7th

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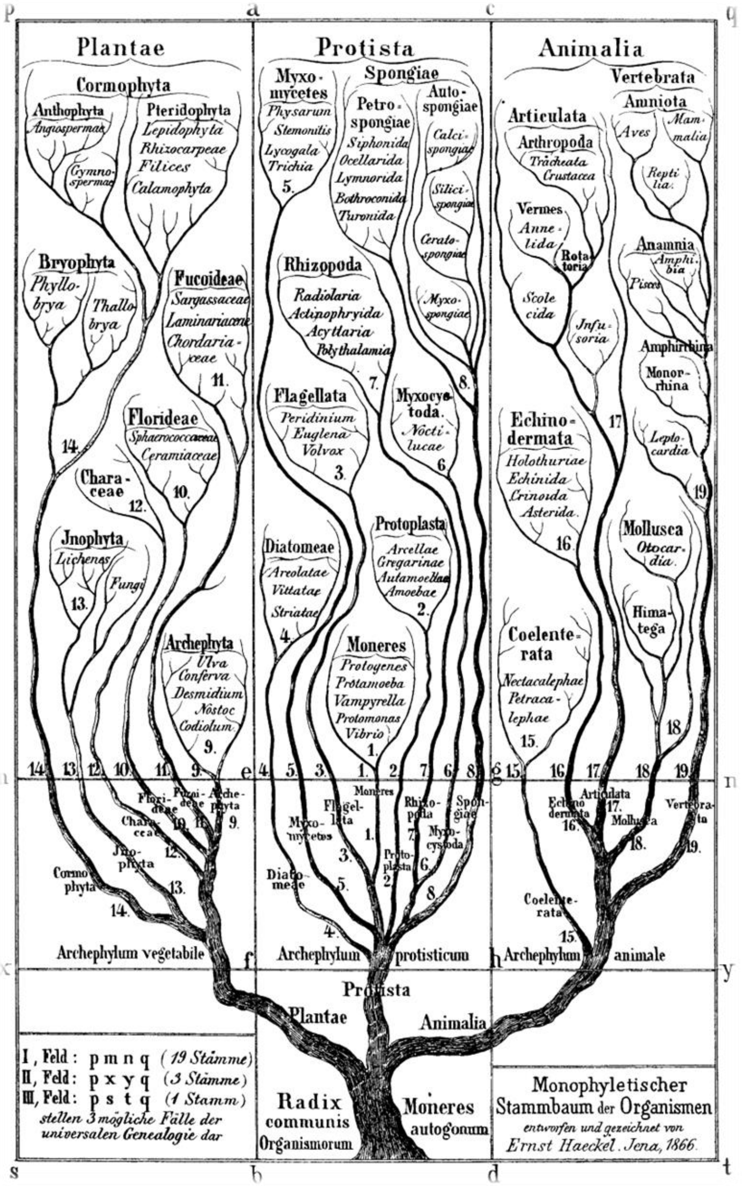
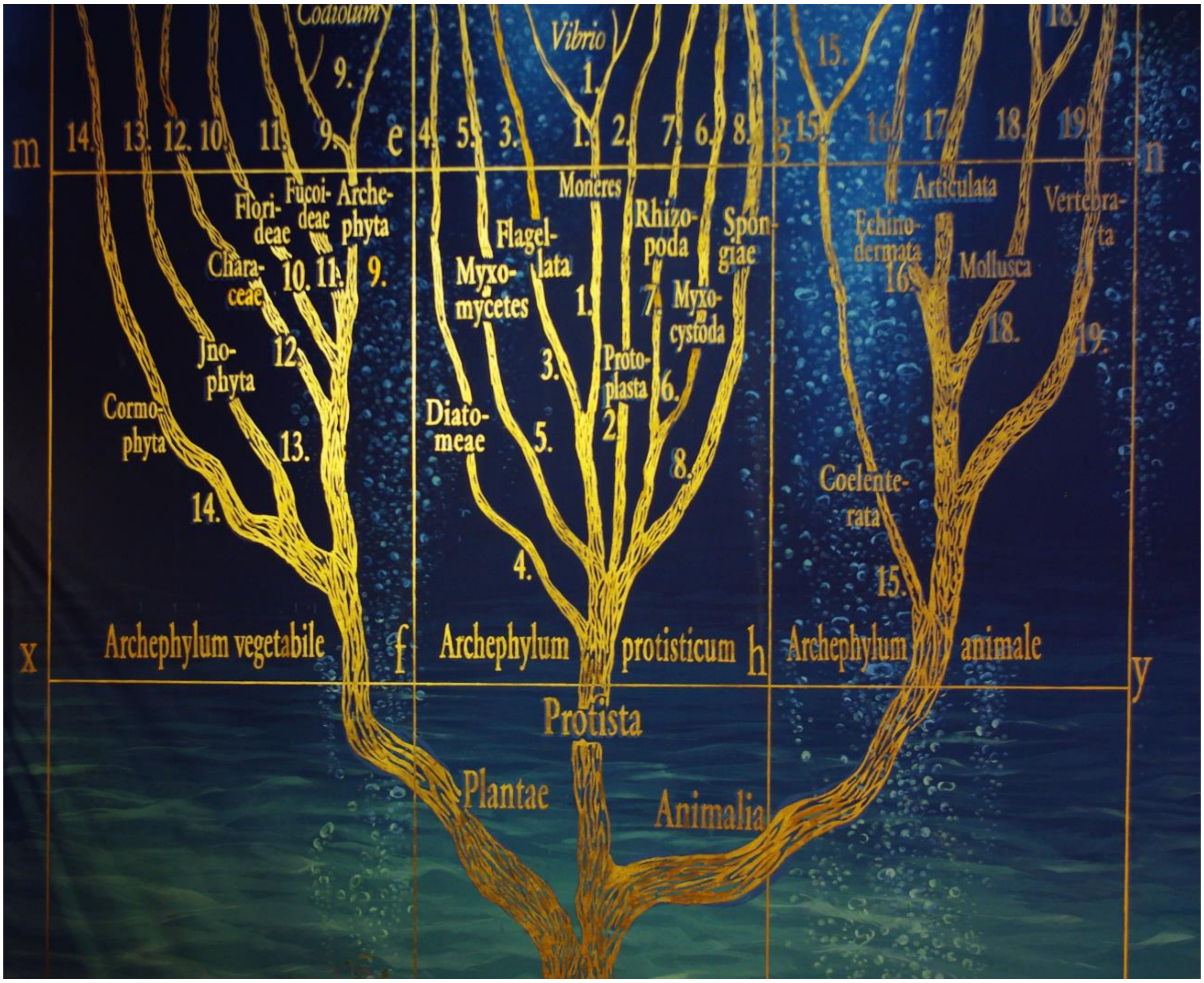
POLISH EVOLUTIONARY CONFERENCE



Gdańsk

September 18-20, 2019



The wall painting in the main hall of the Faculty of Biology (University of Gdańsk) building made by students of Art Academy in Gdańsk: Jacek Zdybel, Katarzyna Marcinkowska, Joanna Mularska, Magdalena Pelak, Klaudia Szalewska, Wojciech Woźniak in 2012. Presents the Ernst Haeckel tree of life, which is Darwin's metaphorical description of the pattern of universal common descent. This is the English version of Ernst Haeckel tree from the *The Evolution of Man* (1879), one of several depictions of a tree of life by Haeckel. Man is at the crown of the tree; for Haeckel, as for many early evolutionists, humans were considered the pinnacle of evolution. Go to fifth floor to appreciate all the tree, including the tree crown. Photo credit: Dorota Kidawa

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POLSKA AKADEMIA NAUK

UNIWERSYTET GDAŃSKI

WYDZIAŁ BIOLOGII
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Welcome to Gdańsk

Situated on the coast of the Baltic Sea, Gdansk is Poland's principal seaport and one of its biggest tourist destinations. With a history stretching over 1,000 years, the opening battles of World War II taking place here and being the birthplace of the Solidarność (Solidarity movement), Gdańsk offers a lot of historical attractions. But there is than that, the whole architecture of old town with the Royal Way, famous promenade street of Polish kings, and historic monumental cathedrals. Besides, there are medieval ports and a lot of oodles cool cafes. For those who prefer spending the time in nature areas, Gdańsk and the whole TriCity area (Gdańsk, Sopot, Gdynia) offers a wide range of nature attractions. The richness of these attractions outstanding, and apart from picturesque sights as the estuary of the Brave Vistula and the Vistula Cutting, natural clifs, beautiful beaches you will also find vast both coniferous and deciduous forests with a lot of interesting floristics specimens and wild fauna hanging around.

Photo credits: Magdalena Hadwiczak

Top **Five** Best Things to Do in Gdańsk

(but there are more than that!)

1

The European Solidarity Centre: a very new museum, situated in the Gdańsk shipyard. However, it has already become one of the best tourist attractions in the city. It is spectacular in both its design and the exhibitions it contains. The Centre celebrates trades unions and their achievements, giving a lot of credit to the Solidarity movement in a series of thought-provoking exhibitions. The building is made of steel and its design is meant to resemble that of a ship, which makes it a worthwhile visit for all architecture lovers (from www.culturetrip.com).

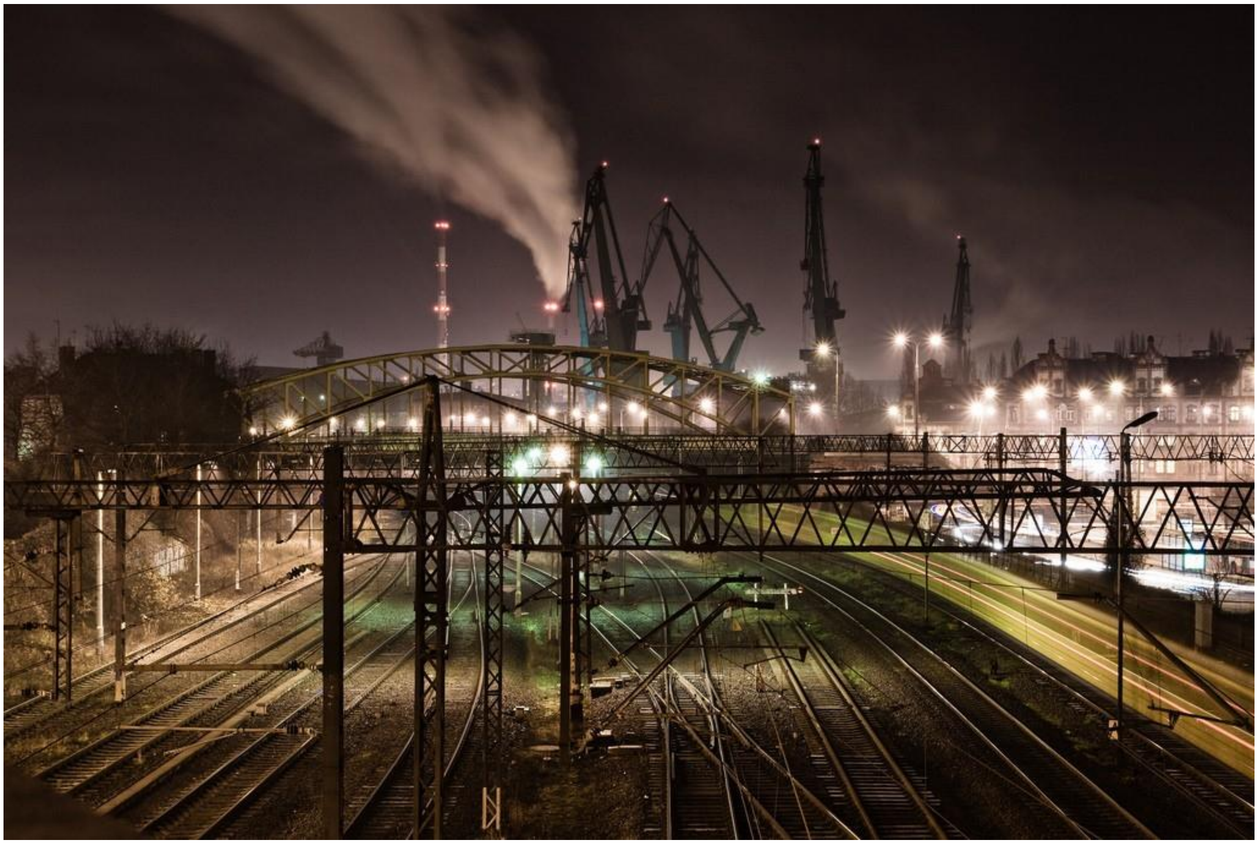

Photo credits: Unknown author

2

The Abbots' Palace: located in the beautiful Oliwa Park, is a rococo artwork in itself. It is worth a visit not only for the beautiful surroundings of the park with its winding paths, relaxing ponds, huge hedges and an abundance of greenery, but also for what is contained inside. It is constituted of two parts, the 'Old Palace', built in the 15th century, and the 'New Palace', added in the first half of the 17th. It now contains the Department of Modern Art of the National Museum of Gdańsk, along with a 'Promotional Gallery' dedicated to the exhibition of works by young artists (from www.culturetrip.com).

Photo credits: Unknown author

3

The Royal Way: a spectacular path from the old city gate to the Motława river. It is also the main Old Town street, famous due to the Polish kings who used to parade along its length when visiting the city. Some of the main sights on the way are the Golden Gate, the Torture House, the Prison Tower and Neptune's Fountain. It is advisable to read something of old Polish history before going on a walk there, however it is also a good chance to admire the beautifully reconstructed buildings, some dating back to the 14th century (from www.culturetrip.com).

Photo credits: Unknown author

4

Ptasi Raj (Birds Paradise) is a nature reserve in Gdańsk located at the former estuary of the Vistula, the purpose of which is to protect breeding and resting places of water and marsh birds. There are approx. 200 species of birds in the reserve, including such interesting names as black-necked grebe, greylag goose, common shelduck, common merganser, spotted crake, water rail, oystercatcher, plover, green sandpiper, bluethroat, or even common eider, particularly rare in our environment. In the reserve, a 6-kilometre nature and educational trail has been set up, featuring information boards which familiarise tourists with the local natural assets and help them observe flora and fauna protected within the reserve. Indeed, it is recommended that visitors take field glasses with them. Waterproof boots can also prove useful since part of the route leads through marshy areas. Ptasi Raj is a real natural paradise, worth visiting not only by bird enthusiasts. It is a mere few kilometres away from the city centre, and can be reached by urban transport (from www.pomorskietravel.com)

Photo credits: Unknown author

5

Kępa Redłowska Nature Reserve - founded in 1938 to preserve the natural beech-forest habitat of wild animals like badgers, bats and foxes. Several walking trails criss-cross the reserve. It makes for an interesting stroll and if you're lucky you may catch a glimpse of an animal scurrying away to its hideout. Groups of boars are known to hang around the area, and though they look fearsome, they are apparently harmless - not that we'd encourage trying to stroke one. Ramblers can find several bunkers left over from WWII spread intermittently around the coastline (from www.inyourpocket.com).

Photo credits: Unknown author

University of Gdańsk

Founded in 1970, the University of Gdańsk is relatively young education and research institution. However, it is a dynamically developing university. It offers education in nearly all fields of academic knowledge, and it is currently one of the most modern academic centers in Northern Poland. The academic staff of the University of Gdańsk conducts scientific and scholarly research on a world-class level, not only creatively expanding the frontiers of knowledge, but also serving the whole of the Pomerania region with their knowledge and experience, thus aiding its dynamic modern development.

UNIWERSYTET GDAŃSKI

Faculty of Biology – **the conference venue**

The Faculty of Biology of the University of Gdańsk is an integral part of the University of Gdańsk since the university establishment, thus it boasts of almost fifty years of scientific research and education. The present building, available since 2012 owing to European Union funds, with modern infrastructure, an auditorium, lecture halls and laboratories equipped with audiovisual systems and specialized research equipment offers excellent conditions for scientific research and education at the highest level. Besides, there many decorations and exhibitions in the building (skeletons of big mammals, museum of amber inclusions, aquarium Malawi, paludarium, formicarium, etc, see below for more details) that makes the place interesting and pleasant to stay in. **We hope you will enjoy it!**

Photo credits: Piotr Rutkowski

Aqarium Malawi: A big aquarium in front of the main entrance in the Faculty Biology building. The residents of the aquarium are cichlids from Lake Malawi. This is an interesting group of fish, with un unusual reproduction system - during the spawning, the female lays eggs that are fertilized by the male, and then the eggs are collected by the female and incubated in the mouth for 3-4 weeks. The fish are vividly colored, especially during the mating period.

Formicarium: the four industrial-like chambers in the lunch room. This an artistic project, made by Jarosław Czarnecki being his *art&science* doctoral thesis (titled: "Simbiosis") on the Faculty of Sculpture and Intermedia Art Academy (Gdańsk, 2014). It is a reconstruction of real nest of *Atta* ants, with all the nest chambers and channels being made of glass and metal.

Paludarium/TEPUI: A big terrarium, in front of the main entrance in the Faculty Biology building, just above the Malawi aquarium. The TEPUI (god's house) biotope paludarium reflects the conditions of the table mountains found in the heart of Venezuelan evergreen equatorial forests.

Museum of Amber Inclusions: main hall, in the corner of left side (from the main entrance perspective). An interesting collection of fossil insects and other invertebrates, locked in the amber over 40 million years ago.

Photos credit: unknown authors

BAŁTYCKI KAMPUS UNIWERSYTETU GDAŃSKIEGO

- Przystanek autobusowy
- Przystanek tramwajowy
- Szybka Kolej Miejska Gdańsk Przymorze - Uniwersytet
- 🟦 budynki planowane
- Przejście podziemne

A	Rektorat i Administracja Centralna UG
B	Instytut Neofilologii Wydziału Filologicznego
C	Wydział Prawa i Administracji
D	Wydział Nauk Społecznych oraz Instytut Geografii Wydziału Oceanografii i Geografii
E	Biblioteka Główna UG
F	Wydział Filologiczny i Wydział Historyczny
G	Wydział Matematyki, Fizyki i Informatyki
H	Instytut Informatyki WMFiI
I	Wydział Biologii
J	Wydział Chemii
K	Międzyuczelniany Wydział Biotechnologii UG i GUMed
L	SWFiS, Biuro Karier, Centrum Transferu Technologii, Dział Studenckich Spraw Socjalnych, „Zatoka Nauki", Instytut Konfucjusza, jednostki administracji
M	Uniwersyteckie Centrum Sportu i Rekreacji
N	„Trzynastka": AZS UG, Parlament Studentów UG, ACK Alternator, Instytut Logopedii
O	Dom Studencki nr 3
P	Dom Studencki nr 4
R	Dom Studencki nr 5
S	Dom Studencki nr 10
T	Hotel Asystencki nr 1
1	Hala Olivia
2	Sklepy i restauracje

Schedule overview

Wednesday, Sept 18		**Thursday, Sept 19**		**Friday, Sept 20**	
		08:45 - 09:00	announcements	08:45 - 09:00	announcements
		09:00 - 10:00	Plenary lecture: Tracey Chapman	09:00 - 10:00	Plenary lecture: Marc-Andre Selosse
		10:00-10:45	talks	10:00-10:45	talks
		10:45 - 11:15	coffee break	10:45 - 11:15	coffee break
		11:15 - 12:30	talks	11:15 - 12:30	talks
		12:30 - 12:45	lunch break	12:30 - 12:45	lunch break
		13:30 - 14:30	Plenary lecture: Hanna Kokko	13:30 - 14:30	Plenary lecture: Jorn Theuerkauf
15:00 - 17:00	registration	14:30 - 14:50	talks	14:30 - 14:50	talks
		15:00 - 15:30	coffee break	15:00 - 15:30	coffee break
		15:30 - 16:15	talks	15:30 - 16:15	talks
		16:15 - 18:00	poster session	16:15 - 16:45	closing remarks
17:00 - 17:15	opening ceremony				
17:15 - 18:15	Plenary lecture: Jan Pawłowski				
18:15 - 18:45	talks				
18:45 - 21:00	welcome reception	19:00 - 23:00	conference dinner		

Saturday, 21 Sept – post-conference trips; ask about details at the reception desk.

