi* (Xu et al., 2009), *Xiaotingia zhengi* (Xu et al., 2011). In order explanation in what way avian flight arised, two mainly hypothesises were suggested. First ground-up hypothesis assume that ancestors of birds were cursorial animals, which during running carry out jumps, later given rise of flight. This hypothesis was for first time proposed by Samuel Wendell Willinston (1879). In past, some versions of ground-up hypothesis was suggested, including WAIR (Wing-Assisted Incline Running). Trees-down hypothesis (created by Marsh, 1880) suppose that birds evolved from small creatures, which jumped from branch to branch. There also scenarios evolution of avian flight, join ground-up and trees-down hypothesis. Author analyse possible phases evolution of flapping flight, potential arboreal adaptations among various coelurosaurians and evidence for and against ground-up and trees-down hypothesis.

Do frequent migrations of the ant *Temnothorax crassispinus* to new nest sites affect life history parameters?

Sławomir Mitrus

Katedra Biosystematyki, Uniwersytet Opolski, Polska

smitrus@uni.opole.pl

Colonies of the ant *Temnothorax crassispinus* inhabit mostly cavities in wood and hollow acorns. Such nest sites are not very durable (e.g. because of decomposition), therefore colonies of the ant could be forced to emigrate to new nest sites during season. In the second half of April 2013, 40 colonies of the ant were collected, and laboratory experiment to study effects of such migrations has been initiated. The colonies are kept in artificial conditions in Petri dishes, with artificial nests. Such an artificial nest has a cavity between a piece of cardboard and $\frac{1}{2}$ microscope slide, kept apart by a plexiglass frame. At the beginning of the experiment, migrations of all colonies were recorded on video, and e.g. the discovery time, and the assessment time (interval from discovery time to the time the first brood or adult was carried into the new nest) have been studied. Migrations will be also recorded in middle of June. Since beginning of May, in experimental group (randomly chosen 20 colonies) every week the artificial nests are destroyed, and the ants have to migrate to new nest. The laboratory experiment will end in the second half of July. Results of the experiment (e.g. number of workers per colony, and sex ratio of sexual individuals) will be presented.

Apolipoprotein E polymorphism - trade-offs between women's fertility and lifespan

Ludwik Odrzywolek¹, Anna Ziomkiewicz², Grażyna Jasieńska¹

¹ Department of Environmental Health, Collegium Medicum of Jagiellonian University, Poland

² Polish Academy of Sciences, Poland

ludwik.odrzywolek@uj.edu.pl

Life-history theory predicts existence of trade-offs between reproduction and lifespan. Some of these trade-offs may have a genetic background. Human apolipoprotein E (ApoE) plays important role in several metabolic processes, such as lipid transport and neuronal repair/protection. It is also involved in pathologies related to advanced age, such as cardiovascular and Alzheimer's disease. ApoE also plays important role in the regulation of steroid hormone action and thus may influence reproduction.

It is well established that carriers of APOE*3 allele have higher risk of health problems than APOE*2 or APOE*4 carriers. Surprisingly, APOE*3 allele is the most frequent in all populations investigated up to now. This high frequency of health-deleterious APOE*3 allele may be explained the fact that, as indicated by some studies, APOE*3 carriers may have better health condition in young age and higher fertility.

We suggest that in order to understand the ApoE impact on trade-offs between fertility and lifespan in human populations, an array of biodemographic variables related to women's fertility and their health condition should be taken into account.

Body attractiveness, nasopharyngeal flora and immunocompetence

Bogusław Pawłowski¹, Judyta Nowak¹, Barbara Borkowska¹, Zuzanna Drulis-Kawa²

¹ Department of Human Biology, University of Wrocław, Poland

² Institute of Genetics and Microbiology, University of Wrocław, Poland

bogus@antropo.uni.wroc.pl

The traits perceived as attractive are supposed to be honest signals of a person's biological quality. Body height, body mass index (BMI) and in women waist-to-hip ratio (WHR) are traits related to body attractiveness. If immunocompetence handicap principal (IHP) is true, people with more attractive values of these traits should be more immunologically competent. To test this, we analyzed whether colonization by potentially pathogenic bacteria in nose and throat, is related to body height, BMI in both sex and to WHR in females. Height and weight of 111 women and 92 men were self-reported. Waist and hip circumferences were measured. BMI and WHR were calculated. Microbiological analysis concerned nasopharyngeal colonization by six common respiratory pathogens (e.g. *Staphylococcus aureus*, *Streptococcus* spp). Bacterial strains identification from nasal and throat swabs were confirmed by colony morphology, standard biochemical assays and latex tests. Carriage participants were compared with non-carriage ones using Kruskal-Wallis test.

