October

Trade-offs in life-against-all odds-history of *Daphnia*

Prof. Dr hab. Piotr Dawidowicz

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

Date: Thursday, 10.10.2018, 13:00, Cent Lecture Theatre 0142

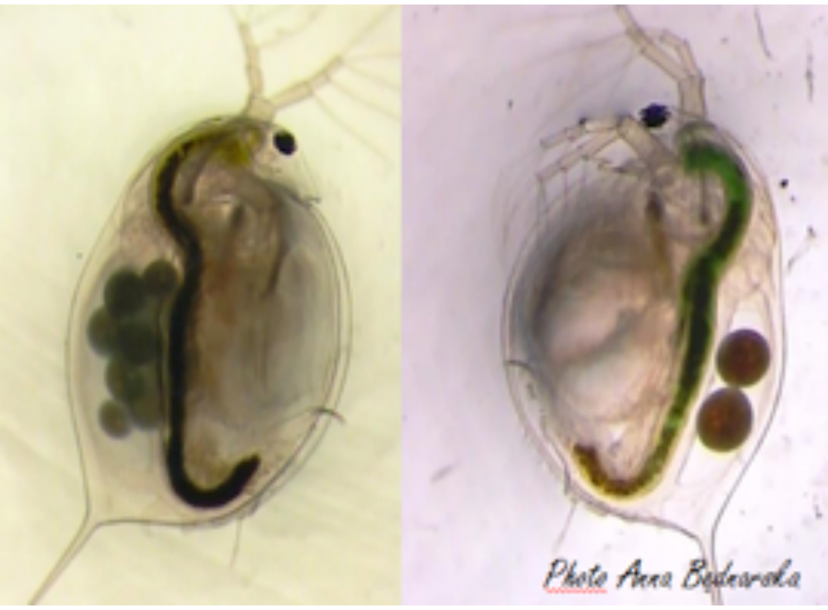

Photo Anna Bednarska

Abstract. *Daphnia*, the magnificent model organism, is particularly suitable for studying physiological and microevolutionary trade-offs. In this lecture I will present experimental evidence, based on phenotypic variation among individual *Daphnia*, of trade-offs between reproduction and somatic growth, reproduction and survival, current reproduction and future reproduction, and others. I will also demonstrate, how expression of a reproductive trade-off may vary among populations of Daphnia subjected to different selection pressures.

November

African swine fever virus (ASFV) in wild boar – *modus operandi*

Dr Tomasz Podgórski

Czech University of Life Sciences, Prague, Czech Republic & Mammal Research Institute, Polish Academy of Sciences, Białowieża, Poland

Date: Wednesday, 14.11.2018, 13:00, Cent Lecture Theatre 0142

Abstract. African Swine Fever (ASF) is a devastating viral disease of wild and domestic suids. It results in high lethality and has severe socio-economic consequences. The disease has been spreading among wild boar – host of the ASF virus in the wild – in eastern Europe for a decade now, following its first occurrence in Georgia in 2007. However, the role of wild boar ecology and behaviour in the epidemiology of ASF is poorly understood and remains largely speculative. I will present the most recent findings on the factors underlying ASF dynamics in Poland and discuss their relevance for disease control and wild boar management. First, host mobility is often expected to enhance spread of infectious diseases. In contrast to these expectations, wild boar movements were found to be poor predictors of ASF dynamics in space and time. Severity of the disease, which quickly hampers extensive movements and restricts disease transmission to only the most immediate individuals, appears to limit the influence of host movements on ASF spread. Wild boar social structure, the short duration of low-level virus shedding, and high virus-induced lethality most likely shape the gradual spread of ASF in space, estimated at 1 – 2 km/month within the wild boar population. Second, host abundance and landscape structure often interact to shape spatial patterns of many wildlife diseases. Occurrence of ASF was positively related to wild boar densities and this effect was stronger at locations near previous ASF incidents. ASF was also more likely to occur in forested areas and this pattern was consistent at low and high wild boar densities. Third, indirect transmission of ASFV, i.e. through infectious carcass, can play a primary role in the epidemiology of ASF in wild boar but its importance relative to direct transmission in this host-pathogen system is unknown. Using simulation models and epidemiological field data, we found that carcass-based indirect transmission is more prevalent than direct route and the role of indirect transmission becomes more important with decreasing host densities. These findings suggest that disease control efforts should target high-density populations and suitable habitats (large forested areas), emphasize removal of carcasses and consider how reductions in host densities may drive carcass-based transmission. The intensity of control measures should decrease with distance from the infected area to match the observed spatial pattern of ASF occurrence probability.