Detailed schedule

Wednesday, Sept 18		
15:00 - 17:00	registration	
17:00 - 17:15	opening ceremony	
17:15 - 18:15	**Jan Pawłowski**	**Environmental DNA: a novel way to explore and monitor present and past biodiversity**
18:15 - 18:30	**Peter Convey**	Terrestrial biodiversity in Antarctica - insights into the evolution of the continent's extant biota
18:30 - 18:45	**Zofia Prokop**	In the face of the global environmental crisis… what's an evolutionary biologist to do?
18:45 - 21:00	welcome reception	

Thursday, Sept 19		
08:45 - 09:00	announcements	
09:00 - 10:00	**Tracey Chapman**	**Sexual selection, sexual conflict and evolutionary change**
10:00-10:15	**Małgorzata Lipowska**	Is evolution of high aerobic exercise capacity facilitated by changes in glucocorticoid stress response?
10:15 - 10:30	**Małgorzata Pilot**	Going to the dogs? Human-induced evolution in the grey wolf
10:30 - 10:45	**Sylwia Buczyńska**	Reproductive effort of laboratory mice selected for low and high basal metabolic rate (BMR): the test of heat dissipation limitation hypothesis
10:45 - 11:15	coffee break	

...continued: Thursday, Sept 19

11:15 - 11:30	**Agata Plesnar-Bielak**	Environment-dependent selection in sexually selected traits
11:30 - 11:45	**Jonathan Parrett**	Sexual selection predicts the persistence of populations within altered environments
11:45 - 12:00	**Aleksandra Łukasiewicz**	Condition-dependence and intensity of sexual conflict in the mite Sancassania berlesei
12:00 - 12:15	**Magdalena Herdegen-Radwan**	Guppy boldness is associated with higher reproductive success, but not due to condition-dependence
12:15 - 12:30	**Jacek Radwan**	Mating preferences can drive expansion or contraction of MHC gene family
12:30 - 12:45	lunch break	
13:30 - 14:30	**Hanna Kokko**	**Gentlemanly males? Always, sometimes, never?**
14:30 - 14:45	**Michela Corsini**	Rearing chicks in a capital city: does urbanisation affect parental visiting rates and nestling body condition?
14:45 - 15:00	**Irene Di Lecce**	Fitness variation of urban birds breeding in natural and artificial nesting sites
15:00 - 15:30	coffee break	
15:30 - 15:45	**Krzysztof Argasiński**	Beyond classical Hamilton's Rule State distribution asymmetry and the dynamics of altruism
15:45 - 16:00	**Rafał Zwolak**	Mast seeding promotes evolution of scatter-hoarding
16:00 - 16:15	**Piotr Łukasik**	Puzzling evolutionary patterns in a nested nutritional symbiosis of a leafhopper
16:15 - 18:00	**Poster session**	
19:00 - 23:00	conference dinner	

Friday, Sept 20

08:45 - 09:00	announcements	
09:00 - 10:00	**Marc-Andre Selosse**	The evolution of interdeppendency between symbiotic organisms by neutral evolution
10:00-10:15	**Małgorzata Lagisz**	Meta-analytical insights into maternal dietary effects on offspring behavior
10:15 - 10:30	**Agnieszka Gudowska**	Seasonality as a predominant control factor of the moult dynamics in birds, a meta-analysis
10:30 - 10:45	**Marcelo Araya-Salas**	Evolutionary dynamics of vocal complexity in a vocal learning clade
10:45 - 11:15	coffee break	
11:15 - 11:30	**Filip Pietluch**	Untangling the puzzle of Archaeplastidia evolution with phylogenies of plastid-encoded proteins
11:30 - 11:45	**Przemysław Gagat**	Antimicrobial peptides and the evolution of mitochondria and plastid targeting signals
11:45 - 12:00	**Michał May**	Comparative transcriptome analysis of mycoheterotrophic orchids *Epipogium aphyllum* and *Neottia nidus-avis*
12:00 - 12:15	**Alejandro Ibañez**	Mental gland mapping across the turtle phylogeny reveals multiple traits losses and sheds light on the evolution of chemical communication in chelonias
12:15 - 12:30	**Wiesław Babik**	Differential introgression across newt hybrid zone, evidence from replicated transects
12:30 - 12:45	lunch break	

…continued: Friday, Sept 20		
13:30 - 14:30	**Jorn Theuerkauf**	Evolutionary ecology in an unusual environment: social organisation and coevolutionary arms race in birds of New Caledonia
14:30 - 14:45	**Katarzyna Janas**	Influence of early growth condition on blue tit nestlings colouration, an experimental approach
14:45 - 15:00	**Piotr Minias**	Infections of enteropathogenic bacteria in wild birds; phylogenetic distribution and ecological predictors
15:00 - 15:30	coffee break	
15:30 - 15:45	**Andre Moura**	Adaptation and diversification of marine predators: integration of genomic and morphological data to determine drivers of ecotype differentiation in bottlenose dolphins (*Tursiops spp*)
15:45 - 16:00	**Bogusław Pawłowski**	Human body fluctuating assymetry and immunocompetence
16:00 - 16:15	**Alicja Pawelec**	Increasing temperatures favors biological invasions: an example of direct, temperature and size dependent food competition between native and invasive fish species
16:15 - 16:45	closing remarks	

Saturday, 21 September – post-conference trips; ask about details at the reception desk.

Plenaries

(alphabetic order, according the Author's name)

Tracey Chapman: "I am an evolutionary geneticist based at the School of Biological Sciences at the University of East Anglia. I am interested in understanding how reproductive traits evolve and function. I use fruit fly model systems to evaluate the potential of sexual selection and sexual conflict to drive evolutionary change. I use the power of these systems to understand the underlying mechanisms involved. I am also interested in translating messages from this research into novel methods for pest insect control."

Sexual selection, sexual conflict and evolutionary change

Tracey Chapman

University of East Anglia, UK

Battles between the males and females over reproductive decisions, such as how often to mate and how much to invest now versus later, are widespread and appear to drive much of the reproductive exuberance we see in nature. Much progress has been made over the past few decades in understanding why and how these battles occur. Broadly speaking, in situations where reproducing partners have little shared interest in each other's reproductive futures, they can sometimes benefit by exploiting, rather than fully cooperating with, their mates. Much work into the details of how these sexual conflicts are manifested has been done in *Drosophila* fruitflies. This has revealed a fascinating covert battleground between males and females mediated by the actions of seminal fluid proteins passed from males to females during mating along with sperm. These proteins affect the behavior and physiology of the female in dramatic ways, by altering her egg laying, sexual receptivity, feeding and immune genes. Males can sometimes gain by using these proteins to make females invest more in current versus future reproductive episodes, even though this can be harmful to females in the longer-term, e.g. by shortening their lifespan. In this situation, females should evolve resistance to these proteins to avoid this harm. Two 'stand out' features of seminal fluid proteins involved in mediating sexual conflict are (a) their functional complexity and (b) their strong interactions with the environment. As well as summarising our current understanding of this field I will explore the origin and maintenance of this complexity and suggest why some male reproductive strategies are 'resistance proof' and hence persist, while others aren't and don't.

Keywords: sexual selection, sexual conflict, life history

Talk on: Thursday, 19 Sept, 09:00

Hanna Kokko: "I am a professor of Evolutionary Ecology at the University of Zurich. I have a longstanding interest in the mathematical logic that underpins biology, with a particular curiosity towards the evolution of reproductive strategies. This really includes everything that involves conflict and possible cooperation between entities (individuals, genes, parts of society…) and this then leads to demographic consequences within or across species."

Gentlemanly males? Always, sometimes, never?

Hanna Kokko

Department of Evolutionary Biology and Environmental Studies,
University of Zurich, Switzerland

As someone who studies sexual conflict for a living, I can attest that the twofold cost of sex (caused by the need for a sexual population to produce males) is the cause of many prolonged headaches in evolutionary biology. However, after explaining some aspects of these intellectual headaches – i.e. why do males even exist? – I will turn to some subtleties. I will present recent work understanding the forces that make males disperse more (or less), or earlier (or later) than their female siblings, discuss why males and females often differ relatively little in their niches (if males refrained from using what the female needs, that'd be quite gentlemanly – but rare), and end with some empirical data: do male black coucals suffer a trade-off between mating and parenting?

Keywords: evolutionary ecology, mathematical modelling

Talk on: Thursday, 19 Sept, 13:30

Jan Pawlowski: "I am an Associate Professor of Biology at the Department of Genetics and Evolution, University of Geneva, where I lead the research group on molecular systematics and environmental genomics. Large part of my activities is devoted to DNA barcoding and metabarcoding. Currently, I am working on the development of eco-genomic tests for biomonitoring and survey of freshwater and marine ecosystems. I am also the chair of the Swiss Barcode of Life, a co-chair of DNAqua-net WG2 and the co-founder of ID-Gene ecodiagnostics Ltd."

Environmental DNA:
a novel way to explore and monitor present and past biodiversity

Jan Pawlowski

Department of Genetics and Evolution, University of Geneva, Switzerland

The environmental DNA (eDNA) corresponds to all genomic material that can be isolated from water, soil, sediment and other type of environmental samples. It contains a mix of DNA from living organisms and their remnants as well as the extra-cellular DNA present in organelles or as free molecules. Depending on environmental conditions, the eDNA can be preserved for hundreds or thousands of years, providing an access to historical genomic material that can be of invaluable contribution to evolutionary and paleoenvironmental studies. The development of eDNA metabarcoding based on targeted high-throughput sequencing, has opened new avenues to explore and monitor biodiversity. Its application in various ecosystems contributes to uncover the immense diversity of prokaryotic and eukaryotic microbiomes. It also enables surveying larger-sized species using their DNA traces left in the water or sediment. Compared to classical approaches based on visual observation and morphological identification, metabarcoding provides a unique insight into the global biodiversity, allowing to explore complex interactions between species and their relations to the surrounding environment. Combined with machine learning and other AI approaches, millions of eDNA sequences can be analysed to predict the response of biodiversity to environmental changes at short- and long-term scales. With the increasing anthropogenic pressures and urgent need to protect and manage biodiversity resources, further research using eDNA as a source of information about present and past biodiversity is of primary importance.

Keywords: environmental genomics, paleogenomics, ancient DNA, biodiversity, biomonitoring, artificial intelligence

Talk on: Wednesday, 18 Sept, 17:15

Marc- Andre Selosse: “I am a professor at Muséum national d’Histoire naturelle (France), University of Gdansk (Poland) and invited professor at Federal University of Viçosa (Brazil). My researches focus on the ecology and evolution of mycorrhizas, a major symbiosis between soil fungi and roots of most land plants, with research models such as Truffles, Sebacinales, orchids and ectomycorrhizal associations, as well as mycorrhizal networks. I have also a general interest for symbiosis and its evolution.“

The evolution of interdependency between symbiotic organisms by neutral evolution

Marc-Andre Selosse

L’Insitute de Systématique, Évolution, Biodiversité,
Department of Plant Taxonomy and Nature Conservation, France
Faculty of Biology, University of Gdańsk, Poland

Symbiosis evolution is often viewed as a progress, with emergence of new adaptive properties. However, symbiosis also enhances the interdependence between partners. I describe several such interdependences, and emphasize that they arise without emergence of new property. Generally, when two partners permanently interact, a mutation in one partner can be complemented by the other. Independency is then lost without any positive selection, in a neutral evolution. The accumulation of such steps makes the reversion to independency unlikely, and drives interdependency in symbiosis.

Keywords: biological interdependency, dependence, drift, regressive evolution, symbiosis

Talk on: Friday, 20 Sept, 09:00

Jörn Theuerkauf: “I am a professor at the Behavioural Ecology Unit, Museum and Institute of Zoology, Polish Academy of Sciences. I received my PhD in Wildlife Biology and Management at the Technische Universität München on the behavioural ecology of wolves in the Białowieża Forest. My research focusses on behavioural, evolutionary and conservation ecology of endangered birds and mammals, co-evolutionary arms race in avian brood parasite-host systems, and the impact of invasive mammals on endemic Pacific birds. Since 2001, I have been studied various bird and mammal species in New Caledonia and other Pacific islands.”

Evolutionary ecology in an unusual environment: social organization and coevolutionary arms race in birds of New Caledonia

Jörn Thereuekauf

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

New Caledonia has a unique insular environment, consisting of large areas of ultramafic soils, which are rich in heavy metals and poor in fertility. This particular environment put an evolutionary pressure on species colonising the island and let to a high rate of endemism and a variety of unusual behaviours. Tool use by the New Caledonian Crow *Corvus moneduloides* is one of the best-known examples, but since 2001, our research group has been studying three other cases of exceptional biology of birds on the island. The first is the occurrence of cooperative breeding in species such as the New Caledonian Parakeet *Cyanoramphus saisseti* and the flightless Kagu *Rhynochetos jubatus*. The second example is an advanced social system in the flightless Kagu with characteristics found otherwise only in human societies, including a high degree of sociality, fraternal polyandry and clannish spatial organisation. The third example is the arms race between the Shining Bronze-cuckoo *Chalcites lucidus* and its exclusive host the Fan-tailed Gerygone *Gerygone flavolateralis*, which is unique because of nestling ejection behaviour by the host and polymorphism in nestling skin colour in both species. It is likely that the environmental conditions of New Caledonia favoured the evolution of many of these adaptations, making the island particularly interesting for research.

Keywords: coevolutionary arms race; cooperative breeding; social organisation; endemic birds; New Caledonia

Talk on: Friday, 20 Sept, 13:30

Oral presentations

(alphabetic order, according the first Author)

Evolutionary dynamics of vocal complexity in a vocal learning clade

Marcelo Araya-Salas, Daniel Caetano, Mike Webster

Cornell Lab of Ornithology, Cornell University, USA; Universidad de Costa Rica, Costa Rica

Improving our understanding of the evolutionary processes that shape biological diversity is at the center of evolutionary biology. There is a growing awareness that alternative means of cross-generational information transmission, as the cultural evolution of socially learned traits, can strongly affect phenotypic variation and potentially shape macro-evolutionary trajectories. Yet, only theoretical models, but no conclusive empirical evidence have supported these ideas. Vocal learning in birds shows a unparalleled level of plasticity, and hence provides an ideal system to investigate the unique macroevolutionary dynamics related to cultural transmission. We explored the evolution of song complexity in a vocal learning avian clade, the hummingbirds, and a sister non-vocal learning clade, the swifts. We measured 4 song structure parameters related to complexity: number of element types, sequence complexity, acoustic space area and element sequence variation between song. Hummingbird species show higher rates of song evolution even though both clades share the same pattern of evolutionary correlation among song parameters. Faster rates of evolution may indicate vocal learning is associated with rapid exploration of the songspace by lineages, although the overall trajectory of song evolution is similar between the clades. Our results suggests an effect of vocal learning on increasing the diversity of vocal complexity on hummingbirds.

Keywords: song evolution, cultural evolution, hummingbirds

Talk on: Friday, Sept 20, 10:30

Beyond classical Hamilton's Rule.
State distribution asymmetry and the dynamics of altruism

Krzysztof Argasinski, Ryszard Rudnicki

Institute of Mathematics of Polish Academy of Sciences, Warszawa, Poland

Most of the formalizations of the Inclusive Fitness and Kin Selection concepts contain two simplifying assumptions: first, is that the models are described in terms of "fitness", an abstract parameter vaguely related to the population growth rate or lifetime reproductive success. The second is that they ignore the division between donors and Receivers of altruism and the distribution of those roles in the population. The Inclusive Fitness and Kin Selection approaches instead of unclear fitness units, can be expressed by explicit demographic parameters describing the probability of death during specific interaction when cooperative trait can be exhibited. This description will be used for the derivation of the model describing the competition between Cooperative and Noncooperative strategies. The obtained approach will be sufficient for description of the cases when the roles are independently drawn during each interaction. However, we can imagine situations when survival and the change of the state are not correlated (such as food support for the infected individual, which keeps him alive, but cannot cure). To cover those cases, new model is extended to the case with explicit dynamics of the distributions of states among carriers of different strategies driven by some general mechanisms. In effect it is shown that even in the case when fluxes between states are driven by selectively neutral mechanisms (acting in the same way on all strategies), the differences in the mortalities in the focal interaction will lead to different distributions of states for different strategies. This leads to more complex rules for cooperation than the classical Hamilton's rule, that in addition to the classical Cost and Benefit contain third component weighted by difference in proportions of Donors among carriers of both strategies. Depending on the sign, it can be termed "selfishness bonus" or "sacrifice bonus" when it increases Cost or Benefit respectively.

Keywords: Kin selection, inclusive fitness, Hamilton’s rule, replicator dynamics

Talk on: Thursday, Sept 19, 15:30

Mating preferences can drive expansion or contraction of MHC gene family

Piotr Benkowski, Jacek Radwan

Adam Mickiewicz University, Poznań, Poland

MHC-based mating rules can evolve as a way to avoid inbreeding or to increase offspring immune competence. While the role of mating preference in the MHC diversity in vertebrates has been acknowledged, their its impact on individual MHC diversity has not been considered. Here, we use computer simulations to investigate how simple mating rules favouring MHC-dissimilar partners affect the evolution of the number of MHC variants in individual genomes, accompanying selection for resistance to parasites. We showed that the effect of such preferences could sometimes be dramatic. If preferences are aimed at avoiding identical alleles, e.g. under strong selection against sib-mating, the equilibrium number of MHC alleles is much smaller than under random mating. However, if the mating rule minimises the ratio of shared to different alleles in partners, MHC number is higher than under random mating. Additionally, our simulations revealed that a negative correlation between the numbers of MHC variants in mated individuals , previously interpreted in terms of choice for optimal MHC diversity in progeny, can arise from simple rules of MHC-disassortative mating. Our results reveal unexpectedly high potential of MHC-based mating preferences to drive MHC gene family expansions or contractions and highlight the need to study the mechanistic basis of such preferences.

Keywords: major histocompatibility complex, dupication, sexual selection, host-parastite coevolution

Talk on: Thursday, Sept 19, 12:15

Reproductive effort of laboratory mice selected for low and high basal metabolic rate (BMR): the test of heat dissipation limitation hypothesis

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

Uniwersytet w Białymstoku, Instytut Biologii, Białystok, Poland

The heat dissipation limitation hypothesis suggests that animals' energy budgets are limited by the ability to dissipate body heat to avoid detrimental overheating. To date, it has been exclusively tested under peak metabolic demands mostly in lactating mice. Here, we compared the parental effort of mother mice divergently selected fir high (H-BMR) and low basal metabolic rate (L-BMR) exposed to an ambient temperature of 23°C and 30°C and fur shaving as a manipulation of the heat dissipation. At 23°C, shaved mother mice from the H-BMR line type consumed more food and their litter mass grew faster, whereas their body temperature was higher at 30°C. In contrast, mother mice from the L-BMR line type had lower body temperature in both ambient conditions, lower food intake and their litter growth was the fastest at 30°C in non-shaved group. Also, warm exposure induced the downsizing kidneys and liver mass, however, these changes were similar in scope in both line types. Shaved mother mice from both line types had higher small intestine mass at 30°C than at 23°C. Our results show that the H-BMR and the L-BMR had different reproductive performance at both temperatures. At 30°C growth of litter mass was higher in the non-shaved L-BMR line type, but at 23°C in shaved mother mice from the H-BMR line type. It suggests that females from the L-BMR line type were not as limited in their ability to dissipate body heat as the H-BMR mice, because they raised bigger litters in warm conditions even without shaving.

Keywords: heat dispassion limitation hypothesis, artificial selection, parental effort, litter mass growth

Talk on: Thursday, Sept 19, 10:30

Terrestrial biodiversity in Antarctica
- insights into the evolution of the continent's extant biota

Peter Convey

British Antarctic Survey, UK

Terrestrial and freshwater life in Antarctica is surprisingly poorly known. Today it is dominated by lower plants and lichens, microarthropods and other microinvertebrates, and microbial groups, although that has not always been the case. Most currently ice-free ground in Antarctica and on at least some of the surrounding sub-Antarctic islands would have been covered and scoured by glacial advances at the Last Glacial Maximum and previous maxima. However, as new baseline survey data become available, combined with modern molecular biological analysis, it has become clear that isolation, long-term persistence, and regionalisation are general features of the Antarctic terrestrial and freshwater biota. Even so, over evolutionary timescales, this biota has still been linked with those of lower southern latitudes, including the tropics, as well as that of the northern polar regions. These advances create a new paradigm in which to consider the evolution and adaptation of Antarctic terrestrial and freshwater biota. Important new cross-disciplinary linkages have also been opened in the fields of understanding the geological and glaciological history of the continent itself and its neighbouring landmasses, and of the climatic and oceanographic process that can both lead to isolation and support colonisation processes.

Keywords: Isolation; refugia; divergence; biogeography; glaciation

Talk on: Wednesday, Sept 18, 18:15

Rearing chicks in a capital city: does urbanisation affect parental visiting rates and nestling body condition?

Michela Corsini, Marta Szulkin

University of Warsaw, Warszawa, Poland

Parental care determines offspring survival. In the last decade, the ubiquity of video recording of passerine breeding events has yielded valuable insight into parental behavior and offspring fitness. Parental effort in nestling provisioning is usually discussed in the context of parental life-history traits (such as clutch size) or resulting brood characteristics (such as brood size or nestling condition). However, the extent to which external environmental factors, and in particular anthropogenic activities, can affect parental investment has rarely been tested. Specifically, knowledge about parental visiting rates to the brood and resulting nestling body condition in urban areas is scarce, and deserves further attention. First, we quantified environmental heterogeneity in a gradient of urbanisation, performed at the nestbox level and across multiple environmental axes using ground-based approaches (human presence, temperature, sound pollution) and remote sensing methodology (light pollution, tree cover, imperviousness, distance to the closest path and to the closest road, NDVI). Second, we tested whether urban-driven environmental heterogeneity impacts i) parental visiting rate and ii) nestling body condition at the nestbox level. The analyses will be presented for two species – the blue tit *Cyanistes caeruleus* and the great tit *Parus major* monitored across two breeding seasons.

Keywords: urbanisation, parental care, nestling body condition

Talk on: Thursday, Sept 19, 14:30

Fitness variation of urban birds breeding in natural and artificial nesting sites

Irene Di Lecce, Joanna Sudyka, Marta Szulkin

Centre of New Technologies, University of Warsaw, Poland

Virtually all inference into fitness variation of hole-nesting passerine birds such as tits has been assessed in nest-box studies. This is because nest-box monitoring is much more convenient than the study of their natural breeding sites, tree cavities. Yet, until nest-boxes emerged in the Anthropocene, the reproductive strategies of hole-nesting birds have been shaped by selective pressures induced by natural cavities. Nest-boxes are often densely distributed in space, which may trigger artificially high breeding densities, they provide altered microclimatic conditions in terms of temperature and humidity, and predation rates observed in nest-boxes populations are usually lower relative to natural cavities. This suggests that life-history variation inferred from nest-boxes may not reflect the natural variation of traits that would be observed in natural cavities. Here, we contrasted the breeding performance of great tits (*Parus major*) and blue tits (*Cyanistes caeruleus*) nesting in natural cavities and nest-boxes located in Las Bielański, an urban forest with elements of primeval ecosystem within Warsaw, Poland. Based on data collected in the first year of sampling (2018), we observed considerable variation in phenology and life-history traits between the two nesting sites: when compared to reproductive events taking place in nest-boxes, blue tits nesting in natural cavities laid eggs later, had a smaller clutch size and a higher hatching success. Blue tit nestlings reared in natural cavities also exhibited larger structural size and left the nest earlier, compared to chicks reared in nest-boxes. Moreover, great tits from nest-boxes started incubating before completing the clutch, which resulted in higher hatching asynchrony. To gain greater insight into the consistency of these trends across years, we will present data collected over two breeding seasons.