Nasopharyngeal colonization with the most frequent *S. aureus*, was observed in 110 subjects (54%). Colonized males appeared to have higher BMI than non-colonized ones (no difference for females). Colonized females had significantly lower WHR. Body height was not related with colonization in neither sex. We confirmed our hypothesis only for BMI in males. Since females with less attractive body shape are less likely to be colonized, we suggest that our results might be explained by higher immunocompetence of those who bear costs of higher level of testosterone.

**Patterns of cranial size variation in two sibling species
Plecotus auritus and *P. austriacus* (Chiroptera: Vespertilionidae)
in a contact zone**

Tomasz Postawa¹, Igor Zagorodniuk², Justyna Bachanek¹

¹ Department of Vertebrate Zoology, Institute of Systematics and Evolution of Animals PAS, Poland

² Laboratory of Animal Ecology and Biogeography, Taras Shevchenko's Luhansk National University, Ukraine

tpostawa@gmail.com

The coexistence in one area of two species with similar ecological requirements can lead to their morphological convergence or divergence. Convergence may be the result of adaptation to new conditions (species share a niche), whereas divergence may be the effect of competition for a resource (species compete for a niche). Compatibility with Bergmann's rule is possible in species with a significant latitudinal range. We tested whether potential differences between two long-eared bat species are consistent with character displacement or Bergmann's rule by investigating variability in cranial morphology of *Plecotus auritus* and *P. austriacus*, which commonly occur in Central and Eastern Europe. We used 111 complete specimens from the allopatric range of *P. auritus* (nine localities) and sympatric *P. auritus* and *P. austriacus* (44 localities) from Poland and Ukraine. A traditional morphometric method was used to evaluate variation in cranial size between the species in their ranges. Discriminant function analysis of cranial dimensions showed larger differences between sympatric populations of *P. austriacus* and *P. auritus* than between allopatric *P. auritus* and a sympatric population of *P. austriacus*. A subsequent analysis showed that most cranial variables (excluding elements of the skull responsible for prey capture and elements partly associated with echolocation) from the sympatric population of *P. auritus* are smaller than those homologues from allopatric populations. Larger individuals from the allopatric population originate from the northern part of the study area; however, we did not detect an association of cranial variability with latitude pattern. The variation in size of the cranium between individuals from allopatric and sympatric ranges of *P. auritus* can be explained by different preferences in each range for prey that vary in hardness. *P. auritus* consumed significantly more hard-bodied insects in allopatry than in sympatry. This example is one of few confirmed morphological cases of competitive character displacement.

Correlated responses to artificial selection for high maximal aerobic metabolism in the bank vole: striped muscle morphology

Ewa Prawdzik, Julia Wyszowska, Dagmara Filak, Magdalena Guńska, Anna Maria Łabęcka, Edyta Teresa Sadowska, Paweł Koteja

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

eprawdzik@gmail.com

Aerobic capacity presumably played a crucial role in the evolution of endothermy and hence evolution of mammalian and avians lineages. Experimental evolution model, lines of bank voles (*Myodes glareolus*) selected toward increased aerobic metabolism achieved during swimming, provide a unique model to study morpho-physiological and biochemical factors underlining evolution of high aerobic capacity and the mechanism limiting aerobic metabolism. Preliminary studies revealed that bipennate leg muscle (*m. gastrocnemius*) mass was higher in selected voles (A; mean±SD, females: 94.5±12.3mg, males: 112.3±13.2mg) than in control ones (unselected, C; females: 83.5±11.8mg, males: 97.6±16.8mg; p=0.03) and was positively correlated with oxygen consumption achieved during forced-exercise on a treadmill (p<0.001). Light microscopy methods were used to test hypothesis that increased aerobic performance is correlated with changes on tissue/cellular level. We used histochemical periodic acid – Schiff reaction to categorize muscle fibers' types and measure cross-sectional dimensions of the fibers as well as progressively hematoxylin staining to assess capillary density in leg muscle of voles from selected and control lines. The results will provide information about differences in muscle structure and the capacity of oxygen transport at the last stage of the pathway from lungs to the working cells.