December

The impact of landscape management on genetic structure: a review and case studies from small mammals and ungulates

Prof. Elena Buzan

Dpt of Biodiversity, University of Primorska, Koper, Slovenia

Date: Wednesday, 12.12.2018, 13:00, Cent Lecture Theatre 0142

Abstract. In my talk, two selected topics will be addressed. In first part I will represent our research connected with the change in rodents communities as consequence of urbanisation and inappropriate waste management. Illegal waste disposal impacts public health and causes aesthetic and environmental pollution and drives the native rodents to local extinction replacing them with invasive commensal species. Waste disposed in places without permitted and controlled facilities can provide a ready source of nutrition and shelter for rodents and thus promote the spread of their ecto- and endoparasites. In our research we have shown that the spread of pathogens already endemic in the environment, where the waste site is located, can be significantly increased. Namely, the seroprevalence of Lymphocytic choriomeningitis virus (LCMV) infection of rodents trapped at illegal waste sites was higher compared to the LCMV infection of rodents from their natural environment.

In second part of may talk I will focus on using genetic diversity data for our understanding of the effects of habitat fragmentation on long-term persistence and viability of keystone species. Presentation will include results of long term study, which have been done on important game subspecies, Northern chamois, in Central Europe and Balkan. I will try to address the issues of the effects of past management on genetic structure and possible hybridization where the subspecies (*Rupicapra r. rupicapra* and *R.r. balcanica*) overlap (i.e., contact zone). Processes occurring at different spatial and temporal scales, fragmentation and losing of the populations connectivity have presumably different impacts on wildlife gene flow and consequently also on the main life-history traits.

January

Reproductive differences between urban and forest populations of great tits

Prof. András Liker

MTA-PE Evolutionary Ecology Research Group, University of Pannonia, Veszprém, Hungary

Date: Wednesday, 09.01.2019, 13:00, Cent Lecture Theatre 0142

Abstract. Urban birds often have lower reproductive success but higher densities than their conspecifics living in natural habitats, and it is still unclear what processes explain this paradoxical pattern. In a study started in 2012, we found that great tits breeding in two urban populations produce consistently fewer nestlings than birds in two nearby forest populations. This difference is likely explained by lower abundance/quality of nestling food in cities than in forests, because in cities (1) caterpillar biomass on trees is 8-20 times lower, (2) caterpillars constitutes a smaller part of nestling diet, and (3) although food volume per nestling shows no habitat difference, nestlings size and mass is lower. Furthermore, a food supplementation experiment showed that supplemented urban nestlings can achieve size and survival rate similar to control forest nestlings, whereas extra food has no effects on forest nestlings. The analyses of the frequencies of second broods suggest no habitat difference in the annual number of broods produced by individual females, and we also did not find consistent differences in the survival rate of breeding adult birds between cities and forest populations. Thus, the persistence and high densities of urban great tit populations can be related to higher survival rates of younger age classes (e.g. fledglings or first winter birds) and/or to immigration from surrounding natural habitats.