Keywords: natural cavity, nest-box, life-history variation

Talk on: Thursday, Sept 19, 14:45

Antimicrobial peptides and the evolution of mitochondria and plastid targeting signals

Przemysław Gagat, Katarzyna Sidorczuk, Filip Pietluch, Stefan Rödiger, Michał Burdukiewicz

Uniwersytet Wrocławski, Wydział Biotechnologii,
Zakład Bioinformatyki i Genomiki, Wrocław, Poland

Antimicrobial peptides (AMPs) are ancient and evolutionarily conserved molecules widespread in all living organisms that participate in host defence and/or microbial competition. They are short, 12 to 50 amino-acid long, do not display any consensus sequences but do share some common features, such as positive charge, hydrophobicity and amphipathicity. These structural characteristics enable AMPs to preferentially disrupt negatively-charged bacterial membranes and do not adversely affect the eukaryotic cells. AMPs are also hypothesized to have greatly contributed to the establishment of bacteria-derived organelles, i.e. mitochondria and plastids, by facilitating two key processes of endosymbiont-to-organelle transformation: (i) endosymbiont gene transfer due to bacterial cell lysis and (ii) evolution of efficient protein import machinery by becoming N-terminal targeting signals for nuclear-encoded, mitochondria/plastid-targeted proteins. Indeed mitochondria and plastid transit peptides (mTP and pTP) seem to share some characteristics with AMPs and some do exhibit antibacterial activities. In order to test the hypothesis, we developed AmpGram, a new tool based on N-grams, reduced alphabets and random forest methods that significantly outperforms all the available AMP prediction algorithms. We tested the hypothesis on mTPs and pTPs extracted from the experimentally verified nuclear encoded, mitochondria/plastid targeted proteins downloaded from the UniProt database. As a control, we used annotated signal peptides, i.e. presequences responsible for protein targeting to the endomembrane system. AmpGram did recognize as AMPs a significant number of mTPs and pTPs but not signal peptides. Based on our results, we propose a new model for evolution of protein import into bacteria-derived organelles with AMPs playing a central role.

Keywords: Antimicrobial peptides, plastid transit peptides, mitochondrial transit peptides, targeting signals, evolution

Talk on: Friday, Sept 20, 11:30

Seasonality as a predominant control factor of the moult dynamics in birds, a meta-analysis

Agnieszka Gudowska, Szymon M. Drobniak

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

Moult is a process, usually occurring annually, in which birds replace their plumage. It is one of the most crucial life-history traits because it restores the functions of plumage and allows a bird to adapt to environmental conditions or special seasonal needs such as breeding and camouflage during non-breeding season. Consequently, moulting has advantages in terms of future performance. However, it also has immediate costs. Expression of such costs may depend on a wide array of physiological and environmental factors experienced by an individual. Using a meta-analytical approach and a representative sample of 146 experimental and observational studies performed on 91 bird species, we quantify internal and external factors which may affect the moult dynamics. Our analysis revealed a moderate magnitude of overall effect size (meta-analytic mean) referring to the overall dependence of moulting on a broad range of factors considered. Generally, the observed average effect for moult dynamics was mainly driven by seasonality. Therefore, changes in the seasonality components like photoperiod, temperature, rainfall pattern or date of snow cover seem to tightly control moult. Moreover, statistically significant interaction of considered factors and geographical locations revealed that birds which moult in cold/temperate climate are the most susceptible to seasonality, whereas birds which moult in sub/tropics are influenced the most by diet and physiology. The internal moderators studied (e.g. age, sex, breeding success) explained absolute magnitude of moult dynamics only to a small extent. However, the result may be biased by quality of reported data in the published literature. Furthermore, we found that experimental studies had stronger effect on moult dynamics than observational one. Knowing that production of a new set of high-quality feathers, depends heavily on timing and rate of moult, we discuss our results in the context of global climate changes.

Keywords: bird, moult, seasonality, phenology

Talk on: Friday, Sept 20, 10:15

Guppy boldness is associated with higher reproductive success, but not due to condition-dependence

Magdalena Herdegen-Radwan

Adam Mickiewicz University, Poznań, Poland

Despite over thirty years of study on animal personalities, their effect on individual fitness is still poorly understood. I measured boldness, a personality trait, and reproductive success in the guppy, *Poecilia reticulata*. I found that bolder males had higher reproductive success than their shyer conspecifics. In this context, it remains an evolutionary puzzle why variation in guppy boldness is maintained in populations. According to the condition-dependence hypothesis, such traits depend on condition, which limits the behavioural choices available to individuals. Because condition is affected by many genes, it can effectively be manipulated by inbreeding, which exposes the effects of deleterious recessive mutations. I compared two personality traits, boldness and tendency to explore, of male guppies from first-generation inbred and outbred treatments. Based on the effect of boldness on guppy fitness, which I showed before, I expected personality traits to be negatively affected by inbreeding. However, inbred guppies did not differ in either personality trait from their outbred counterparts. This finding suggests that mechanisms other than condition-dependence are maintaining personality variation in the guppy.

Keywords: personality, inbreeding depression

Talk on: Thursday, Sept 19, 12:00

Mental gland mapping across the turtle phylogeny reveals multiple traits losses and sheds light on the evolution of chemical communication in chelonias

Alejandro Ibanez, Albert Martinez-Silvestre, Emilia Rydzy, Uwe Fritz, Maciej Pabijan

Department of Comparative Zoology, Institute of Zoology and Biomedical Research,
Jagiellonian University, Kraków, Poland

Intraspecific chemical communication is a widespread phenomenon across the animal kingdom. However, studies aiming to trace the evolution of chemical signaling traits at a large-scale are scarce. Turtles are suitable models to test hypotheses on the evolution and function of chemical communication given that they have a well-developed olfactory sense and several glandular sources of chemosignals. Mental glands (MG) produce secretions that may be involved in communication, particularly during courtship and breeding. A previous study reported the presence of MGs in several taxa within the superfamily Testudinoidea. Here we aimed to reconstruct the evolutionary history of MGs in turtles. We examined specimens from museums and live collections to reassess the occurrence of MGs in extant Testudinoidea, creating a comprehensive dataset spanning most turtle species. MGs show different degrees of development, being large and obvious in some taxa, reduced (likely vestigial) to absent in others. The most parsimonious reconstruction suggested a single origin for MGs in the most recent common ancestor of Testudinoidea, and multiple losses of this trait in each major lineage, particularly in strictly terrestrial genera or species, suggesting the importance of other channels of communication in some clades. By mapping ecological traits of extant species on the tree, we show that there is no strict association between macrohabitat and MG presence, and suggest several hypotheses for future inquiry.

Keywords: chemical communication, mental glands, phylogeny, turtles

Talk on: Friday, Sept 20, 12:00

Influence of early growth condition on blue tit nestlings colouration, an experimental approach

Katarzyna Janas, Julia Barczyk, Dorota Lutyk, Anna Łatkiewicz,
Mariusz Cichoń, Szymon Drobniak

Institute of Environmental Sciences, Jagiellonian University

Brightly coloured feather ornaments are considered to play important role in sexual selection and social communication as an honest signals of bird's condition. Typically, feather colouration mechanisms are divided into pigment-based or structural but in fact, the majority of ornaments, are composite traits, comprising both pigment based and structural components. Although intensively studied in the context of pigment-based component, proximate mechanisms of the condition dependence of structural component, especially in case of non-iridescent structural colouration, is less well understood. The blue tit (*Cyanistes caeruleus*) expresses yellow carotenoid-based breast and blue structural tail feathers colouration at a nestling stage, which gives a unique opportunity to experimentally investigate the influence of an early growth condition on both types of colouration. Importantly, most tail feathers are not replaced during the first moult, thus conditions experienced throughout early development may influence bird's mating success in the first breeding season. We conducted a double-stage brood size manipulation experiment, with nests enlarged at an early or late stage of nestlings development, to investigate condition dependence of carotenoid-based and structural feather colouration of the blue tit nestlings. To analyse feather samples, apart from the reflectance spectrophotometry used to quantify feather colouration, we also applied scanning electron microscopy (SEM) to characterize micro-scale structure of tail feather's barbs. Contrary to expectations, we found no differences in carotenoid based colouration of breast feathers. Keratin-based microscale parameters of barb's internal structure were negatively affected by experimental manipulation, while density of eumelanosomes remained unaffected. This suggests, production of keratin component of non-iridescent structural colouration is, contrary to eumelanin pigment, physiologically costly and sensitive to perturbation during early development.

Keywords: carotenoid-based colouration, structural colouration, condition dependence

Talk on: Friday, Sept 20, 14:30

Meta-analytical insights into maternal dietary effects on offspring behavior

Malgorzata Lagisz

University of New South Wales, Sydney

Mothers are important. Especially so in the mammals. The close connection between mother and offspring in the womb and during lactation period offers multiple critical windows for influencing offspring growth. Growth depends largely on nutritional factors, and there is profound research evidence that suboptimal nutrition of the mother can lead to growth retardation of the foetus and reduced birth and weaning weight. The more subtle long-term influences include metabolic reprogramming leading to altered and disease-prone phenotypes later in life. This phenomenon, known as Barker's hypothesis or thrifty phenotype hypothesis instigated a flourishing research field of developmental origins of health and disease. Developmental foetal programming received much attention in the last few decades. This is reflected in the vast amount and diversity of research on the topic of nutritional maternal effects, especially using rodent models of maternal nutritional manipulations. In my talk, I will present an overview of the meta-analytic work we undertook to synthesise primary animal research related to the intergenerational maternal effects. Particularly, I will address whether maternal nutrition around earliest stages of offspring development can be consistently linked to altered body weight, appetite, personality and learning abilities during offsprings adulthood. The results of meta-analyses show clear effects on offspring body weights, but little influence on offspring appetite when their mothers are subject to caloric restriction or obesogenic diets. Similarly, offspring activity, exploration and anxiety are not uniformly affected by maternal caloric restriction, over-nutrition or protein restriction. In contrast, learning is clearly compromised in offspring of calorie and/or protein-restricted mothers. The effect is larger in studies using positive learning motivation in comparison to studies using negative learning motivation, potentially indicating adaptive trade-off in the effects of early life nutrition.

Keywords: maternal effects, behaviour, meta-analysis

Talk on: Friday, Sept 20, 10:00

Is evolution of high aerobic exercise capacity facilitated by changes in glucocorticoid stress response?

Małgorzata M. Lipowska, Edyta T. Sadowska, Paweł Koteja

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

The locomotor performance achieved in a challenging situation depends not only on biomechanical or physiological limitations, such as the capacity of aerobic exercise metabolism, but also on behavioral characteristics, such as adequate stress coping. The stress response is mediated largely by the hypothalamic-pituitary-adrenal (HPA) axis, through modulated release of glucocorticoids. The hormones affect both the behavioral and physiological traits, in a biphasic, level-dependent way. We used a unique experimental evolution model system to test a hypothesis that evolution of an increased aerobic exercise performance can be facilitated by modification of the glucocorticoid-related stress coping mechanisms. Bank voles (*Myodes glareolus*) from aerobic (A) lines, selected for 22 generations for high values of the maximum swim-induced aerobic metabolism (VO2swim), achieved a 64% higher VO2swim than those from unselected, control (C) lines. The temporal pattern of exercise during the swimming trial also evolved, and the A-line voles achieved VO2swim later in the course of the trial, which indicates a modification in the stress response characteristics. Both VO2swim and the average metabolic rate measured during the entire trial were negatively correlated with the level of blood corticosterone achieved at the conclusion of the trial (Cswim) and with the ratio of Cswim to the base corticosterone level (Cbase). Thus, a high corticosterone response to swimming acts as an inhibitor rather than stimulator of intense activity. However, neither the level of Cswim nor Cbase or their ratio differed between the A-selected and control lines. Thus, the experiment has not provided an evidence that evolution of the increased aerobic performance is facilitated by modification of the glucocorticoid levels. The results, however, do not exclude a possibility that other aspects of the HPA axis function evolved in response to the selection, and as the selection experiment is continued, the possibility can be investigated in further experiments.

Keywords: evolution, aerobic performance, stress response, corticosterone, bank vole

Talk on: Thursday, Sept 19, 10:00

Condition-dependence and intensity of sexual conflict in the mite *Sancassania berlesei*

Aleksandra Łukasiewicz

Evolutionary Biology Group, Adam Mickiewicz University in Poznań, Poznań, Poland

Differing evolutionary interests of males and females may result in sexual conflict, whereby traits or behaviours that are beneficial for male reproductive success (e.g. traits related to male-male competition) are costly for females. Traits associated with male reproductive success are often condition-dependent, yet how condition-dependence affects intensity of sexual conflict is not well understood. Here I used food manipulation during development of the mite, *Sancassania berlesei*, to investigate the effects of juvenile diet quality on male reproductive competitiveness, male-induced harm to female fitness and female resistance to this harm. Among competing males, those exposed to low quality food started mating later, and both mating duration and number of mating attempts were decreased compared to control males. Moreover, males from low quality diet treatment sired fewer eggs then males from control treatment. Unexpectedly, fitness of females exposed to males reared on a poor diet did not differ from females mated with control males. Diet quality did not alter the female resistance to male harm. Overall, expression of traits related to male-male competition, resulting from diet quality manipulation, affected male reproductive behaviour and mating success. However, I found no evidence that intensity of sexual conflict in *S. berlesei* depends on individuals condition.

Keywords: sexual conflitc, condition-dependence

Talk on: Thursday, Sept 19, 11:45

Puzzling evolutionary patterns in a nested nutritional symbiosis of a leafhopper

Piotr Łukasik, Filip Husnik, Anna Michalik

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

Heritable intracellular bacteria that provide insects with essential nutrients undergo dramatic evolutionary changes, leading to very compact genomes that only encode a small set of critically important functions. The reduced symbiont genomes can remain stable for tens of millions of years, but that evolutionary stasis can be broken. For example, when another symbiont colonizes the same insect, some of the original symbiont's functions may become redundant and subsequently lost. These effects can be particularly dramatic in cases when the new symbiont colonizes the cells of a more ancient symbiont, resulting in nested symbioses where partners can become highly complementary. In the leafhopper *Macrosteles laevis*, endobacterial symbiosis has had a different outcome. Cells of its ancient, heritable, nutrient-providing bacterial endosymbiont *Sulcia* became colonized by another bacterium, *Arsenophonus*. The ubiquity of *Arsenophonus* infections within the Polish metapopulation of *M. laevis* and the symbiont's genome characteristics suggest a relatively old association. Unexpectedly, we found no indication that *Arsenophonus* provides essential nutrients or other plausible benefits to its partners. Furthermore, comparative analyses indicated that the persistent intracellular infection did not affect the genome of *Sulcia*. Thus, endobacterial *Arsenophonus* in *M. laevis* appears to be a heritable parasite that has managed to reach fixation within the host metapopulation without providing identifiable benefits. It is now degenerating away without having visibly influenced its symbiotic partners. We discuss how this unusual, asymmetrically evolving symbiotic association may have originated and evolved.

Keywords: Endosymbiosis, nutritional mutualism, parasitism, Hemiptera, genome evolution

Talk on: Thursday, Sept 19, 16:00

Comparative transcriptome analysis of mycoheterotrophic orchids *Epipogium aphyllum* and *Neottia nidus-avis*

Michał May, Marcin Jąkalski, Julita Minasiewicz, Marc-André Selosse

Department of Plant Taxonomy and Nature Conservation,
Faculty of Biology, University of Gdańsk, Gdańsk, Poland

Mycoheterotrophy (MH) is an ability of a plant to obtain carbon from associated fungi. This nutrition mode evolved independently in phylogenetically diverse group of plants to exploit plant-fungal mutualism for carbon resources, but it occurs the most frequently among the Orchidaceae. All orchids are mycoheterotrophic at early steps of developments and are fully dependent on resource supply from appropriate fungus. Although majority of them becomes photosynthetic upon maturity, some species stay mycoheterotrohic also as adult plants. Numerous aspects of MH plants biology, including physiological processes that underlie their functioning, still have not been thoroughly investigated. In our research we aimed at unraveling this aspect of MH plant biology by application of transcriptome analysis among various organs (stems, flowers and mycorrhizal roots) of two species of European mycoheterotrophs from natural populations: *Epipogium aphyllum* Sw. and *Neottia nidus-avis* (L.) L.C. Rich. We have carried out a total RNA sequencing for *E. aphyllum* and *N. nidus-avis* in two biological replicates using Illumina platform. We performed a de novo assembly using Trinity suite, followed by a detailed annotation (e.g. functional annotation based on participation in metabolic pathways and homology to known sequences). Obtained transcriptomes were filtered to eliminate sequences not belonging to the investigated plants (derived mainly from bacteria or fungi). According to BUSCO analysis, our transcriptomes exhibited 69% and 76% completeness in *E. aphyllum* and *N. nidus-avis*, respectively. These values are most likely underestimated due to the lack of transcripts of genes coding for photosynthetic apparatus pathways, most probably linked to their elimination from the nuclear genome. The obtained data were used to perform differential gene expression analysis and to compare their expression levels between various organs, within single species and between them, in the end providing evidence for lineage-specific adaptations to the MH lifestyle.

Keywords: Mycoheterotrophy, transcriptomics, *Epipogium aphyllum*, *Neottia nidus-avis*, RNA-seq

Talk on: Friday, Sept 20, 11:45

Infections of enteropathogenic bacteria in wild birds; phylogenetic distribution and ecological predictors

Piotr Minias

University of Łódź, Łódź, Poland

Birds are common hosts for two genera of enteropathogenic bacteria, *Campylobacter* and *Salmonella*, which are recognized as an important threat to human health and poultry industry. The aim of this study was to identify ecological, life history, and phylogenetic predictors of *Campylobacter* and *Salmonella* occurrence in wild birds. For this purpose, I compiled estimates of *Campylobacter* and *Salmonella* prevalence for 200 avian species and implemented phylogenetically-informed comparative analysis to examine variation in the infection rates. *Campylobacter* had wider phylogenetic distribution and higher average prevalence in birds than *Salmonella*. *Campylobacter* prevalence showed strong associations with basic life-history components of birds, while *Salmonella* prevalence was primarily determined by ecological traits. The results also provided support for biogeographical differences and contrasting temporal trends in the occurrence of these bacteria in birds.

Keywords: *Campylobacter*, comparative analysis, life history, *Salmonella*

Talk on: Friday, Sept 20, 14:45

Adaptation and diversification of marine predators: integration of genomic and morphological data to determine drivers of ecotype differentiation in bottlenose dolphins (*Tursiops* spp.)

Andre E. Moura, Kypher Shreves, Nicholas Oxford-Smith, Marcello Ruta

School of Life Sciences, University of Lincoln, Lincoln, UK

Due to their complete transition from terrestrial to marine environments, cetaceans are a useful model group to study the role of environmental adaptation in driving evolutionary change. Although the general cetacean bodyplan became established some 35 Myears ago, the morphological diversity observed in extant species originated recently. At the intra-specific level, strong population differentiation is usually found at scales smaller than their dispersal capabilities would suggest. This has been suggested to result from adaptation to different environments, given the lack of geographic barriers in the ocean, but few studies have formally tested this. A well known example of small-scale diversification is the genus *Tursiops* (bottlenose dolphins), for which several well described ecotypes are known worldwide, with coastal populations well differentiated from pelagic ones. In this study, we present whole genome data (mtDNA and RADseq) to determine the phylogeographic history and natural selection patterns between the ecotypes, and integrate it with geometric morphometric analyses of worldwide skull morphology. Our results reveal large numbers of genetic sites under putative natural selection between ecotypes, and show that some are in close proximity to genes known to affect skull shape. Skull shape analyses reveal that, while differentiation between coastal ecotypes is likely due to drift from geographic isolation, skull differentiation in pelagic ecotypes likely results from selection towards an oceanic lifestyle. Phylogeographic inference further suggests that pelagic ecotypes are derived, and that skull shape differences relative to coastal ecotypes reflect adaptation to suction-feeding strategies, which might be crucial to survival in open water environments.

Keywords: Adaptation, Cetacea, Genomics, Morphology

Talk on: Friday, Sept 20, 15:30

Sexual selection predicts the persistence of populations within altered environments

Jonathan Parrett, Darren Mann, Arthur Chung, Eleanor Slade, Rob Knell

Adam Mickiewicz University, Poznań, Poland
Queen Mary University of London, London, UK

The effect of sexual selection on species persistence is unclear. The cost of bearing ornaments or armaments might increase extinction risk, but sexual selection can also enhance the spread of beneficial alleles and increase the removal of deleterious alleles, potentially reducing extinction risk. Here we investigate the effect of sexual selection on species persistence in a community of thirty-four species of dung beetles across a gradient of environmental disturbance ranging from old growth forest to oil palm plantation. Horns are sexually selected traits used in contests between males, and we find that both horn presence and relative size are strongly positively associated with species persistence and abundance in altered habitats. Testes mass, an indicator of post-copulatory selection, is, however negatively linked with the abundance of species within the most disturbed habitats. This study represents the first evidence from a field system of a population-level benefit from pre-copulatory sexual selection.