Male polymorphism in *Rhizoglyphus echinopus*

Jacek Radwan¹, Mateusz Twardawa¹, Aleksandra Łukasiewicz²

¹ Evolutionary Biology Group, Adam Mickiewicz University, Poznań,

² Department of Animal Morphology, Adam Mickiewicz University, Poznań, Poland

mathieu1829@wp.pl

Male dimorphism has been described in several species of the mite family Acaridae (Acari: Astigmata). Two basic male morphs occur: heteromorphic (aggressive fighters) with modified, thickened and sharply terminated third pair of legs and homeomorphic (scramblers) with unmodified third pair of legs. Determination of alternative male morph can be heritable (*Rhizoglyphus robini*), or environmentally dependent (*Rhizoglyphus echinopus*, *Caloglyphus berlesei*), where fighter morph is suppressed by substances emanating from colonies. Previous studies have shown that heteromorphic males of *C. berlesi* had higher reproductive success in small colonies, where fighters managed to kill rival males and often monopolise females, but in large colonies the situation was reversed because fighters were killed more often. This indicates that sensitivity to pheromones carrying cues to population size is adaptive. *R. echinopus* shows similar sensitivity to such cues, and thus we predict that the relationship between morph reproductive success and colony size will be similar as in *C. berlesei*. We will present results of the experiment testing this prediction.

Survival pattern of bank voles selected for high aerobic capacity

Agata Rudolf, Katarzyna Chrzęścik, Geoffrey Dheyongera, Edyta Sadowska, Paweł Koteja

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

agata.rudolf@uj.edu.pl

According to the “rate of living theory,” animals with high metabolic rate have increased ageing and mortality rates. Our artificial selection experiment on bank voles (*Myodes=Clethrionomys glareolus*), based on four lines selected for high swim-induced aerobic metabolism (A) and four unselected-control lines (C), provides a suitable model to test the hypothesis. Voles from the selected lines achieved about 50% higher rate of the maximum swim-induced oxygen consumption, and had also significantly increased basal metabolic rate and food consumption. In generation 13, we monitored survival in 2115 young animals (A: 1112, C: 1003) from 17-th to 75-th day of life (from weaning to sexual maturity) and in 167 adults (A: 82, C: 85) from 75-th day to advanced senility (534 days). Statistical analyses were based on proportion of survived animals in each of the eight lines. The survival did not differ significantly between lines either in young animals (mean±SD; A: 0.959±0.03, C: 0.978±0.01; Mann-Whitney U = 2.000, p = 0.083) or in adults (A: 0.776±0.14, C: 0.762±0.14; Mann-Whitney U = 8.000, p = 1.000). Thus, contrary to the expectation of "the rate of living theory", selection for high aerobic metabolic rate did not influence age-related survival. In the next step of the project we ask how the selection affected age-related changes in physiological performance and underlining biochemical traits.

Meta-analysis reveals no egg sexual size dimorphism in birds

Joanna Rutkowska¹, Anna Dubiec², Shinichi Nakagawa³

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

²Museum and Institute of Zoology, Polish Academy of Sciences, Warsaw, Poland

³Department of Zoology, University of Otago, Dunedin, New Zealand

joanna.rutkowska@uj.edu.pl

Maternal effects mediated by egg size may have profound effects on offspring fitness. Sex-biased resource allocation in birds gains increasing interest, but it is not known to what extent the egg sexual size dimorphism (SSD) is a wide-spread phenomenon in this group. To answer that question we performed meta-analysis of 65 studies, which included information on egg SSD of 52 species. Many of those studies suggested adaptive explanation for the reported egg SSD, which helped us to formulate predictions for our analyses. In some species, egg SSD was suggested to promote future size differences between the adults. If that is the case, then across species, adult SSD should be a significant predictor of egg SSD. However, in other species, egg SSD was invoked as an adaptive means by which a female balances nestling mortality differences between sexes, therefore producing bigger eggs for the smaller sex. Based on these two hypotheses, we derived a general prediction that there should be a significant relationship between the magnitude of adult SSD and the magnitude of egg SSD irrespective of the direction. Our analyses found no support for either of those hypotheses. Across species, adult SSD does not predict egg SSD. More importantly, the observed variation in effect sizes in our dataset was to a large extent explained by sampling error and there was no difference in avian egg sizes between the sexes. Although adult SSD is undoubtedly a prominent feature of birds, we conclude that, in general, there is no evidence for egg SSD across the species.