Photo credit: Bálint Preiszner

February

Natural selection: methodological constraints and climatic drivers

Dr Pascal Marrot

CNRS Toulouse, France

Date: Wednesday, 13.02.2019, 13:00, Cent Lecture Theatre 0142

Abstract. Global change results in an increase in temperature mean and variability and generates new environmental conditions for wild populations. In order to respond to this new threat, wild populations can move to another place (dispersion), change their behaviour or their phenology (phenotypic plasticity), or respond by evolutionary change (involving changes in alleles frequency). While many examples of phenotypic plasticity and dispersion have been observed in the wild, empirical detection of evolutionary responses to climate change remains rare. During my PhD, I studied natural selection induced by climate change (both in term of warming and extreme event frequency) acting on monitored population of blue tits (*Cyanistes caeruleus*) in southern France monitored for the past 26 years. Supporting past results for the Mediterranean region (known as a "hot spot" of climate warming), our climatic analyses revealed a strong warming in our study site, especially in spring (+ 0.6°C / decades since 1970). This warming was correlated with an increase in natural selection strength for earlier breeding. In fact, our results indicated an increase in the strength of selection by 46% every +1°C anomalies in maximum April temperature. Beyond this selective impact of the warming trend, we detected an impact of extreme hot days occurrence, independently of mean temperature trend: when 10% of broods in the population experienced this type of extreme climatic event, selection for earlier breeding increased by 39%. This study confirmed the selective impact of warming, pointing out a potential evolutionary response to climate change in the future.

Photo credit: Stephane Tillo

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March

It’s Anthropocene – why are we here and what can we do?

Dr Zofia Prokop

Jagiellonian University, Kraków, Poland

Date: Wednesday, 13.03.2019, 13:00, Cent Lecture Theatre 0142

Abstract. The changes which our single species has made to the biosphere and geosphere (particularly since mid-20th century) are so profound and widespread that, according to the International Commission on Stratigraphy, they go significantly beyond Holocene norms, prompting the formalisation of a new epoch in Earth’s history, which has been termed Anthropocene. The Anthropocene is characterised, among other things, by radical changes in the Earth’s climate, dramatically raised rates of species extinction (current estimates range from 10 to 10000 times above pre-industrial levels), rapid growth of human and livestock populations (currently our combined body weights constitute ca. 32%, and these of our domesticated animals – ca. 65%, of the total biomass of land vertebrates on Earth, with only ca. 3% contributed by wild animals), and increasing proportions of land being occupied by agriculture, industry, and human dwellings. Widespread denial of the responsibility of humans for the current and future state of our Planet’s well-being greatly deepens the extent of this crisis and leaves little hope for its mitigation and reversal.

Along with two other colleagues, I have been recently engaged in exploring the evolutionary underpinnings of human behaviours and predispositions which are causing this crisis. Our most destructive psychological characteristics such as greed for resources or fear of the wild, put together with cognitive limitations and biases, can be viewed as genetic predispositions that once were adaptive, in a similar fashion as our craving for simple carbohydrates – once positively selected, now leading to life-threatening health conditions. Understanding their origin may help us acknowledge, accept and finally move beyond such problematic heritage. We propose an evolutionary dissection of our planet-killer phenotype as a sound basis for developing tools for transforming our individual and collective behaviours. As we have learned to control our fertility, thus our other biological traits can be approached with awareness and regulated to levels compatible with our sustainable existence.

April

When you can actually look into the past. Ancient DNA in studying evolution and population history.

Dr Martyna Molak

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

Date: Wednesday, 10.04.2019, 13:00, Cent Lecture Theatre 0142

Abstract. In genetic studies, making inferences regarding the past of studied populations usually requires an extrapolation of observations made on the current gene pool while making several assumptions regarding the genetic continuity through time. Many factors, however, can distort genetic continuity between the past and the present of a population, thus potentially leading us to incomplete or even incorrect conclusions when inferring about the past. Ancient DNA – genetic material isolated from organic remains, often dating back thousands of years – enables us to obtain information on the actual historical genetic make up of a studied population. Almost like a time machine, ancient DNA allows us to observe changes in the gene pool in real time and reveals demographic, biogeographical and evolutionary processes, otherwise concealed in the genetic variation of the current population.