Keywords: Sexually selected traits, Modified landscapes, Extinction risk

Talk on: Thursday, Sept 19, 11:30

Increasing temperatures favors biological invasions: an example of direct, temperature and size dependent food competition between native and invasive fish species

Alicja Pawelec, Anna Hauler, Małgorzata Grzesiuk

Zakład Hydrobiologii, Wydział Biologii, Uniwersytet Warszawski, Warszawa, Poland

One of the most important problems of modern ecology is to understand the strong, negative impact that invasive species can have on native biocoenosis. This problem is made even worse by an even bigger threat to biodiversity: global warming. Both effects seem to be strongly coupled: increasing temperatures favor biological invasions. We carried out laboratory experiments in order to assess the importance of the effects of interactions between individuals of small groups of co-occurring species, the native common gudgeon *Gobio gobio* and the invasive monkey goby *Neogobius fluviatilis*, both subjected to intensified food competition. Furthermore, because we wanted to investigate whether food competition between those species is dependent on the size of invasive competitors, we ran our experiments using three size classes of the invasive monkey gobies: smaller than, equal to and bigger than the native gudgeons. To reflect the impact of higher temperatures caused by global warming, we used two different water temperatures: 16 ºC preferred by *G. gobio* and 22 ºC preferred by *N. fluviatlis*. We measured feeding competition directly using such parameters as number of prey consumed, time of onset of feeding following introduction to food and total time spent hunting prey. Ours is the first study to provide direct confirmation that invasive species are superior food competitors (they eat more, reach food first and hunt longer) than native species. Surprisingly, we found food competition to be size dependent; the greater threat for native species are invasive fish which are similar to them in size. Higher temperature gives an advantage to the invaders (with significant effects seen at 22 0C; only 6 ºC between the conditions makes big differences). This is especially important given that global temperature rise is predicted to reach 1.5 ºC by the 2030s, and by 2100 over 4 ºC.

Keywords: biological invasions, global warming, food competition, temperature dependent competition, size dependent competition

Talk on: Friday, Sept 20, 16:00

Human body fluctuating asymmetry and immunocompetence

Bogusław Pawłowski, Barbara Borkowska, Justyna Nowak,
Daria Augustyniak, Zuzanna Drulis-Kawa

University of Wrocław, Wrocław, Poland

More symmetric organisms are perceived as more attractive. Fluctuating asymmetry (FA) i.e. small, random deviations from perfect bilateral symmetry, is supposed to inform about developmental instability. According to the good genes hypothesis, a low level of FA is a putative cue to an organism's biological quality. An important aspect of this quality is the immune system functioning (ISF). The aim of this study was to evaluate the relationship between immune system functioning and body symmetry in healthy people. Materials and methods: The composite body fluctuating asymmetry (cFA) was assessed on the basis of six bilatera traits (on hands and feet). The ISF was determined by many innate (total complement and lysozyme activity, nutrophils function) and adaptive immune parameters (T CD3 and B CD19 lymphocytes, total IgA and IgG and response to flu vaccine). 98 men and 92 women were subjected to flu (among them 37 men and 30 women also to tetanus) vaccination. The blood samples were collected before and 4 weeks after the antigen exposure. Immunomodulatory factors: participant's age, body fat and free testosterone level, were controlled. Results: Apart from the weak positive association between CD3 or CD19 and cFA in men, we found no association between the level of body symmetry and the rest of the analysed immune parameters for both sexes. Conclusions: Our results do not confirm the good genes hypothesis prediction and suggest that in western population, human mate preferences for more symmetric bodies are not related to the cue of immune competence i.e. the significant aspect of biological quality.

Keywords: body symmetry, immunity quality, developmental stability, vaccination, good gene hypothesis

Talk on: Friday, Sept 20, 15:45

Untangling the puzzle of Archaeplastidia evolution with phylogenies of plastid-encoded proteins

Filip Pietluch, Katarzyna Sidorczuk, Paweł Mackiewicz, Przemysław Gagat

University of Wroclaw, Faculty of Biotechnology,
Department of Bioinformatics and Genomics, Wrocław, Poland

Photosynthetic eukaryotes play a key role in the Earth's biosphere by converting light into organic compounds that can be subsequently used by other organisms. All eukaryotes with the ability to photosynthesis carry out this process in specialized organelles generally called plastids. Plastids evolved from a free living cyanobacterium engulfed by a heterotrophic unicellular eukaryote in a process called primary plastid endosymbiosis. Two cases of primary plastid establishment were reported. The first primary plastid endosymbiosis gave rise to three eukaryotic lineages: Glaucophyta, Rhodophyta and Viridiplantae, all united into one supergroup the Archaeplastida. The second cyanobacterial endosymbiosis occurred much later within the rhizarian genus *Paulinella*. Some inconsistencies still remain around the primary plastid evolution, such as: (i) the branching order among Archaeplastida, (ii) diversification time of plastid lineages and (iii) the number of primary plastid endosymbioses. In order to untangle the Archaeplastidia evolution, we performed phylogenetic and molecular clock analyses based on concatenated set of 30 highly conserved plastid-encoded proteins derived from 181 taxa representing a large diversity of cyanobacteria and plastids. We used PSI-BLAST to build datasets of homologous plastid-encoded proteins and computed multiple alignments with MAFFT using L-INS-I algorithm. To eliminate poorly aligned positions and divergent regions we used Gblocks. Phylogenetic analyses were calculated in Beast, RaxML, IQtree and MrBayes using best-fit partitioned schemes calculated in Partition Finder, in Phylobayes using site heterogeneous mixture (CAT) model assuming site specific rates and profiles or PhyML using best model choosed by Prottest. Molecular clock analyses were conducted in Phylobayes, MrBayes and Beast with the usage of relaxed models. Our results support the monophyly of Archaeplastidia with Glaucophytes as a basal lineage. They also indicate that the cyanobacterial endosymbioses that gave rise to the Archaeplastida and photosynthetic *Paulinella* may have occurred much earlier than postulated 1.600 and 90-140 million years ago, respectively.

Keywords: Endosymbiosis, Archaeplastida, Cyanobacteria, *Paulinella*, Plastid

Talk on: Friday, Sept 20, 11:15

Going to the dogs? Human-induced evolution in the grey wolf

Małgorzata Pilot, Wiesław Bogdanowicz

Muzeum i Instytut Zoologii PAN, Warszawa, Poland

Domestication is the most striking example of human-induced evolution, and the grey wolf was the first animal that was affected by this process. Domestic dogs thrive in human-dominated habitats, and the continuous expansion of such habitats have resulted in demographic expansion of the global dog population, currently estimated at 1 billion individuals, which in turn has increased the spatial overlap between free-ranging dogs and wild wolves. More frequent wolf-dog encounters are likely to increase the frequency of hybridisation, especially in regions of low wolf density or in the presence of strong hunting pressure. Hybrids living in natural wolf habitats may have lower fitness than non-admixed wolves, but in habitats being rapidly transformed by humans, hybrids can show higher fitness. Dog-derived gene variants may facilitate adaptation of their wild owners to human-dominated habitats, thus leading to human-induced evolution. We studied genome-wide introgression patterns in wolves from across Eurasia, and identified 15 chromosomal blocks having a significant overrepresentation of dog-derived alleles, suggestive of positive selection. Among 105 functional genes located within these chromosomal blocks, we found an overrepresentation of functions associated with nervous system regulation, reproduction, development and metabolism. This result suggests that hybridisation can be an important source of adaptive variation for wolves, and may facilitate their adaptation to living in human-dominated habitats by modifying variation in genes affecting morphological, physiological and behavioural traits. Adaptation of wolves to human-dominated habitats may result in a shift of their trophic niche from apex predators to scavengers of anthropogenic food, leading to ecosystem-level effects.

Keywords: human-induced evolution, hybridisation, grey wolf, domestic dog

Talk on: Thursday, Sept 19, 10:15

Environment-dependent selection in sexually selected traits

Agata Plesnar-Bielak, Anna Maria Skwierzyńska,
Kasper Hlebowicz, Jacek Radwan

Jagiellonian University, Kraków, Poland

The persistence of genetic variation in sexually selected traits is puzzling, given strong directional selection predicted to act on these traits. One of the proposed mechanisms to maintain it is environment-dependent balancing selection acting in heterogeneous environments. It favors one allele in one environment and the other in another one. Such environment-dependent selection might be particularly potent as most environments are highly heterogeneous and/or variable in time. We used a bulb mite model to test the role of environment in shaping the evolution of two sexually selected traits, enlarged legs used as weapons and enzyme polymorphism in 6Pgdh. The expression of the former trait, associated with precopulatory sexual competition, is dimorphic depends on many genes and is modified by environment. The latter trait, affecting sperm competitiveness, is associated with single gene polymorphism. We show that thermal conditions drive the evolution of both traits, but do so in different ways. Evolution at decreased temperature increases the frequency of males possessing enlarged legs, eventually leading to male-monomorphic populations in which all males possess the weapon. This is because total reproductive success of armored males with enlarged legs increases at low temperature. Thus, in comparison to control conditions, decreased temperature strengthens selection for sexual armament expression. On the other hand, the same temperature reduces the strength of selection favoring 6Pgdh allele providing advantage in sperm competition (but does not reverse it). Our results show seasonal temperature fluctuations have the potential to maintain male armaments polymorphism within populations and spatial heterogeneity in thermal conditions may cause differences among populations in sexually selected trait selection, but are insufficient to maintain 6Pgdh polymorphism observed in some natural bulb mite populations. Furthermore, our results suggest that the relative strength of precopulatory and postcopulatory (sperm competition) sexual selection may depend on environmental conditions.

Keywords: Environment-driven selection, sexual selection, genetic variation

Talk on: Thursday, Sept 19, 11:15

In the face of the global environmental crisis. What's an evolutionary biologist to do?

Zofia Prokop

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

The overwhelming evidence from a wide range of biological and Earth sciences reveals the alarmingly deteriorating state of the biosphere. According to recent meta-analyses, current rate of global species extinction is tens to hundreds times higher compared to average over the last 10 million years, and accelerating, threatening the stability of ecosystems on which we and all other species depend. Multiple recent scientific papers and reports, including the one issued this year by the UN's Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES), indicate that we still do have a window of time in which we can conserve and restore nature to the point of sustainability, but this window is closing rapidly, so urgent actions are needed now and at every level from local to global. As biological scientists, we have a set of skills and tools which can be particularly helpful for strengthening and guiding these urgently needed actions. In this talk, I will highlight several ways in which we can (meaningfully and sensibly) engage, as well as argue that we have every responsibility to do so.

Keywords: ecological crisis, climate change, scientists' responsibility

Talk on: Wednesday, Sept 18, 18:30

Differential introgression across newt hybrid zone, evidence from replicated transects

P. Zieliński, K. Dudek, J.W. Arntzen, G. Palomar, M. Niedzicka., A. Fijarczyk, M. Liana,
D. Cogalniceanu, W. Babik

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

Genomic heterogeneity of divergence between hybridizing species may reflect heterogeneity of introgression, but also processes unrelated to hybridization. Heterogeneous introgression and its repeatability can be directly tested in natural hybrid zones by examining multiple transects. Here, we studied hybrid zones between the European newts: *Lissotriton montandoni* and two lineages of *L. vulgaris*, with replicate transects within each zone. Over 1000 nuclear genes located on a linkage map and mtDNA were investigated using geographic and genomic clines. Overall, the five transects were all similar, showing hallmarks of strong reproductive isolation: bimodal distribution of genotypes in central populations and narrow allele frequency clines. However, the extent of introgression differed between the zones, likely as a consequence of their different ages, indicated by the analysis of heterozygosity runs in diagnostic markers. In three transects genomic signatures of small-scale (ca. 2 km) zone movements were detected. We found a limited overlap of cline outliers between transects, and no evidence of stronger differentiation between zones than between transects within zones. Introgression was heterogeneous across linkage groups, with patterns of heterogeneity similar between transects and zones. Predefined candidates for increased or reduced introgression exhibited only a subtle tendency in the expected direction, suggesting that interspecific differentiation is not a reliable indicator for the strength of introgression. These hierarchically sampled hybrid zones of different ages show how introgression unfolds with time and offer an excellent opportunity to dissect the dynamics of hybridization and architecture of reproductive isolation at advanced stages of speciation.

Keywords: hybridization, differential introgression, newts

Talk on: Friday, Sept 20, 12:15

Mast seeding promotes evolution of scatter-hoarding

Rafał Zwolak, Dale Clements, Andy Sih, Sebastian Schreiber

Department of Systematic Zoology, Adam Mickiewicz University, Poznań, Poland

Many plant species worldwide are dispersed by scatter-hoarding granivores: animals that hide seeds in numerous, small caches for future consumption. Yet, the evolution of scatter-hoarding is difficult to explain because undefended caches are at high risk of pilferage. Previous models have attempted to solve this problem by giving cache owners unrealistically large advantages in cache recovery, by kin selection (but individuals that cache and those that pilfer are usually unrelated), or by introducing reciprocal pilferage of “shared” seed resources. However, the role of environmental variability has been so far overlooked in this context. One important form of such variability is masting, which is displayed by many plant species dispersed by scatter-hoarders. We use a mathematical model to investigate the influence of masting on the evolution of scatter-hoarding. The model accounts for periodically varying annual seed fall, caching and pilfering behavior, and the demography of scatter-hoarders. Masting, through its effects on population density, reduces cache pilferage and lowers the reproductive cost of caching (i.e. the cost of caching for the future rather than using seeds for current reproduction). These reductions promote the evolution of scatter-hoarding behavior especially when interannual variation in seed fall and the period between masting events are high.

Keywords: Behavior, evolutionary stable strategies, masting, mathematical model, seed caching

Talk on: Thursday, Sept 19, 15:45

Posters

(alphabetic order, according the first Author)

Seasonal changes in environmental preferences of Black Grouse (*Tetrao tetrix* L.1758) in Biebrza Valley

Michał Adamowicz

University of Warsaw, Warszawa, Poland

Black Grouse *Tetrao tetrix* (L. 1758) is a bird species belonging to the family of Phasianidae family and the Galliformes order. In the Biebrza Valley, as well as in Poland, the number of this bird has been declining for many years. It is a sedentary species. Within its refuges, to which it shows year-round attachment, there is a seasonal variation in habitat preferences. To protect and preserve this critically endangered species in Poland, the knowledge of its ecology is essential. For this reason, it is particularly important to precisely determine the key elements of the environment preferred by Black Grouse during the whole year (including the non-breeding period not very precisely studied in this respect before) in one of the last lowland refuges of this species in Central Europe. Field inspections carried out for 2 years have shown that his environment the Black Grouse needs a patchwork of vast, preferably swampy open areas used for spring lekking and autumn feeding sites, young tree stands which are a winter food base, and drier patches of ground, suitable for breeding, chick leading and moulting - especially in summer and also in the autumn. The presence of bird was noted on the basis of direct observations, the voice heard and found traces. During the research, an attempt was made to determine the number of Black Grouse in the Biebrza Basin.

Keywords: Black Grouse, ecology of the species, environmental preferences, seasonal changes, Biebrza Valley

Poster number in the exhibition corridor: P2

Long-term fitness consequences of divorce in the collared flycatcher *Ficedula albicollis*

Aneta Arct

Department of Animal Ecology and Genetics, Evolutionary Biology Centre,
Uppsala University, Uppsala, Sweden

Divorce has been recorded in 92% of socially monogamous birds and its rate it is known to be highly variable both within and between species. Explaining this variation is important for understanding the evolution of social monogamy and long-term partnerships. Surprisingly, despite decades of effort, the limited availability of long-term study data has prevented a robust characterisation of the divorce behaviour. Here, we analyse 34 years of breeding histories in a population of the collared flycatcher *Ficedula albicollis*, identifying evidence for an adaptive strategy in the divorce behaviour. We found, to our knowledge for the first time, that divorced females showed substantially higher survival rates in comparison to faithful ones. Moreover, multi-divorced females had a higher lifetime reproductive success in terms of the overall number of recruited offspring.

Keywords: divorce, birds, breeding success, life history, fitness, monogamy, mating, adaptiveness, sexual selection

Poster number in the exhibition corridor: P3

Cell size and the oxidative stress in breeding female bank voles *Myodes glareolus*

Elżbieta Bonda-Ostaszewska, Tadeusz Włostowski

University in Białystok, Białystok, Poland

Recent studies demonstrated that reproduction reduces oxidative damage in various tissues of small mammals females. The present work was designed to determine whether the reduction of oxidative stress in reproductive female bank voles was associated with changes in size of cells. We examined the mass of organs and the size of hepatocytes, nephrocytes and myocytes of reproducing, non-reproducing and post-reproducing females of bank voles. TBARS concentration was measured to determine intensity of oxidative damage in tissues. The lowest level of TBARS was found in the tissues of reproducing females. Also, significant increase in liver and kidneys mass and increase in size of hepatocytes and nephrocytes was observed in this group; the simple regression analysis confirmed a negative relation between the cell size and lipid peroxidation in liver and kidneys. Similar relation was not found in the muscles; here the largest myocytes were observed in the muscles of post-reproducing females. These data indicate that reduction of oxidative stress in liver and kidneys, but not in muscles of bank voles during reproduction may be associated with an increase in the cell size.

Keywords: cell size, oxidative stress, reproduction, bank vole

Poster number in the exhibition corridor: P31

Does the chequered blue butterfly (*Scolitantides orion*) has a chance to remain in Polish fauna? Genetic analysis of endangered populations

Magdalena Czajkowska, Anetta Borkowska, Marcin Sielezniew, Izabela Dziekańska

Laboratory of Molecular Biology, Institute of Biology,
University of Bialystok, Bialystok, Poland

Nowadays, the disappearance of many butterfly species is observed in Europe and the main reason of that situation is the loss of natural habitats and their fragmentation, resulting from the processes of natural succession and human activities. A good example is a situation of the chequered blue butterfly (*Scolitantides orion*) in Poland. This xerothermophilous insect is considered as critically endangered in Poland and has survived only in a few localities. Therefore, the knowledge of its genetic population structure is extremely important. We sampled two largest populations of the chequered blue butterfly, inhabiting the Vistula valley near Kazimierz Dolny, but on the opposite banks of the river. Genetic analyzes were carried out on small wing pieces of 65 individuals. A variety of genetic markers (fragments of mitochondrial COI and NADH genes and nuclear gene sequences of Wgl and EF1a, and seven highly variable microsatellite DNA loci) were used to determine the level of genetic variation of the studied populations, the degree of genetic diversity between them, and to detect immigrant individuals. Analyzes revealed that genetic variation is low in both of the studied populations but higher in the sample came from the eastern bank of the river. Similarly, the genetic differentiation between two localities was low. It could suggest the existing gene flow, despite the Vistula river as a geographic barrier. According to the dominant wind direction in this region we hypothesize that occasional migration of individuals occurs more frequently from the west to the east. It may also contribute to a better genetic condition of the population located to the east bank of the river. This study may help to create an appropriate and effective plan for the species protection in the future.

Keywords: Chequered blue butterfly, genetic population structure

Poster number in the exhibition corridor: P11

Landscape genomics of a wild passerine across replicated urbanisation gradients

Sylwia Czarnomska, Marta Szulkin

Wild Urban Evolution & Ecology Lab, Centre of New Technologies (CeNT),
University of Warsaw, Warszawa, Poland

Urban habitat is an extreme example of human-induced alteration of the natural environment and poses different challenges and opportunities for urban dwelling animals. It has been readily demonstrated that urbanization can affects adaptive and nonadaptive evolutionary processes that shape the genetic diversity within and between populations. However, most of these studies are hampered by the fact that inference is often made on only one or few urban/rural contrasts. Moreover, while urban areas are often considered as homogeneous entities, these are in fact a mosaic of highly contrasted environments. The impact of this heterogeneity on genomic structuring in wild vertebrates is to date very limited. The goal of our project was to quantify the extent to which (1) cities induce a consistent signal at the genomic level, (2) urban heterogeneity influences patterns of genetic variation and (3) populations exhibit replicated, urbanisation-driven signatures of selection. For that purpose we applied a high density Affymetrix 500K Great Tit SNP chip to genotype 288 pre-breeding adult great tits (*Parus major*) collected in eight Polish cities and four large natural forests. Within each city, birds were sampled in up to 5 different urban habitats (urban center, residential area, urban park, natural corridor, adjacent forest). Each location was quantified on multiple environmental axes (e.g. light pollution, percentage of impervious surface, canopy cover, distance to roads), which were further synthesised with a principal component analysis (PCA) to calculate an overall urbanisation score subsequently used in a genome-environment association (GEA) study.

Keywords: population genetics, urban evolution, urbanisation, SNP chip, urban mosaic

Poster number in the exhibition corridor: P45

Ectoparasite and sex effects on recruitment and natal dispersal in the blue tit

Anna Dubiec, Adam Krupski, Edyta Podmokła, Szymon Drobniak, Lars Gustafsson

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

Parasites are considered to be one of the major factors affecting life history traits and behaviour in animal populations. While their role in affecting reproductive success and adult survival is well explored, it is relatively poorly known how parasite-related rearing conditions shape postnatal life. We studied the effect of the common avian haematophagous ectoparasite – the hen flea – on the probability of recruitment to the breeding population in the small cavity-nesting passerine – the blue tit. Infestation levels of the nesting material were manipulated during three breeding seasons. Two types of nests were created: devoid of ectoparasites and infested with hen fleas at the beginning of the incubation period and shortly after nestlings hatched. Treatment affected the size of nestlings in a sex-specific manner: both body mass and tarsus length were more strongly reduced in male than female nestlings in flea-infested nests. Infestation levels did not explain variation in the recruitment probability, however, male fledglings recruited at higher rate than female fledglings. Moreover, while the treatment did not affect the natal dispersal distance, females tended to disperse further than males. These results indicate that haematophagous ectoparasites may have limited influence on the patterns of recruitment in avian passerine hosts and confirm the role of sex as an important predictor of this trait.