Maximum cold-induced food consumption in bank voles selected for high swim-induced aerobic capacity

Edyta T. Sadowska, Katarzyna M. Chrząścik, Geoffrey Dheyongera, Agata Rudolf, Paweł Koteja

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

edyta.sadowska@uj.edu.pl

To test a hypothesis that high capacity for energy assimilation in cold-exposed endotherms could evolve as a correlated response to selection for increased locomotor-related aerobic capacity, we studied bank voles (*Myodes=Clethrionomys glareolus*) from lines selected for high swim-induced aerobic metabolism (A) and unselected control lines (C). After 13 generations, voles from the four selected lines had about 50% higher aerobic capacity, 12% higher basal metabolic rate, and about 7% higher routine food consumption rate than voles from the four control lines. Body mass of the animals (mean age \pm SD: 114 \pm 7.6days, N=96) maintained in room temperature (+20°C) was higher in the selected (LSM \pm SE; 24.9 \pm 0.4g) than in the control lines (22.6 \pm 0.6g, p=0.007). The maximum cold-induced rate of food consumption, achieved after gradual exposure to low ambient temperatures (overall 46 days from +20°C down to -16°C or to maintain positive body mass balance), was significantly higher in the selected than in the control voles (mass-independent LSM \pm SE; A: 12.19 \pm 0.18g/day, C: 11.51 \pm 0.20g/day, p=0.044). The coefficient of digestibility did not differ significantly between the lines (A: 72.83 \pm 0.53%, C: 72.21 \pm 0.57%, p=0.527), so the difference in food consumption reflects a difference in energy budgets. Although the selected voles have higher basic costs of maintenance during the extreme cold exposure, they maintained body mass as well as control ones (A: -0.41 \pm 0.22g/day, C: -0.32 \pm 0.22g/day, p=0.389). The results suggest that selection for increased locomotor-related aerobic capacity would not be a factor behind the evolution of high capacity for energy assimilation during prolonged cold-exposure.

Searching for genes determining mating types in selected species of the *P. aurelia* complex

Natalia Sawka¹, Deepankar Pratap Singh², Olivier Arnaiz³, Małgorzata Prajer¹, Sebastian Tarcz¹, Casey L. McGrath⁴, Tom Doak⁴, Eric Meyer²

¹ Instytut Systematyki i Ewolucji Zwierząt Polskiej Akademii Nauk, Polska

² Laboratoire de Génétique Moléculaire, Institut de Biologie de l'Ecole Normale Supérieure, France

³ Centre de Genetique Moleculaire, France

⁴ Department of Biology, Indiana University, United States

sawka@isez.pan.krakow.pl

In each species of the *Paramecium aurelia* complex, two mating types are distinguished: O (Odd) and E (Even). The O and E types are homologous in all species, but they are determined by one of three different systems: maternal inheritance (synclonal), random determination (caryonidal), or Mendelian determination. Previous work in *P. tetraurelia* identified three genes that are required for expression of mating type E (*mtA*, *mtB*, and *mtC*). *mtA* encodes an E-specific transmembrane protein likely involved in agglutination with O cells, while *mtB* and *mtC* appear to encode transcription factors required for *mtA* transcription. In *P. tetraurelia*, mating type O is determined during macronuclear development by the excision of the *mtA* promoter as an IES; the rearrangement is regulated by the scnRNA pathway, explaining the maternal inheritance of mating types.

We have started a survey of selected species from each of the 3 systems to test whether mating type E is characterized by expression of *mtA* orthologs in all species, and to determine whether this always requires *mtB* and *mtC* orthologs. The final aim is to identify the mating-type determination mechanism in each species and to determine how is it possible to evolve from a maternal inheritance system to a random determination one, or the reverse, or to a Mendelian one.

The results obtained so far are consistent with the idea that *mtA* expression is always associated with type E, but the mechanisms of mating-type determination appear to vary widely among *P. aurelia* species.

"Escape into the niche" mechanism as novel evolutionary screenplay

Edwin Sieredziński

Department of Parasitology, Faculty of Biology, University of Warsaw, Poland

colonelvolf@gmail.com

During phylogenetic research of animals the largest controversies were related to most specialized taxa. Endeavor by molecular approach often yielded long-branch attraction. Taking into consideration classical paradigm by LANCASTER (1891), it should recognize these taxa as derivate. Moreover, congruence issue implicating from various – molecular, morphological and paleontological – data is appeared. It should rethink about new attempt.