In my talk I will demonstrate the possibilities of using ancient DNA to explore historical biogeography, demography and population genetics as well as to improve phylogenetic inferences. I will present examples from the research projects I was involved in, which cover various ancient human populations, Palaeolithic mammals, as well as disease-bearing microorganisms and viruses.

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May

Wildlife policy and politics in Poland: Socio-political determinants of conservation policy concerning the European bison, the moose and the wolf

Dr Krzysztof Niedziałkowski

Institute of Philosophy and Sociology, Polish Academy of Sciences

Mammal Research Institute, Polish Academy of Sciences

Date: Wednesday, 08.05.2019, 13:00, Cent Lecture Theatre 0142

Abstract. Recent years have witnessed heated discussions concerning the management of wildlife in Poland. They addressed the questions whether certain species should be lethally regulated, where, to what extent and by whom. They also engaged a number of social actors who tried to influence management rules according to their interests, beliefs and values. The outcome of these struggles depended on the arguments used, the resources of the social actors, and the wider socio-political context of the discussions. In my project I used social scientific theories and tools to analyse the management of three wildlife species: the European bison, the moose, and the wolf, since 1945. The first species has traditionally been a strictly protected symbol of nature conservation, but with its growing numbers it has also been increasingly perceived as too numerous and in need of lethal regulation, also in the form of trophy hunting. The second species has traditionally been classified as a game animal, but following the dramatic decline of the population in the late 1990s its hunting was suspended. The third species, persecuted after World War II and treated as a pest, over time became a game animal and, in the 1990s, a protected species. Based on the written sources and 46 interviews with people involved in the discussion concerning wildlife management I identify the main coalitions of social actors influencing policy changes, their arguments, and resources. I also show that decision-making concerning these species was strongly influenced by wider socio-political changes, such as democratization, the EU accession and changes of the government. I suggest that social scientific research can facilitate a better understanding of the determinants of population dynamics of wildlife.

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June

What can we learn from microbial symbionts about their animal hosts?

Dr Öncü MARACI

Department of Animal Behaviour, Bielefeld University

Date: Wednesday, 12.06.2019, 13:00, Cent Lecture Theatre 0142

Abstract. Animal bodies harbour complex and dynamic microbial ecosystems consisting of bacteria, fungi, archaea, protozoa and viruses. An increasing number of studies documented the functions of microbial symbionts in physiology, metabolism, behaviour, fitness and evolution of their animal hosts. These new findings have fundamentally altered our understanding of animal biology. One of the most striking discoveries is that, microorganisms can modulate the hosts' communicative behaviour and social interactions in many animal taxa. Although the exact mechanism of this interplay has not been fully discovered, one possible mechanism is that olfactory signals produced by microorganism as metabolic by-products might influence hosts' behaviour. The composition of the symbiotic microbiota is influenced by several host-specific factors, resulting in substantial inter-individual variations. In turn, the variations in microbial communities would consequently affect social and communicative behaviour by influencing recognition cues of the hosts. Hence, it is crucial to elucidate the factors affecting microbial community structure in terms of understanding the potential function of microbial symbionts in olfactory communication. Furthermore, an increasing number of studies showed anthropogenic stress can alter the composition and functioning of microbial communities. More recently, it has been also proposed that microorganism can influence the adaptive capacity of their host, making them more resilient to potentially stressful anthropogenic perturbations. Therefore, understanding the structural changes in microbial symbionts in response to urbanisation related stressors might open new windows to further investigate the function of microbial communities in facilitating the adaptation of their animal hosts to anthropogenic stress. In this talk, I will present some preliminary data on the factors influencing the gut microbe composition in two estridild finch species and some ideas about future perspectives.

Illustrative Drawing: Andrew Rae for Quanta Magazine