Keywords: ectoparasitism, recruitment probability, natal dispersal

Poster number in the exhibition corridor: P5

Natural blood doping through anthocyanin supplementation in migratory songbirds

Maciej Działo[1], Amadeusz Bryła[1], Kristen DeMoranville[2], Edyta T Sadowska[1], Lisa Trost[4],
Barbara J Pierce[3], Scott R McWilliams[2], Ulf Bauchinger[1]

[1]Jagiellonian University, Kraków, Poland
[2]University of Rhode Island, Kingston, USA
[3]Sacred Heart University, Fairfield, USA
[4]Max Planck Institute for Ornithology, Seewiesen, Germany

Red blood cells (RBCs) play a key role in aerobic metabolism by providing the oxygen required to meet the energetic demands of effective organs. During migration, birds must upregulate their metabolism, which increases reactive species production. These molecules can cause considerable damage to RBCs and impair their oxygen-carrying capacity, however, the consumption of dietary antioxidants may mitigate damage to RBCs. Migratory birds were found to consume fruits high in the anthocyanin – a potent antioxidant. It is, however, unknown if the availability of anthocyanins in the diet is beneficial for the aerobic machinery of migrants. We employed a two-factorial design in female European starlings (*Sturnus vulgaris*) by manipulating dietary anthocyanin availability (with and without supplementation), and migratory flight activity (flying versus non-flying in a wind-tunnel) to test for the effects on hematological variables. Birds in the flight group flew on average 600 km over a two week period while birds in the non-flight group remained in room-sized aviaries. Individuals supplemented with anthocyanins had on average 15% higher RBC number and 4% lower RBC size compared to non-supplemented individuals, a result that was independent of flight manipulation. Hematocrit and hemoglobin content did not differ between experimental groups. It is possible that dietary antioxidants were able to protect RBCs from damage, so birds maintained a higher number of RBC, however, other explanations such as the direct effect of anthocyanins on RBCs proliferation cannot be excluded. A greater number of smaller RBCs may ultimately secure migratory performance and the fitness of migrants by enhancing RBC hemorheological properties and the exchange of respiratory gases. The flexible response to dietary anthocyanins is novel for endurance athletes in general and raises the question if birds are actively pursuing natural blood doping.

Keywords: birds, blood, antioxidants, wind-tunnel, phenotypic flexibility

Poster number in the exhibition corridor: P8

The evolution of vision in vertebrates:
The size of sensor and processor in avian visual system

Arkadiusz Fröhlich, Simon Ducatez, Daniel Sol

Department of Forest Biodiversity, Institute of Forest Ecology and Silviculture,
Faculty of Forestry, University of Agriculture, Kraków, Poland

The size of vertebrate eye evolved adjusting to ambient light conditions and visual quality needs. However, visual scenes are projected to visual brain regions, which recognize colors, patterns and motions. According to principle of proper mass, the relatively large visual brain regions facilitate processing of more complex visual stimuli and/or accelerate reaction time (Reaction Fluency Hypothesis). Here, we hypothesized that in birds, the size of visual brain regions (Tectum Opticum; TeO hereafter) did not coevolve with the size of eye (Mosaic Evolution Hypothesis), but rather with high complexity of habitat, mobility of prey and foraging technique (Reaction Fluency Hypothesis). To test these hypotheses, we compiled database containing the axial eye length, the corneal diameter and the mass/volume of TeO (and whole brain) using already existing literature. We showed that the size (relative to body size) of the eye and TeO do not correlate among birds. We confirmed Reaction Fluency Hypothesis, showing that vertivores and species of closed habitats are more likely to have enlarged TeO (relative to body size). Although these birds were also more likely to have large eyes, the major drivers of the size of eye were nocturnality and aquatic feeding (Ambient Light Hypothesis). The foraging technique, related with moving speed did not explain the size of TeO, nor the size of eye, but flightlessness does. Our results showed, how different components of visual system, such as sensors (eyes) and processors (visual brain regions) might evolve in vertebrates and gave support for comparative analyses.

Keywords: Eye Size, Tectum Opticum, Optic Lobe

Poster number in the exhibition corridor: P35

Hatching delays vs breeding success and physiological condition in two extreme years in the Great Tit *Parus major*

Michał Glądalski, Mirosława Bańbura, Adam Kaliński, Markowski Marcin, Joanna Skwarska,
Jarosław Wawrzyniak, Piotr Zieliński, Iwona Czyżewska, Jerzy Bańbura

Department of Experimental Zoology and Evolutionary Biology,
Faculty of Biology and Environmental Protection, University of Łódź, Łódź, Poland

Temperature variation affects various life stages of organisms. Temperature has a major influence on the optimal laying-incubation-hatching dates of insectivorous passerines, because it poses energetic constraints and affects the timing of food abundance. A combination of warm weather and mild rainfall in spirng provides good conditions for the development of plants and rich arthropod communities, while low temperature slows down these processes. Delays in hatching usually occur when females of the Great Tit face a cold spell and may be considered as beneficial because they allow for better family planning decisions. In extreme situations (sudden and extreme drop in temperature in spring of 2017 vs. normal spring in 2018) hatching delay is not enough to protect nestlings against food shortages later during their growth and this suggests that extreme weather events during laying-incubation period may decrease reproductive success of birds.

Keywords: breeding success, climate change, natural experiment, body condition

Poster number in the exhibition corridor: P4

Coevolution between host and host-associated phytophagous: a case study on Norway spruce and the *Monochamus* sawyer beetle

Jakub Goczał, Andrzej Oleksa

University of Agriculture, Krakow, Poland

Pleistocene glaciations had a profound influence on a current distribution and evolution of temperate biota. Moving glacier forced many plant and animal species to retreat from their primary distribution areas. When the glacier declined, the species that had survived in scattered refuges have started colonizing new areas. In many taxa, the long time of geographic isolation resulted in an allopatric speciation and formation of new species. Main aim of the study was to investigate how about 5,000 years of geographic isolation of two Norway spruce (*Picea abies*) subpopulations (Alpine-Carphatian and boreal) affected the genetic and morphological structure of its host-associated phytophagous beetle – *Monochamus sartor*. By using of microsatellite markers and geometric morphometrics we documented that the genetic and morphological structure of the species differ significantly between Alpine-Carphatian and boreal subpopulations of its host plant. Obtained results point to the importance of host range fragmentation as an important driver of diversification of phytophagous organisms.

Keywords: phylogeography, host-plant interactions, glaciation

Poster number in the exhibition corridor: P38

Coordinated chick provisioning in an Arctic seabird

Antoine Grissot, Marion Devogel, Dorota Kidawa, Dariusz Jakubas,
Marcelo Araya-Salas, Katarzyna Wojczulanis-Jakubas

Department of Vertebrate Ecology and Zoology,
Faculty of Biology, University of Gdańsk, Gdańsk

Poland An increasing number of studies report coordinated chick provisioning by avian parents. Although the pattern of parental coordination varies across species, broad occurrence of the coordination suggests that it has an adaptive value: it may increase individual fitness via higher offspring survival, faster offspring growth rate and/or higher body reserves of the parents. However, what drives the pattern of coordinated provisioning in a species remains unanswered. Here, we examined coordination of chick provisioning in the Little Auk (*Alle alle*), a planktivorous seabird species that breeds in the Arctic, and tested to what extent coordination represents a flexible response to current foraging conditions. During the chick rearing period, parents exhibit a dual-foraging strategy (i.e. alternating long foraging trips, serving to maintain the adults' body reserves, with several short trips aimed to provision the chick). It has been previously shown that Little Auk parents coordinate their foraging trips during this period, avoiding performing long trips simultaneously and thus enabling a more even distribution of feeding through time. Here we examined coordination of parental provisioning across five breeding seasons varying in terms of environmental conditions and examined chick body condition in relation to the level of parental coordination to test potential adaptive value of the coordination. We found no significant differences between study seasons, which represented a wide range of experienced environmental conditions, on coordination level, and this level was not linked with chick body condition. There was high variability between pairs, and this variability was similar across study seasons. Future studies are needed to further investigate the effect of environmental conditions on coordination, using finer scale parameters, and to test to what extent the pattern of coordinated provisioning is pair specific and related to life-history traits.

The project funded by NCN grant, no; 2017/25/B/NZ8/01417.

Keywords: coordinated provisioning, Little Auk (*Alle alle*), seabird, parental care

Poster number in the exhibition corridor: P6

Pharmaceutical contaminations of freshwater ecosystems influences *Daphnia* population on individual and molecular level

Małgorzata Grzesiuk[1], Anna Bednarska[1], Damian Mielecki[2], Elżbieta Grzesiuk[1]

[1]Autonomous Department of Microbial Biology, Faculty of Agriculture and Biology, Warsaw University of Life Sciences (SGGW), Poland

[2]Institute of Biochemistry and Biophysics PAS, Warsaw, Poland

Poland Drugs are used in medical treatment on a large scale and as a waste pollute freshwater ecosystems. Increasing amount of so-called civilization diseases, such as different type of cancer, in large extent contribute to this form of contamination. The aim of the present research was to determine how the exposure to chemotherapeutics: cyclophosphamide (CP) and cisplatin (CDDP), at registered in environment concentrations, influence population and life history parameters plus proteome profile of naturally occurring in surface waters water flea: *Daphnia pulex* and *Daphnia pulicaria*. The parameters significant for crustaceans, survivorship and population growth rate, were importantly decreased by CDDP treatment but not influenced by CP. On the contrary, the individual growth rate was affected only by CP and alone in the case of *D. pulicaria*. Decrease in number of eggs was observed in both *Daphnia* clones treated with CP or CDDP. Interestingly, *Daphnia* males were less sensitive to tested chemotherapeutic than females. Proteome profile disclosed that tested anticancer medicines modified expression of some proteins involved in *Daphnia* metabolism. Moreover, males exposed to CDDP showed increased level of enzymes contributing in DNA repair. Summing up, the polluting environment chemotherapeutics reduced fitness of naturally occurring *Daphnia* species. In consequence this may affect performance of the aquatic food webs on different trophic levels. Supported by NCN grant UMO-2016/21/B/NZ8/01542

Keywords: pharmaceuticals, alkylating agents, cyclophosphamide, cisplatin, life history, proteome

Poster number in the exhibition corridor: P48

Diversity of circular extrachromosomal DNA molecules among the Euglenids

Natalia Gumińska, Paweł Hałakuc, Rafał Milanowski

Department of Molecular Phylogenetics and Evolution, Faculty of Biology,
University of Warsaw, Biochemical Research Centre, Warszawa, Poland

Circular extrachromosomal DNA (eccDNA) molecules have been observed for a long time. With the advent of high-throughput sequencing techniques they have recently become the subject of increased research interest. To date, endogenous circular DNAs have been reported in many organisms, such as human, yeast, plants and protists. They are known to play an important role in the plasticity of eukaryotic genomes and their response to external stimuli. Some of these molecules arise as the result of cellular machinery errors, cancerogenesis, aging or as a response to stress conditions, while others are present constantly during the cell cycle. To better understand the evolutionary context of the formation and accumulation of circular DNAs of chromosomal origin, we have decided to investigate the circulomes of two *Euglena* (Excavate algae) species, *Euglena hiemalis* and *Euglena longa*. These organisms belong to one of the basal taxa of eukaryotes, thus displaying ancestral features likely to be present in Last Eukaryotic Common Ancestor (LECA). We have analyzed the data from whole genome (de novo) sequencing and circular fraction enrichment. Herein, we present our findings concerning circular rDNA as well as other putative eccDNAs diversity among the Euglenids. Our results may shed new light not only on the evolution of Euglenids, but also on the evolution of Eukarya as a whole.

Keywords: eccDNA, Euglenids, rDNA, *E. hiemalis*, *E. longa*

Poster number in the exhibition corridor: P24

The physical form of released nonconventional introns in *Euglena gracilis*

Natalia Gumińska, Michalina Komorowska, Rafał Milanowski

Department of Molecular Phylogenetics and Evolution, Faculty of Biology,
University of Warsaw Biochemical Research Centre, Warszawa, Poland

Euglenids (Euglenida) are unicellular Excavate flagellates. Their nuclear genes, apart from conventional, spliceosomal introns, also contain nonconventional introns, which exhibit some exceptional traits: variable, noncanonical borders and an ability to form a stable RNA secondary structure, which brings together intron ends, placing adjacent exons in close proximity. Interestingly, while spliceosomal introns are frequently lost in different lineages, nonconventional introns are inserted in new positions within the genes. Although they were first described nearly thirty years ago, the mechanism of their removal still remains unknown. To gain insight into this topic, we have investigated the physical form of released introns in three genes (tubA, tubB and gapC) in model organism, *Euglena gracilis*. Applying experimental approach based on reverse transcription followed by an inverse PCR, we observed, as expected, conventional lariats consistent with a two-step transesterification removal for spliceosomal introns. On the contrary, released nonconventional introns adopt circular form with full-length ends. This new type of intronic circRNA may play a role in intron mobility due to the frequent insertions of nonconventional introns. The proliferation of nonconventional introns in genomes of Euglenids can have significant evolutionary implications as a determinant of variability. This is particularly important in clonal organisms such as Euglenids.

Keywords: nonconventional intron, circRNA, Euglenids, *E. gracilis*

Poster number in the exhibition corridor: P25

The evolution of phenotypical characters in the *Micarea prasina* group (Pilocarpaceae)

Beata Guzow-Krzemińska[1], Emmanuël Sérusiaux[2], Pieter P.G. van den Boom[3], A. Maarten Brand[4], Annina Launis[5], Anna Łubek[6], Martin Kukwa[1]

[1]University of Gdańsk, Faculty of Biology,
Department of Plant Taxonomy and Nature Conservation, Gdańsk, Poland
[2]Evolution and Conservation Biology Unit, University of Liège, Liège, Belgium
[3]JA Son, The Netherlands; [4] Leiden, The Netherlands
[5]Botany unit, Finnish Museum of Natural History, University of Helsinki, Finland
[6]The Jan Kochanowski University in Kielce, Institute of Biology, Kielce

Lichens are nutritionally specialized fungi which associate with autotrophic partners, either eukaryotic algae or cyanobacteria, or both. Traditionally, morpho-anatomical characters together with secondary metabolites have played an important role in the lichen classification. However, the value of chemical traits have been questioned by many authors as in many cases molecular data do not correspond with the chemical variation, and therefore the correlation between them has to be evaluated for each taxonomic group de novo. Recently, several new *Micarea* species have been described from Europe and their phylogenetic position has been evaluated based on three loci, i.e. mtSSU rDNA, Mcm7 and ITS rDNA. Two main lineages were found within the group. The *Micarea micrococca* clade consists of twelve species, of which most species produce methoxymicareic acid, with the exceptions of *M. levicula* and *M. viridileprosa* producing gyrophoric acid. The *M. prasina* clade consists of species producing micareic acid, with the exception of *M. herbarum* which lacks any detectable substances and *M. subviridescens* that produces prasinic acid. Ancestral state reconstructions were used to evaluate infra-group divisions and the role of secondary metabolites and selected morphological characters on the taxonomy in the *M. prasina* group. It was concluded that the ancestor of the *M. prasina* group probably had a thallus consisting of goniocysts, which were lost several times during evolution, while isidia and soredia evolved independently multiple times in different lineages. This research supported the view that the ancestor of *M. prasina* group did not produce any secondary substances, but they were gained independently in different lineages, such as methoxymicareic acid which is restricted to *M. micrococca* and allied species or micareic acid present in the *M. prasina* clade.

Keywords: ancestral states reconstruction, lichen-forming fungi, *Micarea*, phylogeny, secondary metabolites

Poster number in the exhibition corridor: P21

Seasonal changes of metabolic heat production and heat loss in a blackcap *Sylvia atricapilla*

Weronika Jadach, Anna Kowalczewska, Roger Colominas-Ciuró, Anna S. Przybylska, Małgorzata Jefimow, Michał S. Wojciechowski

Nicolaus Copernicus University, Toruń, Poland

Every year millions of small passerines migrate in autumn from breeding areas in Temperate Zone to the wintering grounds in Africa and back in spring. During migration birds have to fly across the Sahara desert where ambient temperature (Ta) is higher than body temperature and water availability is low. Prior to migration birds increase organ and muscle size necessary for intense work during migration flight. Body size increase results in increase of basal metabolic rate (BMR). This in turn, should result in increased evaporative heat loss (EHL) to maintain constant body temperature. Here we tested the hypothesis that an increase in BMR is accompanied by an increase in EHL. We measured metabolic rate (MR) and evaporative heat loss in blackcaps (*Sylvia atricapilla*) during and out of the migration seasons at 22, 33 and 37°C by indirect calorimetry. Moreover, in autumn and spring, we measured MR at Ta's between 18 to 37°C to determine the relationship between MR and Ta. Birds were kept under constant 12h photoperiod at Ta = 20°C. Bird body mass increased during autumn and spring but presumably this resulted from changes in fat mass. We found that BMR did not differ between seasons. However, metabolic rate below lower critical temperature was lower in autumn than in spring, which was accompanied by broadening of the thermoneutral zone in spring. Changes in the relationship between MR and Ta together with estimated changes in body composition suggest that greater fat mass in spring results in lower heat loss at Ta's below lower critical temperature. This would result in the observed differences in thermoregulatory characteristics of birds. The study was supported by the National Science Center grant 2017/25/B/NZ8/00541.

Keywords: metabolic heat production, heat loss, migration, bird

Poster number in the exhibition corridor: P9

The acoustic parameters of the little auk chicks' begging calls in the artificially induced stress conditions

Dorota Kidawa, Paulina Koriat, Mateusz Barcikowski

Department of Vertebrate Ecology and Zoology,
Faculty of Biology, University of Gdańsk, Gdańsk, Poland

Chicks' begging performance entails a high energetic cost, thus it should be an honest and reliable signal of chick needs. The body condition of chicks may influence the intensity of begging (the number and rate of calls) as well as the structure and acoustic parameters of the chick voice, such as the duration of individual syllables, the pauses between syllables, the frequency range or the amplitude of emitted sounds. Single-chick broods of the little auk (*Alle alle*) provide an opportunity to study the role of begging signals in a parent–offspring interactions, without the effect of sibling competition. The aim of the study was to investigate changes in the acoustic parameters of the chicks' begging calls in the artificially induced stress conditions. Glucocorticoids, the end hormones of the hypothalamo-pituitary-adrenal axis, are one of the front-line hormones that participate in the control of the whole body homeostasis and the organism's response to stress. Corticosterone, the principal glucocorticoid in birds, was used as an experimental factor to simulate the stress reaction. Circulating corticosterone may change behaviour through mobilising energy reserves. Elevated baseline corticosterone levels have been suggested as a reliable indicator of poor condition or health, thus, reflecting how an individual copes with different perturbations. The results of the bioacoustics analyses showed that little auk chicks with the increased corticosterone level not only intensified their begging call rate but also uttered calls at higher frequencies and higher entropy levels. Such changes in vocalizations allow chicks to provide the parents with more information about their body state and food demands, therefore, it may constitute an adaptive mechanism that guards against the decrease in the chicks' body condition during the stressful periods. The study was supported by the National Science Center grant, no: DEC-2011/01/N/NZ8/04569 and DEC-2017/26/D/NZ8/00005.

Keywords: begging calls, acoustic parameters, stress, seabirds

Poster number in the exhibition corridor: P7

Six in one? Cryptic diversity of a non-marine ostracod morphospecies *Heterocypris salina* (Brady, 1868) revealed by mtDNA analyses

Adrianna Kilikowska, Karina Sas, Anna Wysocka, Monika Mioduchowska,
Lucyna Namiotko, Tadeusz Namiotko

Department of Genetics and Biosystematics,
Faculty of Biology, University of Gdańsk, Gdańsk, Poland

Cytochrome oxidase subunit I (COI) gene was used to assess the level of cryptic diversity within a halophilic ostracod morphospecies *Heterocypris salina*. DNA from a total of 94 individuals from 10 all-female localities in Greece, Italy, Morocco and Poland was amplified. The final alignment consisted of 559 base pairs of the COI gene showing 166 variable and 160 parsimony informative sites. The 20 recursive steps in the Automatic Barcode Gap Discovery (ABGD) analysis resulted in four different sequence partitions, ranging from one to six preliminary species hypotheses (PSH). The best correspondence between the PSH and the constructed COI gene tree was found at the partition, in which each of the six recognized PSH corresponded well to the main lineages with high bootstrap support. Interestingly, *H. salina* from Greece (Crete) diverged from the other molecular operational taxonomic units (MOTUs), however, only one mtDNA haplotype was found in this location. On the contrary, individuals from some localities in Morocco or Poland showed high intra-site diversity resulted in recognising representatives of two or three PSH and MOTUs co-occurring at these sites. In general, comparison of pairwise haplotype distances within *H. salina* morphospecies exhibited high genetic diversity ranged from nearly 0.0% to 23.5% confirming presence of cryptic diversity.