Such case is comprised by Dicyemida, parasites of marine invertebrates. These animals have H1 histone, instead of protamine, as Porifera and Cnidaria (CZAKER, 2011). It is undoubtedly primordial feature, which does not correlate with Dicyemida position between Lophotrochozoa. Therefore subsequent question is appearing: can Dicyemida be a descendants of unknown antic group?

Similar case pertains to Nymphomyiidae, neotenic midges family from regions of wordl. GRIMALDI and ENGEL (2004) suggested place between Culicomorpha, pointing out difficulties with *Baeonotus* classification. However, Nymphomyiidae are descendants of primeval Diptera what can signalize paleontological data (HUANG et al., 2013; KRZEMIŃSKI 2003).

Hitherto investigations are not sufficient for Pentastomida. Current researches often classify this group between Ichtyostraca (Maxillipoda) with fish lice (ZRZAVÝ, 2001). Thus it does not interlink with paleontological data – tongue worms have been existing since Cambrian period (WALLOSEK et al., 1994).

These cases are enjoining novel conception – “escape into the niche”. A number of taxa are withdrawn to extreme habitats and undergo modification afterwards. Regarding it, recapture of their phylogenetic development – and systematical position, too – is arduous. Striving toward holistic portrayal of evolution becomes necessity, what let to prove mentioned phenomenon.

Different mate strategies in two morphs of bulb mite

Anna Skrzynecka, Agata Plesnar- Bielak, Michał Kolasa, Jacek Radwan

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

anna.skrzynecka@uj.edu.pl

The bulb mite *Rhizoglyphus robini* with two male morphs, exhibiting different ways of securing mating partners, is an example of species with alternative reproductive phenotypes. Aggressive fighters, possessing a sharply terminated third pair of legs, which they use to mortally stab other males, coexist in population with unarmed scramblers. Morphs may also differ in some aspects of mating behaviour. Copulation in *R. robini* usually lasts about 20 min, but pairs may remain associated for a much longer time. Such postinsemination association probably function as mate guarding: a male that can prevent female from re-mating benefits by increasing his paternity, but simultaneously such behavior may be costly in populations with aggressive fighters. In our study we checked whether mate guarding strategy depends on morph and social context. We established experimental populations differing in morph ratio to check if males can modify behaviour based on their social experience. We also compared mites from lines selected for increased proportion of either fighters or scramblers (33 generations resulting in ca. 80 % of appropriate morph in each line). We found that association time was not affected by social context. However, scramblers from «scrambler selection lines» remained with females twice longer than fighters from «fighter selection lines». Our results indicate that morph ratio can be an important selective force determining guarding behavior, although mites cannot modify this behavior due to social context. This suggests that guarding behavior is genetically controlled rather than socially plastic and depends on the evolutionary history of a population.

Phylogeography of two species of voles (*Microtus*) in Poland inferred from cytochrome b and microsatellite DNA analyses

Joanna Stojak¹, Allan D. McDevitt², Jeremy B. Searle³, Jeremy S. Herman³, Jan M. Wójcik¹

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

² School of Biology and Environmental Science, University College, Dublin, Ireland

³ Department of Ecology and Evolution, Cornell University, Ithaca, United States

jstojak@ibs.bialowieza.pl

In this project, we utilised well-preserved museum specimens of common voles (*Microtus arvalis*) and field voles (*Microtus agrestis*) collected from different populations in Poland in the 1960/70s. To perform phylogeographic analyses the complete cytochrome *b* gene (mtDNA) was amplified in several overlapping fragments in ~100 individuals in each species and 11 (*M. arvalis*) and 13 (*M. agrestis*) microsatellite loci were analysed from ~200 individuals of each species. Preliminary results of cytochrome *b* revealed that at least two mtDNA lineages in these two species occur within Poland when analysed with existing data on a European-wide scale. They do however show contrasting patterns in their distribution in Poland. We assume that one of lineages of the common vole colonised Polish territory from the Carpathian refugium, because fossils of this species from Last Glacial Maximum (LGM) were abundant in this region. The same however is not true of the field vole and the origin of the lineages present is so far uncertain. In contrast, preliminary results of the microsatellite data suggests a similar pattern of genetic structuring and distribution of these genetic clusters in Poland. Therefore, it is clear that ancient and contemporary events are leaving different signals in related vole species. Additional samples are currently being collected from unsampled sites in Poland and in adjacent countries to further enlighten post-glacial colonisation processes and factors shaping contemporary genetic structure in small mammals in central and eastern Europe.