Keywords: *Heterocypris salina*, cryptic diversity, mtDNA

Poster number in the exhibition corridor: P17

Study of functional modules stability - transcriptomic analysis of *Saccharomyces cerevisiae*

Joanna Klim, Marek Skoneczny, Anna Kurlandzka,
Urszula Zielenkiewicz, Szymon Kaczanowski

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

‘Functional modules’ are a group of genes or their products participating in the same biological process, which are linked by at least one genetic or physical interaction. An important property of a module is that its members have more relations among themselves than with members of other modules, which is reflected in the network topology. In our research, we took a closer look at the dependencies between genes of functional modules related to NUP133 and COG7. Both of the genes have orthologues in other organisms and exhibit numerous genetic interactions. Nup133 is a nuclear pore complex protein whereas Cog7 is a part of vesicular transport module. The purpose of our research was to determine whether a lack of NUP133 or COG7, respectively, causes compensatory inactivation of other genes belonging to the tested modules. For that, we conducted experimental evolution of *S. cerevisiae* mutant strains in long-term cultures in a chemostat. After c.a 200 generations evolved populations (and wild-type strain as a control) were subjected to genome sequencing for identification of changes resulting from each primal mutation. Our results indicate the emergence of a relatively small number of non-synonymous mutations in the whole yeast genome and probably only few compensatory mutations. In both cases mutations in evolved populations in majority localized in probable promoter regions which indicate that the evolution of gene expression may play an important role in compensatory changes in cellular machinery after gene inactivation. To verify whether mutations in 5’ upstream regions substantially influenced transcription, we conducted microarray analysis of the evolved yeast populations. Initial results indicate that significant changes in the gene expression were observed for around 10% of genes of post-evolutionary mutant strains. This work was supported by the grants from the National Science Centre of Poland, no.: 2018/29/N/NZ2/00902 and 2014/13/B/NZ8/0471.

Keywords: *S. cerevisiae*, experimental evolution, genetic interactions, gene expression profiling

Poster number in the exhibition corridor: P26

Does forest management influence the ectomycorrhizal fungal communities in managed acid lowland beech forests?
The case study of the Trójmiejski Landscape Park (Pomerania, North Poland)

Joanna Korybut-Orlowska[1], Tomáš Figura[2,3], Marcin Pietras[4]

[1]University of Gdansk, Falculty of Biology, Department of Plant Taxonomy and Nature Conversation, Gdansk, Poland; [2]Institut de Systématique, Evolution, Biodiversité (ISYEB), Muséum National d'Histoire Naturelle, Paris, France; [3]Department of Experimental Plant Biology, Faculty of Science,Charles University, Prague, Czech Republic; [4]Institute of Dendrology Polish Academy of Science, Kórnik, Poland

Landscape parks, due to their relatively large size and high natural, ecological, cultural and landscape values, as well as a balance between people activity and nature conservation, are among best places to study ecology of fungi. Because fungi are essential component of biodiversity, studies in such areas given ability to use fungi as bioindicators, showing potential impact of human activity on natural or seminatural ecosystems. Moreover, landscape parks are regarded as hot-spots of fungal diversity. The following work focuses on examining the species richness and diversity of ectomycorrhizal fungal communities of acid lowland beech forest in the Trójmiejski Landscape Park. Ten research areas were selected for the study. Samples were taken in two gradients: (1) with varying degrees of phytocoenosis transformation (gradient PH), (2) and at various stages of forest management operations (gradient F). New generation sequencing (Illumina) was used to determine the composition of fungi communities in both research gradients. In these studies, particular emphasis was placed on ectomycorrhizal fungi. In total, 469 operational taxonomic units (OTUs) of fungi were obtained from root samples, of which 154 were OTUs of ectomycorrhizal fungi. Total richness for gradient PH was 134 and 117 for F, of which 99 OTU was the same for both. The highest total richness was characteristic for young beech forest from natural regeneration and the largest number of OTUs occurring only in this habitat (17). The average richness for gradients F is consistent with the hypothesis of moderate disorders, saying that just after the onset of the disorder, the species richness increases. The average and total richness for the PH gradient is very similar for each stage, but with the distortion of phytocoenosis, the number of OTUs in the characteristic stages decreases. This study clearly shows, that suitable forest management do not affect negatively the ectomycorrhizal fungi assemblages of acid lowland beech forest.

Keywords: ectomycorrhizal fungi, acid beech forest, forest management, next-generation sequencing, NGS

Poster number in the exhibition corridor: P22

Adaptation strategies of Bolivian lichens - biodiversity study of photobionts

[1]Magdalena Kosecka, [1]Agnieszka Jabłońska, [2]Adam Flakus, [3]Pamela Rodriguez-Flakus,
[1]Martin Kukwa, [1]Beata Guzow-Krzemińska

[1]Department of Plant Taxonomy and Nature Conservation,
Faculty of Biology, University of Gdańsk, Gdańsk, Poland
[2]Department of Lichenology, W. Szafer Institute of Botany,
Polish Academy of Sciences, Kraków, Poland
[3]Laboratory of Molecular Analyses, W. Szafer Institute of Botany,
Polish Academy of Sciences, Kraków, Poland

Photobionts are assigned to approximately 40 different genera of eukaryotic algae and prokaryotic cyanobacteria. The most common photobionts comprise the green algal genera *Trebouxia* and *Trentepohlia* and the cyanobacterium *Nostoc*. Sterile crustose lichens are characterized by a complete or partial disappearance of reproductive structures of mycobionts. In these taxa propagation occur mostly or only through the production of vegetative diaspores, i.e. soredia or isidia (or pseudoisidia, granules, goniocyst, etc.). Moreover, it may be assumed that in this case lichen photobionts may be transferred only through vertical transmission and the continuity of the interaction mycobiont, photobiont is not interrupted. Maintaining constant relationships, with subsequent evolution, should lead to the formation of a monophyletic groups, in which association occurs only with a given symbiont and its close relatives. Sterile tropical lichens are still understudied, either in terms of diversity, genetic variability, or interactions between bionts. Here we would like to present data on the diversity of Trentepohliaceae and Trebouxiophyceae associated with epiphytic sterile lichens from Bolivia. The results also include evaluation of the impact of habitat conditions on distribution of Trentepohliaceae and *Trebouxia* genetic diversity and their ability to occupy different geographical and climatic areas in Bolivia.

Keywords: *Trebouxia*, Trentepohliaceae, sterile lichens

Poster number in the exhibition corridor: P23

Investigation of the trade-off between current and future reproduction through brood-size manipulation in a nest-hole breeding bird

Victor Kovalov, Sadowska E. T., Niedojadlo J., Bury A., Żmuda A., Zagkle E., Speakman J., Cichoń M., Bauchinger U.

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

Reproduction is an essential life-history trait, and typically a costly one. In long-lived species with multiple reproductive events competition for allocation of resources between reproduction and self-maintenance processes may occur, and indicate a trade-off between current and future reproduction. At present we still do not fully understand which self-maintenance component might be constrained. Here, we present a project design, aimed to provide empirical evidence for such a trade-off and the potential cost for current reproduction. We employ brood-size manipulation in great tits (Parus major) as an experimental approach to increase reproductive workload and measure different parameters to answer following questions: (1) what is the energy source for increased reproduction costs? We may test either for a positive relationship between Daily Energy Expenditure (DEE) and Basal Metabolic Rate (BMR) (increased intake hypothesis), or alternatively for a negative relationship (compensation hypothesis). (2) Which component of the self-maintenance system might be suppressed? If an individual reallocates resources from the immune system, we may observe lower immunocompetence through low bacterial killing capacity (BKC) and/or high value of H/L index (Heterophils to Lymphocytes ratio). (3) Do offspring pay a cost for increased reproductive parental workload? Measurements of hatchling growth and fledgling survival will allow us to test if parents do compensate for the increased reproductive costs in response to our experimental manipulation. Currently, data on females, males and offspring for two field seasons are available including parental DEE measurements. Based on these data we will formulate the possible outcome scenarios for the future analysis of blood smears and measurements of BKC with the goal to invest the possible trade-off between the immune system as a self-maintenance trait and the investment into current reproductive effort.

Keywords: life-history traits, *Parus major*, immunocompetence

Poster number in the exhibition corridor: P1

Partitioning of evaporative heat loss in zebra finches

Anna Kowalczewska, Roger Colominas-Ciuró, Małgorzata Jefimow, Michał S. Wojciechowski

Nicolaus Copernicus University, Toruń, Poland

Surviving in hot and dry conditions requires a compromise between effective heat loss and water saving. When ambient temperature exceeds body temperature, the only way to dissipate heat is to evaporate water from the skin and respiratory tract surfaces which brings a significant loss of water. However arid-adapted birds are able to tolerate periods of hot weather and restricted water availability. We asked whether prolonged exposure to hot and desiccating conditions results in adjustments in cutaneous and respiratory heat loss. To answer this question we used 40 male zebra finches (*Taeniopygia guttata*) that were acclimated to different thermal and water conditions. Ten out of 20 birds exposed to 23°C were water-deprived for half of the daylight hours. The remaining 20 birds were exposed to 40°C during the day and half of them was also water-deprived for 6 h/day. After a 3-month acclimation we measured cutaneous (CHL) and respiratory (RHL) heat loss by open-flow respirometry at 25 and 40°C. Acclimation to hot or water restriction did not affect CHL or RHL. At moderate ambient temperatures, at 25°C CHL was ~30% greater than RHL. At 40°C RHL was positively correlated with body temperature and was ~3 times higher than CHL. When hyperthermia, birds were drooping wings and exposing underwing apteria which increased CHL and allowed lowering bird body temperature. It suggest a crucial role of CHL for heat dissipation at high ambient temperatures. The study was supported by the National Science Center grant 2017/25/B/NZ8/00541.

Keywords: heat loss, heat production, partitioning, bird

Poster number in the exhibition corridor: P10

Multimodal nestling signalization of needs in different light conditions

Kinga Kułaga, Paweł Podkowa, Adrian Surmacki

Department of Behavioural Ecology, Adam Mickiewicz University, Poznan, Poland

More effective signalization of hunger by nestlings can increase parental feeding rate. Number of feedings is one of the many factor regulating condition and further survival among offspring. Nestling begging signals can be transmitted visually through displaying the color of mouth, but also by vocalization. It is hypothesized that under different daylight conditions nestlings favor one or the other form of signal transmission. For example, in dark conditions, lauder vocalization may be more effective than visual signals due to reduced conspicuousness of nestlings gapes. On the other hand color of mouth might be more informative when light level within nests becomes sufficient. We present the literature review and the results of preliminary studies conducted on secondary cavity nesting species in May 2017 in the Wielkopolski National Park. The aim of the work was to determine whether use of the visual and voice signals of needs in Great Tit (*Parus major*) nestlings vary under different light conditions. We monitored 10 nest boxes with limited access to light and 10 with increased internal light level. In each of them we mounted digital voice recorder and trail camera. When nestlings were 8-days-old, we took sound and video recordings and measured the color of nestlings' mouths by using spectrophotometer. In the next step nestlings' calls during feeding were analyzed for frequency(Hz) and energy of the signal (dB) by using Raven bioacoustic software. Finally, the acoustic parameters of the begging calls from different light conditions were compared with the brightness of nestlings mouths. The preliminary results show that nestlings vocalize with a higher intensity in the dark conditions. Although further research is necessary, it can be suggested that this phenomenon is a kind of adaptation to prevailing conditions which may increases the chance to survive.

Keywords: signalization of needs, light conditions, nestling, Great Tit

Poster number in the exhibition corridor: P36

Historical biogeography of *Anthriscus* sect. *Cacosciadium* (Apiaceae)

Renata Kurzyna-Młynik, Łukasz Banasiak, Krzysztof Spalik

University of Warsaw, Faculty of Biology,
Biological and Chemical Research Centre, Warszawa, Poland

Anthriscus sect. *Cacosciadium* comprises seven taxa recognized as separate species or as subspecies of a widespread *Anthriscus sylvestris*. This complex occurs from East Asia to Western Europe and to western North Africa, with isolated localities in the mountains of tropical East Africa. In Europe, it includes five taxa that show a remarkable ecological diversity inhabiting both primary and secondary lowland habitats as well as primary alpine screes and mountain shady forests, the last being a very rare feature among umbellifers. We have investigated the evolutionary history and biogeography of this group using dated phylogenetic trees inferred from nuclear rDNA ITS sequences and three plastid intergenic spacers: *rpoB-trnC*, *trnS-trnG* and *trnH-psbA*. Plastid phylogenetic trees suggest Middle Eastern and origins of both the genus and its sect. *Cacosciadium*. The genus is c. 8.0 My old while sect. *Cacosciadium* originated c. 1.7 Mya. The migration of A. sylvestris complex to Europe did not occur through the Anatolian and Balkan peninsulas but around the Mediterranean through northern Africa to the Iberian Peninsula and then eastwards. The dispersal to Europe occurred c. 0.45 Mya, i.e., prior to the advent of the Elster glaciation. The occurrence of a single Asiatic haplotype in the Balkans and a single European haplotype in the Caucasus documents subsequent seed flow. ITS phylogenetic trees did not show any distinct phylogeographic pattern and the most common ribotype occurred almost throughout the entire range of sect. *Cacosciadium* suggesting a lack of barriers to gene flow. The occurrence of bristled fruits in southeastern Europe and western Asia and their absence in northern African and western European *A. sylvestris* suggest secondary gene flow from Asia Minor to Europe through the Balkans.

Keywords: diversification, phylogeography, reticulate evolution

Poster number in the exhibition corridor: P16

The complete chloroplast genome sequence of *Dactylorhiza majalis* and *Platanthera chlorantha* (Orchidaceae)

Félix Lallemand[1], Joanna Korybut-Orłowska[2], Michał May[2], Anna Ihnatowicz[3], Marcin Jąkalski[2]

[1]Institut de Systématique, Evolution, Biodiversité (ISYEB),
Muséum National d'Histoire Naturelle, CNRS, Sorbonne Université, EPHE, Paris, France
[2]Department of Plant Taxonomy and Nature Conversation,
Falculty of Biology, University of Gdańsk, Gdańsk, Poland
[3]Faculty of Biotechnology, University of Gdańsk and Medical University of Gdansk,
Gdańsk, Poland

Orchids form one of the largest and most diverse family of angiosperms in the world. Due to high variability and specialized biotic interactions with their pollinators and mycorrhizal fungi , they are an interesting subject for evolutionary and ecological research. The aim of this work was to obtain and characterize the complete chloroplast genome of two orchid species, namely *Dactylorhiza majalis* and *Platanthera chlorantha*, as a prerequisite for population genetic as well as taxonomic studies. Both species belongs to the Orchidoideae subfamily. With the main focus of researchers being put on the Epidendroideae subfamily, currently only slightly more than a dozen complete chloroplast genomes are available within Orchidoideae, and only one of those belongs to the member of the genus *Platanthera*. Sequencing library was generated using the Accel-NGS® 1S Plus Library (Swift Biosciences Inc., USA) and DNA was sequenced using the Illumina HiSeq 4000 platform. Assembly and annotations were based on the Geneious algorithm followed by careful manual inspection. As a result, both species have plastome with a circular structure, respectively 154 260 bp and 154 108 bp. They consist of several areas typical of plant chloroplast genome, i.e. a large single copy region (LCS), a small single copy region (SSC), and two separating inverted repeats (IRa, IRb). Both genomes code for 134 genes, including 113 unique ones.. The total GC content in both cases is approximately 37%. Our result show plastids with apparently intact photosynthetic abilities in *P. chlorantha*, and *D. majalis*, which is in agreement with indirect evidence for autotrophy published by Bidartondo et al. (2004) for these species. The plastome sequences we provided here constitutes a valuable aid for analyzing the genetic diversity of the Orchidaceae family and specifically in untangling complex evolutionary history in studied species.

Keywords: plastome, next-generation sequencing, NGS, *Dactylorhiza majalis*, *Platanthera chlorantha*

Poster number in the exhibition corridor: P13

Host specialization-generalization trade-offs in an invasive wheat curl mite

Alicja Laska[1], Anna Radwańska[1], Kamila Karpicka-Igntowska[1], Lechosław Kuczyński[1],
]Mateusz Konczal[2], Anna Skoracka[1]

[1]Population Ecology Lab, Faculty of Biology, Adam Mickiewicz University, Poznań, Poland
[2]Evolutionary Biology Group, Faculty of Biology, Adam Mickiewicz University, Poznań, Poland

Life history traits are often subjected to trade-offs. For example, high host specialization restricts use of a variety of hosts but enables a more efficient use of a single one. Although trade-offs are ubiquitous in nature and they have played a central role in the development of life-history theory, understanding of mechanisms underlying this phenomenon is rare. This is true especially for the evolution of host specialization. Therefore, we are studying genetic and phenotypic mechanisms of trade-offs in an obligate plant parasite *Aceria tosischella* (wheat curl mite, WCM) laboratory evolved towards specialization and generalization. Despite the wheat curl mite is one of the most important mite pests of wheat with great invasive potential, the mechanisms of its host specialization have been poorly understood. The invasive and polyphagous lineage of the WCM has been subjected to experimental host adaptation in three separate treatments (each replicated 10 times): towards specialization on a single host plant species, either wheat or barley; and towards specialization on each of these host plant species separately. Altogether, we are evolving 30 populations in which phenotypic and genetic changes are measured and analyzed every 15 generations. The project aims to bring new comprehensive knowledge about the importance of trade-offs in host adaptation and thus may help to explain the mechanisms underlying host specialization process in phytophagous organisms. Explaining trade-offs between adaptation to homogeneous and heterogeneous environment is crucial for our better understanding of changes in host range, niche breadth and invasive potential of species. The study is funded by National Science Centre, Poland (Grant no: 2017/27/N/NZ8/00305).

Keywords: trade-off, host adaptation, plant-feeding mites

Poster number in the exhibition corridor: P37

The phylogeny of the genus *Encyclia* (Orchidaceae: Laeliinae)

Monika M. Lipińska, Magdalena Dudek, Dariusz L. Szlachetko

Departament of Plant Taxonomy and Nature Conservation,
Faculty of Biology, University of Gdańsk, Poland

The Neotropical genus *Encyclia* has been described in 1828 by Hooker. It comprises over 150 species of orchids that occupy mainly seasonally dry habitats in tropical and subtropical America and are usually restricted to one or a few ecoregions. The phylogeny of *Encylia* has been subjected to an extended investigation since the beginning of the 20th century. The previous taxonomic treatments of *Encyclia* have resulted in a complex succession of invalid and misapplied nomenclature involving the following eight generic names: *Epidendrum* L., *Encyclia* Hook., *Dichaea* Lindl., *Prosthechea* Knowles & Westc., *Epithecia* Knowles & Westc., *Hormidium* Lindl. ex Heynhold, *Anacheilium* Hoffmanns., and *Microepidendrum* Brieger. In our research we sampled more than 100 species of *Encylia* and herby we present the preliminary results of the phylogenetic analysis with the usage of the low-copy genes as the molecular markers.

Keywords: *Encyclia*, Neotropics, phylogeny, taxonomy

Poster number in the exhibition corridor: P14

The sources and effects of an altered gut microbiome in an experimental evolution model on bank voles: research plan and preliminary results

Małgorzata M. Lipowska, Edyta T. Sadowska, Paweł Koteja

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

Gut microbial community, or microbiome, plays a major role in its mammalian host fitness, including the ability to digest cellulose in rodents caecum. The microbiome structure can result from an interplay of genetic (nature) and environmental factors (nurture), such as diet or bacteria present in the environment. An artificial selection experiment gives an opportunity to study how factors acting on each of these levels influence both the gut microbiome structure and the animals performance in a trial challenging the host-microbiome interaction. We performed an experiment on bank voles (*Myodes glareolus*) from lines selected for the ability to grow on low-quality herbivorous diet, which have been already found to host different caecal microbiome than those from unselected, control lines. To test if the difference is determined by genetic differences between the lines (nature) or can be altered by a horizontal transfer of bacteria from environment (nurture), we co-housed young animals with ones from the same or the other type of line. Subsequently, the animals were given either standard or low-quality herbivorous food, to investigate how the microbiome change with diet, and how do all these factors interplay in determining the animal's ability to gain or maintain body mass. During the feeding trial, half of the animals were kept in metabolic cages to measure food consumption and feces excretion, whereas the remaining animals underwent the trial in regular cages. Voles from the selected lines gain body mass faster when fed standard diet, and lose less body mass when fed low-quality herbivorous diet, than those from the unselected control lines. The line type of cohabitant did not affect body mass changes. Interestingly, low-quality diet had lesser impact on animals kept in metabolic cages, indicating potential effect of housing conditions on microbiome and digestion efficiency. However, the caecal microbiome is yet to be analyzed.

Keywords: evolution, microbiome-host interaction, herbivorous capability, bank vole

Poster number in the exhibition corridor: P32

Evidence of an ancient bottleneck influencng contemporary genetic diversity of endangered peat bog pine (*Pinus uliginosa* N.)

Bartosz Łabiszak, Julia Zaborowska, Witold Wachowiak

Adam Mickiewicz University in Poznań, Evolutionary Biology Group, Poznań, Poland

Understanding the interplay between genetic, demographic and environmental factors affecting genetic diversity of endangered species is of key importance in conservation genetics. Loss of genetic diversity, as an outcome of numerous threats, including habitat destruction, fragmentation, pollution, environmental change due to unsuitable use and exploitation of land, may lead to particularly severe consequences for forest ecosystems. This is because many forest tree species have long lifespan, limited dispersal ability and they slowly reach their reproductive maturity. Decline of genetic diversity is especially dangerous for rare, endemic or threatened tree species with small and isolated populations such as a peat bog pine (*Pinus uliginosa* N.). Natural distribution of this geographically restricted and ecologically specialized coniferous tree species is limited to a few known isolated stands. In recent years, especially in Poland, severe decrease in populations size had been observed, coupled with lack of natural regeneration and decline of older trees. Here, we used genetic and palaeo - environmental data to investigate the effects of past demographic events on contemporary population structure and distribution of genetic diversity of remaining stands of this pine species. We combined population genetic methods, phylogeographic modeling within coalescent-based approximate Bayesian computation (ABC) framework and ecological niche modeling, to explore the complex history of *P. uliginosa*. Surprisingly, we detected signatures of an ancient genetic bottleneck dated at around 26,400 years ago indicating drastic reduction of the population size during the Last Glacial Maximum, but no signatures of more recent population decline.

Keywords: LGM, genetic diversity, demography, population structure

Poster number in the exhibition corridor: P20

The genetic basis for the quiescence cell formation in *Saccharomyces cerevisiae*

Agnieszka Marek, Dominika Włoch-Salamon, Monika Opałek

Jagiellonian University, Kraków, Poland

The ability of *Saccharomyces cerevisiae* to sense and respond adequately to amino acid content in environment is critical for cell survival. During starvation for one or more nutrients, a certain fraction of yeast population exit the mitotic cycle and enter quiescence. Quiescent cells better survive long-term starvation and keep the ability to re-enter G1 phase. In the experiment with artificial selection, we have obtained strains that produce significantly lower fraction of quiescent cell relative to the ancestral strain despite the lack of nutrients such as glucose and nitrogen. These strains, during the experiment acquired several mutations, including ones in the SPS-sensing pathway (Ssy1-Ptr3-Ssy5) which is responsible only for sensing the presence of amino acids in the environment. Additionally we have also detected mutations in the amino acid permease genes AAP (Asi1, Bro1) involved in the transport of nutrients into the cell. Based on the obtained data, it can be assumed that selected mutations cause constitutive activation of SPS/AAP- sensing pathway and constant information about the presence of nutrients despite their lack in the environment. This results in the blocking transformations to quiescent state of most of the cells in the population. To test this hypothesis we transferred selected mutations on the ancestral strain background and check their production of quiescent cells. We want to measure the level of Stp1 within these strains and in experimentally evolved strains. Stp1 is the transcription factor, that is activated by the SPS- pathway genes in response to nutrients uptake. Stp1 actives then transcription of amino acid permease genes . We would like to correlate the received data with the amount of the non-quiescence cells. The obtained results will allow to confirm/exclude possible genetic based mechanism of the quiescence cell formation in yeast which can be important in aspects of biofilm formation and other fungal infections.

Keywords: *Saccharomyces cerevisiae*, Quiescent, STP1

Poster number in the exhibition corridor: P27

Gut microbiome profile of the bivalve DUI species *Unio crassus* (Bivalvia: Unionidae) is strongly related to phylogeography

Monika Mioduchowska, Katarzyna Zając, Krzysztof Bartoszek, Piotr Mandecki,
Jarosław Kur, Tadeusz Zając

Department of Genetics and Biosystematics,
Faculty of Biology, University of Gdańsk, Gdańsk, Poland

Poland Micro-organisms play important functions in the biology of all animals and also their micro-evolutionary processes and population phenomena. At present, studies on the microbiome profile of molluscs are still in progress, and the mechanisms that determine host-microbial associations are largely unknown, also with regard to endosymbionts. However, there are examples of the enormous evolutionary potential of the mollusk-microbiome coevolution. In turn, diet is one of the main components determining the community structure of an organism, and hosts are known to select their gut microbes selectively and/or functionally. Based on previous results of phylogeographical relationships among *U. crassus* populations from rivers in Poland which showed independent maternally (F-type) and paternally (M-type) inherited mitochondrial DNA lineages, we carried out analyses of the microbiome profile of populations from very different habitats, representing different evolutionary lineages. We focused on showing differences in the hosts microbiome composition that would indicate niche selection by bacteria for which *U. crassus* represents a favourable environment. Sequencing of the V3-V4 amplicon of the 16S rRNA gene resulted in 1051647 reads, with 58424 reads / 65 OTUs per sample on average. There were no significant differences in gut microbiome composition between the two sexes of the target species. However, we did observe different phyla in geographically isolated populations, which is consistent with previous research on the gut microbiome of bivalves. Although both extrinsic (environmental) and intrinsic (host) factors are crucial in shaping the microbiome profile of aquatic organisms, it seems that host genetic factors may be the driving force in bacterial colonization control.

Keywords: freshwater mussels, microbiota, next-generation sequencing (NGS)

Poster number in the exhibition corridor: P33

Application of metagenomics to the microbiome of *Branchipus schaefferi* Fischer, 1834 for the identification of endosymbiotic bacterial species

Monika Mioduchowska, Barbara Faltynowska-Domańska, Alois Pavlicko,
Krzysztof Bartoszek, Bartłomiej Gołdyn

Department of Genetics and Biosystematics,
Faculty of Biology, University of Gdansk, Gdańsk, Poland

Endosymbiotic bacteria are commonly identified in numerous invertebrate species, particularly in terrestrial insects. The host-endosymbiont coexistence in the case of freshwater invertebrates is considered a rare phenomenon. To this day, merely two publications, describing the occurrence of bacterial endosymbionts in freshwater Anostraca, have been published. This does not signify, however, that they are present only in a few freshwater invertebrates. There are three main problems associated with the identification of these bacteria occurring in unknown freshwater invertebrate hosts: a) endosymbiotic bacteria cannot be cultured on microbiological media; b) their identification is only possible with the use of molecular biology techniques, including species-specific primers; c) if the endosymbiont makes up less than 1% of the host microbiome, its identification by the PCR method may be insufficient. However, the latest, more sensitive and precise high-throughput sequencing technique, known as the next generation sequencing, provides insight into theentire profile of the microbiome, as well as the identification of bacterial sequences present in the host in trace amounts. As a result of the application of NGS and a new bioinformatictools, endosymbiotic bacteria, commonly described in other invertebrates, have been identified: *Candidatus Gortzia*, *Flavobacterium* sp., *Polynucleobacter* sp., *Rickettsia* sp., *Sphingomonas* sp. and *Wolbachia* sp.. Due to the complex host-symbiont correlations, from facultative parasitism to obligatory mutualism, the influence of discovered potential bacterialendosymbionts on *Branchipus schaefferi* (including coevolution and manipulation of hosts' reproduction) requires further research.

Keywords: Branchiopoda, Operational Taxonomic Unit, 16S rRNA, bacterial endosymbiont

Poster number in the exhibition corridor: P34

Can lower enemy pressure determine non-optimal habitat preferences in an alien *Impatiens balfourii* in Europe?

Kamil Najberek[1], Wojciech Solarz[1], Wojciech Pusz[2], Katarzyna Patejuk[2], Paweł Olejniczak[1]

[1]Institute of Nature Conservation, Polish Academy of Sciences, Kraków, Poland
[2]Department of Plant Protection, Wroclaw University of Environmental and Life Sciences, Wrocław, Poland

Vascular plants are intensively studied group of alien species, and the Impatiens genus holds a special place among them. Spectacular invasions in different parts of the world make this genus extremely harmful. However, there are still knowledge gaps in the context of high differences in levels of invasiveness, even between closely related representatives of this genus. Examples of such species in Europe are the non-invasive *Impatiens balfourii* and highly invasive *I. glandulifera*. We assumed that varying levels of invasiveness among Impatiens species may be driven by the fact that evolution processes that they undergo after introduction may be far from being parallel. In the present studies, the tested trait was the ability to release from the enemy in populations differing in age. The enemy release hypothesis (ERH) assumes that within their native range alien species are suppressed by natural enemies (such as herbivores or pathogens) and liberation from this limiting factor after introduction may lead to a rapid spread in new areas. It was demonstrated that *I. glandulifera* individuals from younger populations release from enemy more effectively than those from older populations. In the present studies we checked this assumption regarding *I. balfourii*. We also tested if occurrence of along roadsides, that is, the preferred habitat of *I. balfourii*, may be connected with lower pressure of enemies there. We demonstrated that at the same time this habitat may in fact be a trap for the species because of very frequent mowing of roadsides. We demonstrated that although *I. balfourii* releases from its enemies in a similar way as *I. glandulifera*, it is still a poor disperser. Thus, we assume that maladaptive habitat preferences may significantly decrease the invasion success of this species.
This work was supported by the National Science Centre in Poland under Grant number 2018/02/X/NZ9/00165.

Keywords: Biological invasions, post-introduction evolution, pests, polinators, seed pathogens

Poster number in the exhibition corridor: P39

A dense linkage map for the hybridising toads, *Bombina bombina* and *B. variegata*

Beate Nürnberger, Stuart J.E. Baird, Anna Bryjová, Dagmar Čížková,
Mark L. Blaxter, Jacek M. Szymura

Jagiellonian University, Kraków, Poland

The two European fire-bellied toads diverged about three million years ago. Yet, to this day, they produce abundant fertile hybrids wherever their distribution ranges adjoin. In typically narrow hybrid zones, recombination not only breaks up two diverged genomes but also mixes two distinct ecological strategies: *B. bombina* typically reproduces in lowland ponds whereas *B. variegata* is an upland puddle breeder. We have developed a dense linkage map for a genomic dissection of the evolutionary forces that shape the *Bombina* hybrid zone and in order to map the sex determining region. From a draft assembly of a *B. variegata* genome, we designed molecular baits to enrich genomic libraries for 5000 loci. This involved careful filtering of candidate sequences, given the very large (approx. 8 Gb) and repeat-rich *Bombina* genome. We sequenced enriched libraries of two grandparents, the three F1s and 162 F2 offspring from an interspecific cross. To determine the taxon of origin for each haplotype at each marker locus, we devised a likelihood-based inference approach that involves model-based clustering of individuals' unphased diplotypes. For each locus, these clusters correspond to the two homozygotes and the *B. bombina* x *B. variegata* heterozygote expected in the F2 cross. The linkage map was built with LepMap3 and resulted in 12 linkage groups, corresponding to the 12 chromosome in the *Bombina* genome. It comprises about 4800 markers. The sex of late-stage F2 tadpoles was determined from histological sections. Sex-specific segregation distortion identifies several candidates for the sex determining region. These will be subject to further analysis. Currently, we are analysing sequence results from several hundred natural hybrids from Romania and Poland.

Keywords: linkage map, hybrid zone, *Bombina*

Poster number in the exhibition corridor: P12

Role of yeast Q and NQ cells balance in starvation survival

Monika Opałek, Katarzyna Tomala, Donna K. McCullough, Dominika Włoch-Salamon

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

In stationary phase of haploid yeast populations, two cells fractions can be distinguished. Representing 70-80 percent of population, spore-like quiescent (Q) cells are derived from virgin yeast cells after first signals of nutrient exhaustion. Q cells are stress resistant and prepared for long-term survival. In contrary, heterogeneous fraction of nonresistant to stress nonquiescent (NQ) cells is composed of cells stopped in various stages of mitotic cell cycle, without common phenotype. Presence of both cells types (Q and NQ) in mature laboratory yeast strains populations can be viewed as (i) beneficial for overall populations survival (e.g. dead NQ cells can serve as nutrients source for Q cells), or (ii) with no particular influence on population survival, but rather as a byproduct of yeast physiology. The importance of Q/NQ cells balance for populations long-term starvation survival was tested experimentally. Populations composed of both Q and NQ cells in various proportions (number of Q cells: number of NQ cells, 3:1; 1:1 and 1:3) and monocultures (Q, NQ) were exposed to long-terms starvation for 13 weeks. Each week, fractions from starved populations were re-grown in complete medium (YPD). Proportions of Qs and NQs descendants and populations survival rate (as a percentage of cells that re-entered mitotic cell cycle) were calculated based on OD and fluorescence measurements. The results confirmed that Q cells are more resistant to stress factors and they are prepared for longterm starvation. By 9th week, in populations with initial proportions 1:1 and 3:1 Q:NQ cells, the fraction of Qs descendants, after regrowth, was nearly twice higher than initially. However, the presence of NQ cells seems to have neither positive nor negative effect on Q cells survival rate. All populations, regardless NQ cells proportion, parallelly decreased their survival rate in time, reaching ca 1 percent by 9th week. The results do not support hypothesis about adaptive importance of non-quiescent cells during survival during starvation.

Keywords: quiescence, *Saccharomyces cerevisiae*, starvation

Poster number in the exhibition corridor: P28

Interpreting palaeohabitats of the Eocene amber forests on Fulgoroid planthoppers (Hemiptera: Achilidae) and biting midges (Diptera: Ceratopogonidae)

Agata Pielowska, Alicja Brysz, Jacek Szwedo

University of Gdansk, Faculty of Biology, Department of Invertebrate Zoology and Parasitology,
Laboratory of Evolutionary Entomology and Museum of Amber Inclusions,
Gdańsk, Poland

Amber forests of the Eocene were diverse through time and space. Paris Basin amber of Oise, Cambay amber of India, Fushun amber of China, and the best known Baltic amber of Europe present wide spectre of palaeohabitat and palaeoenvironments. Fossil materials are very often scarce, equally often not complete, and unfortunately do not compose a full picture accessible to researchers working on recent taxa. There are always missing pieces, and commonly there is more information missing than the data we have. To counter this situation many paleontologists seek ways to transfer data between different groups, hoping to mask those missing pieces. While making such links between closely related e.g. families is rather obvious and does not possess great amount of risks such attempts between more distant taxa is more risky. Yet sometimes all of those closely related groups have more missing data than known one and any links are inpssible to make. Therefore comparisons between less close taxa may sometimes be necessary. This study is an attempt to make such link between two families: a Fulgoroid planthoppers (Hemiptera) Achilidae and Nematoceran flies (Diptera) Ceratopogonidae families. Both families have fossil representatives of many lower-level taxa (subfamily- and tribe-level) present in a wide spectrum of fossil sources: both families are present in Lower Cretaceous and Eocene ambers and sedimentary rocks, with Ceratopogonidae present also in Upper Cretaceous ambers and Oligocene sedimentary rocks.

Keywords: Achilidae, amber, Ceratopogonidae, Eocene, feeding

Poster number in the exhibition corridor: P19

The role of major histocompatibility complex in urbanization process of birds

Ewa Pikus, Piotr Jedlikowski, Piotr Minias

University of Łódź, Łódź, Poland

The Major Histocompatibility Complex (MHC) class I and II molecules play an important role in the adaptive immunity of vertebrates, as they initiate an immune response against intracellular and extracellular pathogens, respectively. The large diversity of MHC allelic variants within individuals and within populations increases the chance for effective defense against a wide spectrum of pathogens. The aim of the study was to determine whether urbanization processes in a common waterbird species, the common coot *Fulica atra*, are associated with changes in the allelic composition and diversity of MHC class II genes. For this purpose, birds from four populations were examined, two of which were urban (Warsaw - an old urban population, Lodz, a new urban population), and two rural (Sarnow and Zeromin).There was strong divergence at the MHC between the old urban population and both the new urban population and two rural populations. There was also moderate, but significant divergence at the MHC between the new urban population and two rural populations, while no divergence was found between the populations from nonurban landscape. The total number of MHC alleles, as well as the number of alleles per individual, was significantly lower in the old urban population as compared to the new urban population and the populations from non-urban areas. However, no differences in MHC diversity were found between the new urban population and both rural populations. At the same time, the analysis of microsatellite loci provided no support for neutral genetic divergence between populations. This suggests that the processes of urban colonization by wildlife may require adaptive changes in MHC gene pool as a response to the pathogen and parasite faunas characteristic for urbanized areas.

Keywords: major histocompatibility complex, immune system, urbanization

Poster number in the exhibition corridor: P46

Genetic variation of selected *Loxospora* species

Łucja Ptach, Beata Guzow-Krzemińska

Department of Plant Taxonomy and Nature Conservation, Faculty of Biology,
University of Gdańsk, Poland

Lichens represent symbiotic relationship between fungi and algae or cyanobacteria. In the genus *Loxospora* A. Massal. mycobionts belong to Ascomycota and associate with unicellular chlorococcoid photobionts. The goal of this study was to examine genetic variation of mycobionts of three species: *Loxospora cismonica L. elatina* and *L. ochrophaea*. To understand their genetic variation, haplotype networks for each species were created. Specimens of *Loxospora* were provided by The New Yourk Botanical Garden Herbarium and University of Gdańsk. Analyses were based on ITS rDNA and mtSSU rDNA markers. The BLAST search was used to compare the new sequences to those available in the GeneBank. The sequences identified as *Loxospora* were used in further analyses. Moreover, additional sequences of *Loxospora* spp. available in GenBank were also downloaded. Based on haplotype networks of ITS rDNA 3 haplotypes were identified for *L. cismonica*, 5 haplotypes for *L. elatina* and 7 haplotypes for *L. ochrophaea*. In case of mtSSU rDNA marker, 2 haplotypes were identified for *L. elatina* and *L. ochrophaea*. Moreover, *L. elatina* and *L. ochrophaea* shared the same haplotypes in both markers. Phylogenetic analysis confirmed uncertain species delimitation within those two species.

Keywords: ITS rDNA, *Loxospora*, mtSSU rDNA, lichens, genetic variation

Poster number in the exhibition corridor: P15

Morphometric and genetic analysis of skeletal elements in mouse

Wioleta Rasmus, Diethard Tautz

Max Planck Institute for Evolutionary Biology, Germany

The house mouse is a perfect model system for genetic and evolutionary studies, with its skeletal elements being used to explore the concept of morphological integration. Morphological integration is a tendency of covariation between characters, resulting from similar developmental patterns. Typically, it is present in homologous body parts, such as vertebrates' front and hind limbs. The research recently conducted at our department have pinpointed genes, which are associated with covariation between pairs of homologous bones of front and hind limb, such as humerus and femur, ulna and tibia. Furthermore, they have proved the polygenic nature of length of these bones. Evolution of such traits - which do not follow simple Mendelian inheritance is still not well understood, therefore I aim to explore it during my PhD studies. Our research team have launched parallel selection experiment in which fourteen separate lines of house mouse (*Mus musculus domesticus*) will be bred for 5 generations in order to distort the integration between homologous bones: ulna and tibia. We use isoflurane anesthesia to restrain the mice and x-ray cabinet to obtain digital roentgen images, as methods to obtain the phenotype data – length ratio between these bones in live animals, on which the selective pressure will be implied. Furthermore, the mice will be scanned using micro-tomography, which provides high quality 3-dimensional models of other skeletal elements, importantly, it will allow to detect any morphological changes which may be the effect of selection on correlated traits. One of the main part of the experiment, is going to be genome-wide association mapping of involved animals, which will bring understanding of genetic basis of evolution of novel morphological characteristics.

Keywords: morphometrics, GWAS, zoology, genetics, mouse

Poster number in the exhibition corridor: P44

Embryology of cetaceans and their evolution - case of whale embryogenesis

Edwin Sieredziński

Independent researcher

Whale embryones and foeti are very rare specimens, therefore state of knowledge about prenatal development of cetaceans (and other marine mammals) is very low. Interpretation in evolutionary and phylogenetic terms becomes impede – many authors have completely dissonant opinions, for example about Mysticeti embryonal dentition character (Eschricht 1846, Eschricht 1849, Kükenthal 1891, Kükenthal 1893). Endeavour of synthesis embryological and palaeontological data is seldom (e. g. Yamato & Pyennson 2015), although such approach was applied in another mammals groups (for examples, monotremes, Watson (1916)). Embryological data could help in a number of cetacean evolution issues – as dentition reduction in sperm whales, lack of dentition in baleen whales and beaked whales, evolution of the skull of baleen whales, development of hind limbs. Work hypotheses could be formulated on basis of paleontological data, it would be argumentation a rebours, most often praxis in embryological and paleontological data synthesis is opposite. Moreover, such material as whale foeti and/or embryones is very rare. These specimens can be not denoted to particular species, for example, whale embryo from Jedrzejow, (Świetokrzyskie Voivodeship, Poland). Therefore additional obstacles, linked to taxonomy, may appear. According to unidentified foeti and embryones, they can belong to various groups of cetaceans because stage of knowledge is so harsh in this area. Embryological data can be useful in cetacean evolution research, but these animals are heavily modified – thus these date should be synthesised with another from different sources (as above-mentioned, fossils). Congruence issue would be occurred. Nowadays, molecular techniques enable to identify embryones and foeti to particular species (for example, based on mtDNA), moreover, CT tomography and 3D printing allow search of hard tissues. Cetacean (and other marine mammal) embryology can be non invasive in morphological level. These data can useful from evolutionary synthetic approach to search cetacean evolution.

Keywords: cetaceans, embryology, congruence issue, synthesis of embryological and palaeontological data

Poster number in the exhibition corridor: P42

Why are baleen whales so huge?
Big sizes of some filter feeders or Neogene global geotectonic changes?

Edwin Sieredziński

Independent researcher

Baleen whales have been the biggest animals ever living on Earth. Their gigantism is sparsely explained by ecologists and palaeontologists, enormous sizes were linked to increase of oceans productivity during Neogene and Pleistocene (Slater et al. 2017). Moreover, these conclusions do not include another factors e. g. rather huge size of filter feeders and many geotectonic changes in the end of Tertiary period. During hitherto history of animal kingdom filter feeders were often biggest animals in marine ecosystems. This trend has pertained to anomalocarids, Cetiocaridae family (Vinther et al. 2014), pachycormid fish *Leedsichthys* (Bardet et al. 1993, Friedman et al. 2010, Liston 2010) and contemporary sharks *Rhincodon typus* and *Cetorhinus maximus* (Knickle et al. 2018). Filter feeders could have achieved huge size because of few factors – pressure of predation and ecosystem productivity and capacity. First mentioned determinant is linked to occurring big marine predators as sharks *Carcharodon* or sperm whales *Livyatan* and *Zygmophyseter* – escape in giant size would be answer for these predators pressure. However it should be less significant than increase of sea waters productivity (regarding Slater et al. 2017). Important factor is also body structure and physiology – baleen whales are bigger than sharks and *Leedsichthys*. Next reason has consisted in geotectonic changes on Earth from Miocene to today. Nowadays epicontinental seas are not met (beside Baltic Sea and Hudson Bay), also continental glaciers developed in polar regions. This changes brought about increase of productivity of sea waters, upwelling zones were also appeared due to changes in oceanic circulation. Thus baleen whales (especially rorquals) achieved huge sizes in Pliocene, for example *Balaenoptera sibbaldina* with comparable size to recent blue whale (Demere et al. 2005). Giant sizes of baleen whales are derivative of global changes in marine ecosystems. But it is part of broader issue – gigantism of some filter feeders.