Characterization of sex-biased genes from the transcriptome of a male-dimorphic mite

Michał T. Stuglik, Wiesław Babik, Jacek Radwan

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

michal.stuglik@uj.edu.pl

The different sexes experience different selective pressures, which can lead to highly divergent phenotypes that are achieved via sex-biased gene expression. As a result of sexual selection and sexual conflict, sex-biased genes are expected to evolve at a faster rate than other genes in the genome. Furthermore, because sexual selection acts more strongly on males, male-biased genes are expected to evolve faster than female-biased genes. We aimed to test these predictions in a model species for sexual selection and conflict research, the bulb mite *Rhizoglyphus robini* (Acari, Acaridae), in which armored, aggressive fighter males coexist with unarmored scrambler males. We sequenced and de-novo assembled transcriptomes of adult males and females. Expression of 4.0% of 114,456 transcriptome-based gene models (TGMs) was male-biased, whereas 1.3% of TGMs had female-biased expression and this difference was highly significant. For TGMs with protein-coding capacity, the proportion with orthologs identified in the spider mite (*Tetranychus urticae*) genome was lower for male-biased than for unbiased genes, but was very similar for female-biased and unbiased genes. Mean amino acid distances between male-biased *R. robini* genes and their *T. urticae* orthologs were significantly greater than those between unbiased genes and their orthologs; female-biased gene orthologs had distances similar to those of the unbiased orthologs. The higher number and faster evolution of male-biased genes are consistent with the hypothesis that sexual dimorphism is driven mostly by male-biased sexual selection. This hypothesis is further supported by the result that the fighter morph, which is behaviorally and morphologically adapted to intense intrasexual competition, was characterized by a considerably larger number of overexpressed (compared to female expression levels) genes than the less sexually dimorphic scrambler morph.

How long to remain in diapause in unpredictably changing habitats?

Mirosław Ślusarczyk¹, Piotr Bernatowicz²

¹ Department of Hydrobiology, University of Warsaw, Poland

² Department of Paleobiology and Evolution, University of Warsaw, Poland

m.slusarczyk@uw.edu.pl

Most organisms inhabiting temporary changing habitats entail protective dormant forms to cope with periodic deterioration of environmental conditions. Dormant forms of some organisms do not resume development at first favourable season, yet postpone it till further occasion, being capable to arrest development for years, decades or even centuries. According to theoretical expectations proportion of dormant forms that hatch at first occasion should be inversely related to probability of occurrence of unfavourable conditions. The ultimate length of diapause has not been however tested so far. In the present study we examined how long should organisms postpone development in unpredictably changing habitats with stochastic and individual based models.

DNA barcoding of unicellular eukaryotes - is it sufficient for fully species delineation in the *P. aurelia* species complex?

Sebastian Tarcz, Natalia Sawka, Ewa Przyboś

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

tarcz@isez.pan.krakow.pl

Ciliates from the genus *Paramecium* are model organisms in biochemistry, cell biology, physiology, genetics as well as in the field of evolution and speciation. Although species of the *Paramecium* genus are some of the best known protozoans, the problems concerning their speciation, determination of boundaries between species as well as biogeography has not been thoroughly elucidated. The *Paramecium aurelia* complex (Ciliophora, Protozoa) is composed of fifteen sibling species, which are morphologically indistinguishable but sexually isolated. Therefore, the *P. aurelia* complex seems to be an ideal model for testing hypotheses about recent speciation events. From the biological point of view, the sibling species of the *P. aurelia* complex may be identified by mating reactions (conjugation) with the standard strains and complimentary mating types of particular species. In turn, comparison two “barcoding” DNA fragments (ITS1-5.8S-ITS2-5’LSU rDNA and *COI* mtDNA) in 120 representatives of all species of the complex revealed that some of them appear on the trees as monophyletic clusters (e.g. *P. undecaurelia*) whereas the other were polyphyletic (*P. octaurelia*). Present project is an extension of above analysis using almost sixty strains collected from around the world and representing three species of the complex (*P. tetraurelia*, *P. septaurelia* and *P. octaurelia*). The revealed discrepancies, which are manifested by different mating behavior and haplotypes not characteristic of particular species, may be explained by incomplete lineage sorting. On the other hand hybridization and introgression in natural populations of these species cannot be excluded. However, there are no scientific data which may confirm their presence.

Integration of the polecat dentition

Kamila Topolska, Mieczysław Wolsan

Muzeum i Instytut Zoologii PAN, Polska

ktopolska@miiz.waw.pl

Morphological integration is the cohesion among phenotypic traits that reflects the effects of interactions among biological processes producing the structure. Here we investigated the integration of the dentition in the European polecat (*Mustela putorius*). We first measured the lengths and widths of permanent tooth crowns in 15 males and 15 females originated from Poland. We then explored the pairwise relationship between all the variables by using the Pearson product-moment correlation coefficient. Results show that premolars are more integrated than molars; corresponding upper and lower cheek teeth are more integrated than noncorresponding cheek teeth; contiguous cheek teeth of an arcade are more integrated than noncontiguous cheek teeth; and the second lower molar is least integrated.

Phylogeny and history of dispersion of Carpathian species of *Bryodaemon* Podlussany, 1998 (Coleoptera: Curculionidae)

Beniamin Waclawik

Wydział Biologii i Nauk o Ziemi, Uniwersytet Jagielloński, Kraków, Poland

beniamin@wacławik.eu

For resolving causes of today's species and populations distribution in Europe, most relevant and reliable data are these obtained on recent events such as climatic oscillations during the Quaternary. Because of recurrent cooling and warming periods, ranges of many species cyclically contracted and expanded. Thus, these changes had huge impact on distribution, that we can observe today and also they could have influence on speciation caused by division of ranges. By resolving phylogenetic histories of species and connecting them with geographical data, we can attempt to reconstruct phylogeographical paths of many taxa-we try to get to know how they expanded, in which refugia (areas with more stable climate) they survived during periods of suboptimal conditions, or even when speciation could occur.

Phylogenetic research based on molecular data is one of most dynamically developing fields of evolutionary biology. Studies using DNA markers are very helpful in research on clades that include many species or/and have complicated evolutionary history. A very good example of such clade is beetle family Curculionidae (weevils).

This research was made on four Carpathian species of weevils *Bryodaemon* Podlussany, 1998 (Coleoptera: Curculionidae). Their morphological similarity, mostly montane distribution and overlapping of ranges point to Quaternary climate oscillation as main cause of their divergence and dispersion. Main goal of research was to confirm (or not) their monophyly, and to resolve their phylogeographical history. Basing on three molecular markers (one mitochondrial and two nuclear), phylogenetic trees of 13 populations of these species were constructed. Species monophyly was confirmed, and obtained phylogenetic trees allowed to get to know their phylogeography. There was made attempt to answer which refugia could be connected with history of the genus, and what possible climate changes could lead to dispersion and divergence of species.

Physiological range of temperature limits the Temperature-Size Rule acting

Aleksandra Walczyńska

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

aleksandra.walczynska@uj.edu.pl

The performance curve for population growth rate r was measured in the wide range of temperature for three species: *Coleps hirtus* (Protista), *Lecane inermis* (Rotifera) and *Aeolosoma hemprichi* (Oligochaeta). These data were linked with body size of individuals across temperature for the examination of temperature-size rule (TSR) acting. The results show that TSR operates only within the range between minimal and optimal temperature, regarding r as a measure of fitness. It seems that these two temperature values delineates the physiological range outside which an organism is physiologically constrained against displaying the size plasticity as response to temperature. This result has important implications for general size-temperature studies because it shows that the temperature arbitrary chosen is not indifferent for an organism and the preceding knowledge on its thermal preferences is needed. An application of this finding could cause a decrease in the number of species that are known from the literature as the exceptions from TSR.

When did the fire-bellied species arise? Thus spoke fossils and mitochondrial DNA

Anna Wandycz¹, Maciej Pabijan¹, Sebastian Hofman¹, Jacek M. Szymura¹, Marcin Piwczyński², Karolina Węcek¹