Keywords: gigantism, baleen whales, filter feeders, determinants of body size

Poster number in the exhibition corridor: P43

Priority effects and seasonal time constraints jointly shape competition in larval damselflies

Szymon Sniegula, Mateusz Raczyński, Frank Johansson, Robby Stoks

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

Climate change might affect competition between organisms through temperature-induced changes in hatching and emergence dates. Advanced hatching modifies priority effects, where advanced organisms may take competitive advantage in gaining resources over no advanced ones through, for example, a larger size. Furthermore, organisms competition might be mediated by the length of the growth season. Indeed, time constrained individuals often accelerate development and growth rates in the presence of predation risk. In a common-garden rearing experiment in the laboratory, we tested the effects of intraspecific competition and hatching dates on larval development, growth and survival rates in more (high latitude) and less (central latitude) seasonally time constrained populations of the damselfly *Lestes sponsa*. By manipulating hatching dates, we created two size groups of larvae per latitude: advanced hatched large and non-advanced hatched small larvae. We reared the larvae from these groups in non-mixed and mixed groups, and this at native and non-native temperatures/photoperiods, indicating different degrees of seasonal time constraints. In non-mixed groups, high-latitude larvae emerged earlier and grew faster than central-latitude larvae, but only at native temperatures/photoperiods, supporting adaptive adjustment of larval development and growth rates to seasonal time constraints. At native temperatures/photoperiods, advanced central-latitude larvae reared in mixed groups emerged earlier and grew faster than those reared in non-mixed groups. This suggests that advanced hatched larvae gained more resources when competing with non-advanced ones, but only when time for development/growth was not strongly limited. Advanced larvae reared in mixed groups had the highest survival rate, indicating that advanced individuals put cannibalistic pressure on non-advanced ones. The results suggest that a shift in the relative timing of hatching can cause temperature-dependent priority effects, mediated through cannibalism, growth and development, which may change the population dynamics of important intermediate predators in food webs. This research was funded by National Science Centre, Poland, grant 2017/25/B/NZ8/01852.

Keywords: climate change, phenology, competition, cannibalism, seasonal time constraint

Poster number in the exhibition corridor: P41

Hemiptera tree, Hemiptera on the Tree (of Life)

Jacek Szwedo

Laboratory of Evolutionary Entomology and Museum of Amber Inclusions,
Department of Invertebrate Zoology and Parasitology,
Faculty of Biology, University of Gdańsk

Hemiptera is the fifth larger insects order on terms of species taxic diversity, and the most diversified regarding morphological disparity reflected in over 300 currently recognised families extant and extinct. Their fossil record could be traced back to the Carboniferous, with molecular calibrations suggesting older, Devonian period as time of origination. The group was established by Linnaeus, but since these time its concept and content changed many times. Currently, the order is divided into six suborders: Paleorrhyncha (extinct), Sternorrhyncha, Fulgoromorpha, Cicadomorpha, Coleorrhyncha and Heteroptera. The first classification and relationships proposals had been proposed in the 19 th century. The development of palaeoentomology, and data brought by these investigations shaped the first relationships trees presented in the beginning of 20th century. Also cladistic methodology approach enabled to propose some new interpretations of classification and relationships of the Hemiptera. End of 20th century brought molecular earthquake of newly available data, which reshaped the evolutionary and classification proposals for the Hemiptera. Development of these techniques and accumulation of palaeontological data, together with new morphological data, in the beginning of 21st century resulted in several new proposals. However, there is still no full consensus. There are several reasons: selection and sampling of taxa, mistakes in identification, wrongly selected or wrongly dated fossils used for calibration of the molecular clock, misinterpretation of morphological structures, unclear homologies, lack of reliable data for certain crown groups, etc. Despite these biases, the general shape of the tree of Hemiptera could be presented, with relationships of most groups more or less solved. The second is the placement of the Hemiptera on the Tree of Life. Here the situation seemed to be more or less stable, but recent findings of fossils and reinterpretations of crucial morphological characters put some new questions on relationships of the Hemiptera with other paraneopteran insects.

Keywords: phylogeny, classification, evolution, insects

Poster number in the exhibition corridor: P18

The effect of rapamycin on the wing beat frequency in aging *Drosophila melanogaster*

Ewa Tatarczyk, Marcin Czarnołęski

Institute of Environmental Science, Jagiellonian University, Kraków, Poland

Rapamycin is an immunosuppressive medicine which binds and regulates activities of Target of Rapamycin (TOR) proteins. It increases lifespan and reduces cell size in vertebrates and invertebrates. We studied fruit flies *Drosophila melanogaster* to examine whether supplementation of larval food with rapamycin maintains flight performance in aging flies. We used 10 isolines of flies, and each isoline was subjected either to control conditions - development in a standard food or to rapamycin treatment - supplementation of larval food with rapamycin. On the 10th and 25th day after wclosion, we measured flight performance (wing beat frequency) under two temperatures combined with two oxygen levels. Following expectations, flies tested in warm and normoxic conditions had higher wing beat frequency than either cold or hypoxic flies. Against predictions, wing beat frequency did not differ between rapamycin and control flies. Instead, we found profound differences between isolines in the wing beat frequency. Our results suggest that access to rapamycin during the larval development does not reduce effects of aging among adult flies, at least at the level of flight performance. We discuss our results in the context of current theories concerning life history evolution and optimal cell size. The study was supported by NSC grant to MCz (OPUS 2016/21/B/NZ8/00303).

Keywords: cell size, performance, flies, ageing, life history

Poster number in the exhibition corridor: P47

Dynamics of epistatic interactions in *Caenorhabditis elegans* under various stressors

Katarzyna Toch, Mateusz Buczek, Marta Labocha

Institute of Environmental Sciences, Jagiellonian University, Kraków, Poland

Epistasis is a peculiar phenomenon which we observe when a single mutation is having different phenotype depending on its genetic background. It is known for having a far-reaching contribution to evolution of sex and recombination, complex traits development, livestock improvement and speciation. What is more interesting, it has been recently acknowledged for its important role in evolution of microbial drug resistance, disease diagnosis and forensic analysis. Studies on epistasis keep uncovering new genes which might be involved in certain genetic pathways and point to the functions of studied genes. However, most such studies are performed in standard laboratory conditions, and change in the environment can drastically affect the epistatic landscape – in new environment new interactions are uncovered and some of the already known interactions are lost from the sight. Using RNA interference method we screened over 6000 gene-gene interactions in *Caenorhabditis elegans* in standard as well as in three different stressful conditions – 37^{o}C heat shock (HS), hydrogen peroxidase (H_2O_2) and methyl-methanesulfonate (MMS) treatment – and calculated their interaction scores (S-scores). We found that in two tested stressful environments – HS and H_2O_2 – epistasis tends to be more suppressing in comparison to standard condition (mean S-score 0.241 and 0.22, respectively). We did not find such clear situation in MMS treatment (mean S-score 0.08). Therefore we did not unambiguously confirm that harsh conditions alleviate effects of deleterious mutations via epistatic interactions. Nevertheless, we propose that observed phenomenon might have an effect on the strength of selection, when organism is facing unfavorable environment.

Keywords: Genetic interactions, epistasis, *Caenorhabditis elegans*

Poster number in the exhibition corridor: P30

Role of amino acid signalling in transition to quiescent state in yeast

Dominika Włoch-Salamon, Monika Opałek, Agnieszka Marek,
Aleksandra Kałdon, Barbara Mickowska

Faculty of Biology, Jagiellonian University, Kraków, Poland

Production of spores, persister and quiescent cells is a strategy that helps microorganism to survive environmental stresses, and restart divisions when conditions improve. About 80% of carbon starved *Saccharomyces cerevisiae* population differentiate into non-dividing quiescent cells (Q), while the rest stays in non-quiescent state (NQ). We applied experimental artificial selection to evolve yeast strains with reversed natural proportions of Q/NQ cells. Whole genome sequencing of the clones isolated from evolved populations revealed frequent mutations in all of the 3 genes (SSY1_PTR3_SSY5) forming amino acid sensing pathway SPS. Analysis of the amino acids content determined by ion-exchange chromatography revealed significant average increase of the total amino acid content of ca 15% in the evolved populations. Our result indicates that disruption in the amino acid signalling prevents transition to quiescence. Constitutive SPS pathway activation, despite nutrient deprived environment resulted in the high proportions of non-quiescent cells, what in consequence leads to increased total amino acid content in yeast cells. Our experiment was relatively simple to perform in the standard laboratory conditions and do not involve any genetic modification of the yeast strain. We noticed increase of all mammalian exogenous amino acids except methionine. We consider that discovered phenomenon is not only possible new explanation for genetic base of transition to quiescent state but might be a good start-up point to develop evolution-based method to obtain yeast enriched in amino acids for the future use for food industry. (please check related posters by Agnieszka Marek and Monika Opałek).

Keywords: amino acid uptake; SPS pathway, non-quiescent cells, nonGMO

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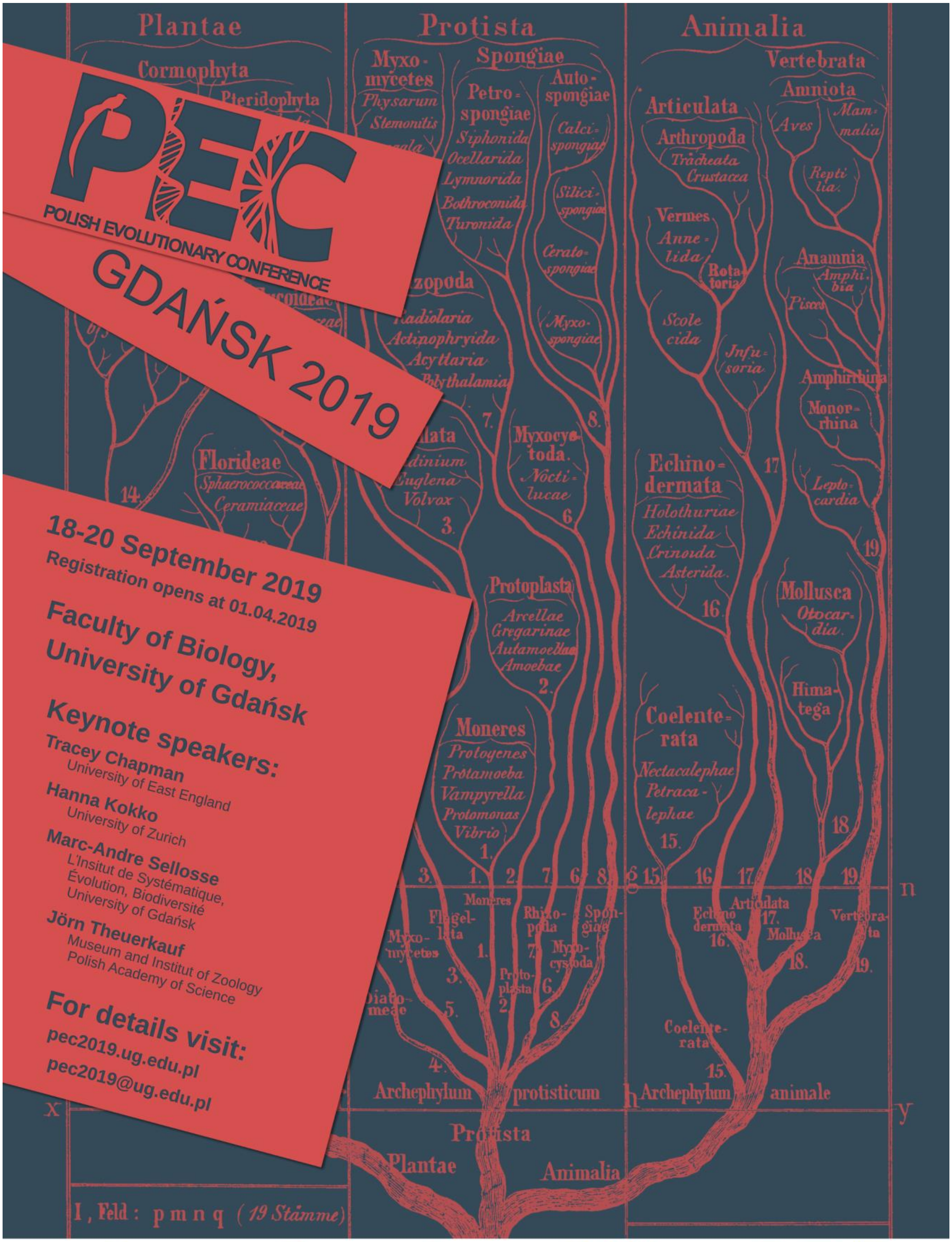
List of 7th PEC participants:

Adamowicz Michał	University of Warsaw	Warszawa	Poland
Araya-Salas Marcelo	Cornell University; Universidad de Costa Rica	New York/San Jose	USA/Costa Rica
Arct Aneta	Uppsala University	Uppsala	Sweden
Argasinski Krzysztof	Institute of Mathematics, Polish Academy of Sciences	Warszawa	Poland
Babik Wiesław	Jagiellonian University	Kraków	Poland
Bańbura Jerzy	University of Łódź	Łódź	Poland
Bańbura Mirosława	University of Łódź	Łódź	Poland
Bauchinger Ulf	Jagiellonian University	Kraków	Poland
Bladowska-Pawlowska Alina	attendee	Geneva	Switzerland
Bonda-Ostaszewska Elżbieta	University in Białystok	Białystok	Poland
Borkowska Anetta	University of Białystok	Białystok	Poland
Brzęk Paweł	University of Białystok	Białystok	Poland
Buczyńska Sylwia	University of Białystok	Białystok	Poland
Cendrowska Martyna	University of Gdańsk	Gdańsk	Poland
Chapman Tracey	University of East Anglia	Norwich	UK
Chmielewski Sebastian	Adam Mickiewicz University	Poznań	Poland
Cichoń Mariusz	Jagiellonian University	Kraków	Poland
Convey Peter	British Antarctic Survey	Cambridge	UK
Corsini Michela	University of Warsaw	Warszawa	Poland
Czajkowska Magdalena	University of Białystok	Białystok	Poland
Czyżewska Iwona	University of Łódź	Łódź	Poland
Devogel Marion	University of Gdańsk	Gdańsk	Poland
Di Lecce Irene	Centre of New Technologies, University of Warsaw	Warszawa	Poland
Domański Jakub	University of Gdańsk	Gdańsk	Poland
Drzewińska-Chańko Joanna	University of Łódź	Łódź	Poland
Dubiec Anna	Museum and Institute of Zoology, Polish Academy of Sciences	Warszawa	Poland
Działo Maciej	Jagiellonian University	Kraków	Poland
Fröhlich Arkadiusz	University of Agriculture	Kraków	Poland

Gagat Przemyslaw	University of Wrocław	Wrocław	Poland
Glądalski Michał	University of Łódź	Łódź	Poland
Goczał Jakub	University of Agriculture	Kraków	Poland
Grissot Antoine	University of Gdańsk	Gdańsk	Poland
Grzesiuk-Bieniek Małgorzata	Warsaw University of Life Sciences	Warszawa	Poland
Gudowska Agnieszka	Jagiellonian University	Kraków	Poland
Gumińska Natalia	Biochemical Research Centre, University of Warsaw	Warszawa	Poland
Guzow-Krzemińska Beata	University of Gdańsk	Gdańsk	Poland
Herdegen-Radwan Magdalena	Adam Mickiewicz University	Poznań	Poland
Ibañez Alejandro	Jagiellonian University	Kraków	Poland
Jadach Weronika	Nicolaus Copernicus University	Toruń	Poland
Janas Katarzyna	Jagiellonian University	Kraków	Poland
Jankowska-Jarek Martyna	University of Gdańsk	Gdańsk	Poland
Kaczanowski Szymon	Institute of Biochemistry and Biophysics, Polish Academy of Science	Warszawa	Poland
Kaliński Adam	University of Łódź	Łódź	Poland
Kania Wojciech	Museum and Institute of Zoology, Polish Academy of Sciences	Gdańsk	Poland
Kidawa Dorota	University of Gdańsk	Gdańsk	Poland
Kilikowska Adrianna	University of Gdańsk	Gdańsk	Poland
Klim Joanna	Institute of Biochemistry and Biophysics, Polish Academy of Sciences	Warszawa	Poland
Kokko Hanna	University of Zurich	Zurich	Switzerland
Komorowska Michalina	Biochemical Research Centre, University of Warsaw	Warszawa	Poland
Korybut-Orłowska Joanna	University of Gdańsk	Gdańsk	Poland
Kosecka Magdalena	University of Gdańsk	Gdańsk	Poland
Kovalov Viktor	Jagiellonian University	Kraków	Poland
Kowalczewska Anna	Nicolaus Copernicus University	Toruń	Poland
Kozłowski Jan	Jagiellonian University	Kraków	Poland
Książek Aneta	University of Białystok	Białystok	Poland
Kukwa Martin	University of Gdańsk	Gdańsk	Poland
Kułaga Kinga	Adam Mickiewicz University	Poznań	Poland

Lagisz Małgorzata	University of New South Wales	Sydney	Australia
Laska Alicja	Adam Mickiewicz University	Poznań	Poland
Lipińska Monika	University of Gdańsk	Gdańsk	Poland
Lipowska Małgorzata M.	Jagiellonian University	Kraków	Poland
Łabiszak Bartosz	Adam Mickiewicz University	Poznań	Poland
Łukasiewicz Aleksandra	Adam Mickiewicz University	Poznań	Poland
Łukasik Piotr	Jagiellonian University	Kraków	Poland
Marek Agnieszka	Jagiellonian University	Kraków	Poland
Markowski Marcin	University of Łódź	Łódź	Poland
May Michał	University of Gdańsk	Gdańsk	Poland
Minasiewicz Julita	University of Gdańsk	Gdańsk	Poland
Minias Piotr	University of Łódź	Łódź	Poland
Mioduchowska Monika	University of Gdańsk	Gdańsk	Poland
Moura Andre	University of Lincoln	Lincoln	UK
Najberek Kamil	Institute of Nature Conservation, Polish Academy of Sciences	Kraków	Poland
Opałek Monika	Jagiellonian University	Kraków	Poland
Parrett Jonathan	Adam Mickiewicz University; Queen Mary University of London	Poznań/London	Poland/UK
Pawelec Alicja	University of Warsaw	Warszawa	Poland
Pawlowski Jan	University of Geneva	Geneva	Switzerland
Pawłowski Bogusław	University of Wrocław	Wrocław	Poland
Pielowska Agata	University of Gdańsk	Gdańsk	Poland
Pietluch Filip	University of Wrocław	Wrocław	Poland
Pikus Ewa	University of Łódź	Łódź	Poland
Pilot Małgorzata	Museum and Institute of Zoology, Polish Academy of Sciences	Warszawa	Poland
Pinszke Agata	University of Gdańsk	Gdańsk	Poland
Plesnar-Bielak Agata	Jagiellonian University	Kraków	Poland
Prokop Zofia	Jagiellonian University	Kraków	Poland
Ptach Łucja	University of Gdańsk	Gdańsk	Poland

Radwan Jacek	Adam Mickiewicz University	Poznań	Poland
Rasmus Wioleta	Max Planck Institute for Evolutionary Biology	Ploen	Germany
Redlisiak Michał	University of Gdańsk	Gdańsk	Poland
Remisiewicz Magdelena	University of Gdańsk	Gdańsk	Poland
Sadowska Edyta	Jagiellonian University	Kraków	Poland
Selosse Marc-Andre	L'Insitut de Systématique, Évolution, Biodiversité; University of Gdańsk	Sorbonne/Gdańsk	France/Poland
Sidorczuk Katarzyna	University of Wrocław	Wrocław	Poland
Sieredziński Edwin	Independent researcher		Poland
Skwarska Joanna	University of Łódź	Łódź	Poland
Sniegula Szymon	Institute of Nature Conservation, Polish Academy of Sciences	Kraków	Poland
Spalik Krzysztof	University of Warsaw	Warszawa	Poland
Sudyka Joanna	Centre of New Technologies, University of Warsaw	Warszawa	Poland
Szulkin Marta	Centre of New Technologies, University of Warsaw	Warszawa	Poland
Szwedo Jacek	University of Gdańsk	Gdańsk	Poland
Szymura Jacek M.	Jagiellonian University	Kraków	Poland
Tatarczyk Ewa	Jagiellonian University	Kraków	Poland
Taylor Jan R.E.	University of Białystok	Białystok	Poland
Thereuekauf Jorn	Museum and Institute of Zoology, Polish Academy of Sciences	Warszawa	Poland
Toch Katarzyna	Jagiellonian University	Kraków	Poland
Vong Alexandre	Independent researcher		France
Wawrzyniak Jarosław	University of Łódź	Łódź	Poland
Wesławski Marcin	Institut of Oceanology, Polish Academy of Science	Sopot	Poland
Wojciechowski Michał	Nicolaus Copernicus University	Toruń	Poland
Wojczulanis-Jakubas Katarzyna	University of Gdańsk	Gdańsk	Poland
Wójcik Jan M.	Institut of Mammals Biology, Polish Academy of Science	Białowieża	Poland
Zaborowska Julia	Adam Mickiewicz University	Poznań	Poland
Zdrojewska Karolina	University of Gdańsk	Gdańsk	Poland
Zwolak Rafał	Adam Mickiewicz University	Poznań	Poland



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University of Gdańsk

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