¹ Instytut Zoologii, Uniwersytet Jagielloński, Kraków, Poland

² Katedra Ekologii i Biogeografii, Uniwersytet Mikołaja Kopernika, Polska

anna.wandycz@uj.edu.pl

The European fire-bellied toads, *Bombina bombina* and *B. variegata* hybridize in a narrow zone whenever their parapatric ranges meet. Here we provide phylogeny and time estimate of their divergence based on 18 complete mitochondrial DNA sequences from all extant species and fossil calibration. The small- and large-bodied *Bombina* were recovered: ((*B. bombina*, *B. variegata*)*B. orientalis*), and (*B. maxima*, (*B. microdeladigitora*, (*B. lichuanensis*, *B. fortinuptialis*))) with $2n=24$ and $2n=28$ chromosomes respectively. Further subdivisions were found within *B. variegata*. The earliest split between large- and small-bodied *Bombina* took place either in the Middle Oligocene or the Early Miocene. East Asian *B. orientalis* and European *Bombina* diverged in the Early or Middle Miocene. The separation of *B. bombina* and *B. variegata* occurred in the Late Miocene. Climatic changes in Late Pliocene and Pleistocene induced episodes of vicariance events that led to the formation of the Carpathian *B. variegata* lineage, two *B. v. scabra* lineages in the Balkans and the allopatric *B. v. pachypus* in the Apennines. In ecologically specialized *B. bombina* mtDNA lineages is low, with an Anatolian lineage as the sister group to the European mtDNA clades.

Miocene diversification in the genus *Bombina* resulted in six allopatric major mtDNA lineages that further diversified during the Pliocene and Pleistocene and have survived till now. Narrow habitat requirements of fire-bellied toads combined with extensive environmental changes in the Neogene throughout the Palearctic may have contributed to a putatively high extinction rate in these Archeobatrachians resulting in the spectacular disjunction of their ranges in Eurasia.

Can the lost variation be found by sequencing multiple mitogenomes from recent and archival wisents

Karolina Węcek, Jacek M. Szymura

Instytut Zoologii, Uniwersytet Jagielloński, Kraków, Poland

karolina.wecek@uj.edu.pl

The European bison or wisent (*Bison bonasus*) has experienced a drastic population size reduction following World War I. The modern herds, managed as two separate lines (the Lowland line and the Lowland-Caucasian line), originated from only a few founders. The current wisent population is characterized by a low level of genetic variability observed at neutral markers and mtDNA control region (CR). However, low variation in the CR may not be representative for the whole molecule, as recent studies in mice showed a *lower* mutation rate in the CR than the coding mtDNA segments. We seek an answer the question if low genetic variability extends indeed over the whole molecule, and was associated with the bottleneck. We have obtained nucleotide sequences of three complete mtDNAs of *B. bonasus* from the Lowland line and one mtDNA from the Lowland-Caucasian line, all of which appear identical, shared the same mtDNA haplotype. Comparison of this haplotype with two other mtDNAs and various mtDNA fragments deposited in GenBank showed surprisingly large variability. Further studies will show whether these nucleotide substitutions represent real polymorphisms, sequencing errors or result from other phenomena, e.g. “paternal leakage”. We also extracted archival DNA from hair samples acquired from two founders of all extant wisent herds to assess if genetic purging took place upon the bottleneck produced by the restitution or the pre-bottleneck population already was depauperate. So far there is little evidence for nucleotide mtDNA variability in *B. bonasus* preceding the bottleneck.

Effects of evolution of intromission on courtship and male and female morphology in water mites of the genus *Arrenurus*

Mariusz Więcek

Institute of Environmental Biology, Adam Mickiewicz University, Poland

roztoc@wp.pl

The role of female preference for particular male traits was emphasized in studies on sexual selection. However, there is growing evidence that sexual conflict can drive morphological and behavioural diversification (Arnqvist & Rowe 2005). Within the water mite genus *Arrenurus*, there are species in which sperm transfer is under female control, and others under male control. In the present study I reconstruct phylogenetic relationships among main *Arrenurus* subgenera based on mitochondrial (COI) and nuclear (D2 28S rDNA) markers, and map morphological structures engaged in reproduction onto a phylogeny reconstruction. I hypothesize that male reproductive morphology, which is currently the main rationale for the subgeneric classification of the genus *Arrenurus*, will not prove to be a perfect predictor of phylogenetic relationships. Additionally, I observe complete courtship sequences to test the hypothesis that duration and complexity of courtship would be reduced in intromittent species, in which the male does not have to "convince" the female to take up sperm. The approximately 20 target species will include species having a range of elaboration of male genitalia and grasping structures. In addition to observing complete courtship sequences, I used SEM to describe details of male and female morphology. I present first results of the study and discuss what evolutionary processes may drive morphological and behavioural diversification in the genus *Arrenurus*.