

THE CZECH ACADEMY OF SCIENCES

INSTITUTE OF VERTEBRATE BIOLOGY



BIENNIAL REPORT

2015–2016

BRNO 2017

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INSTITUTE OF VERTEBRATE
BIOLOGY

THE CZECH ACADEMY OF SCIENCES

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A periodical continuation of the Institute's previous bulletins: *Vertebratologické Zprávy* (1969–1987), *Zprávy ÚSEB* (1988–1991) and the ILE Biennial Report (1993–1994).

Edited by Josef Bryja, Alena Fornůsková, Jan Zima, Hana Slabáková, and Marcel Honza

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Front cover: Smooth newt, *Lissotriton vulgaris*, as a model system for behavioural thermoregulation research in ectothermic vertebrates. (Photo by L. Gvoždík)

Back cover: a) Aerial respirometry system for measuring energy metabolism in small vertebrates. (Photo by L. Gvoždík)

b) Water temperature measurements over an aquatic thermal gradient, photographed using a thermal imaging camera. (Photo by L. Gvoždík)

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PREFACE

Dear reader,

You have just opened the Biennial report, which is traditionally published every other year by the Institute of Vertebrate Biology (IVB). The purpose of this report is to provide information on the scientific results published by the Institute's staff between 2015 and 2016 and important events that occurred over that time, both in a style that is accessible to the interested layperson.

I believe that the information contained in this report will be of interest not only to our co-workers but also to colleagues from other institutions and to the general public. What is more, it should also stimulate our potential new students and post-doctoral researchers in deciding where to direct their professional career. Finally, I believe that the information provided in this and previous reports on the development of the Institute and the milestones that have influenced the direction of the Institute over time could prove an inspiring and useful resource to writers and contributors.

At the IVB, we focus on groundbreaking research in fields such as evolutionary biology, biodiversity and medical zoology. These research activities are primarily of a fundamental nature and focus on observation and experiment in order to gain a better understanding of the processes that affect the fascinating world of the animal kingdom. Such studies have produced around 110 scientific publications per year in peer-reviewed journals. Also of note is the growing number of

achievements of a more applied character. It is my wish here to express a vote of heartfelt thanks to all the research teams for their excellent results over the past two years. In addition to our scientific output, I am also pleased to announce the successful completion of our new state-of-the-art breeding facility in 2016, which we now plan to open in summer 2017.

Probably the most significant event for the IVB over the past two years was the international evaluation of the Institute for 2010-2014. I am happy to say that the Institute was evaluated very positively, which is reflected in an increase in the Institute budget of cca 10% for 2017. Of course, these funds are never enough to cover all our expenses, especially when it comes to funding research projects. As ever, thanks must go to all our scientists who proved highly competitive and successful in obtaining research grants. These grants contributed significantly to the IVB budget, representing an additional 45.8 and 49.7 million CZK in 2015 and 2016, respectively.

Finally, I would like to express once again what a personal pleasure it has been to work at the IVB. I always feel that the pleasant and constructive atmosphere that is so typical at our Institute is one of the primary prerequisites for our ongoing success and will allow us to reach even greater heights over the coming years.

Dear reader, I wish you pleasant reading.

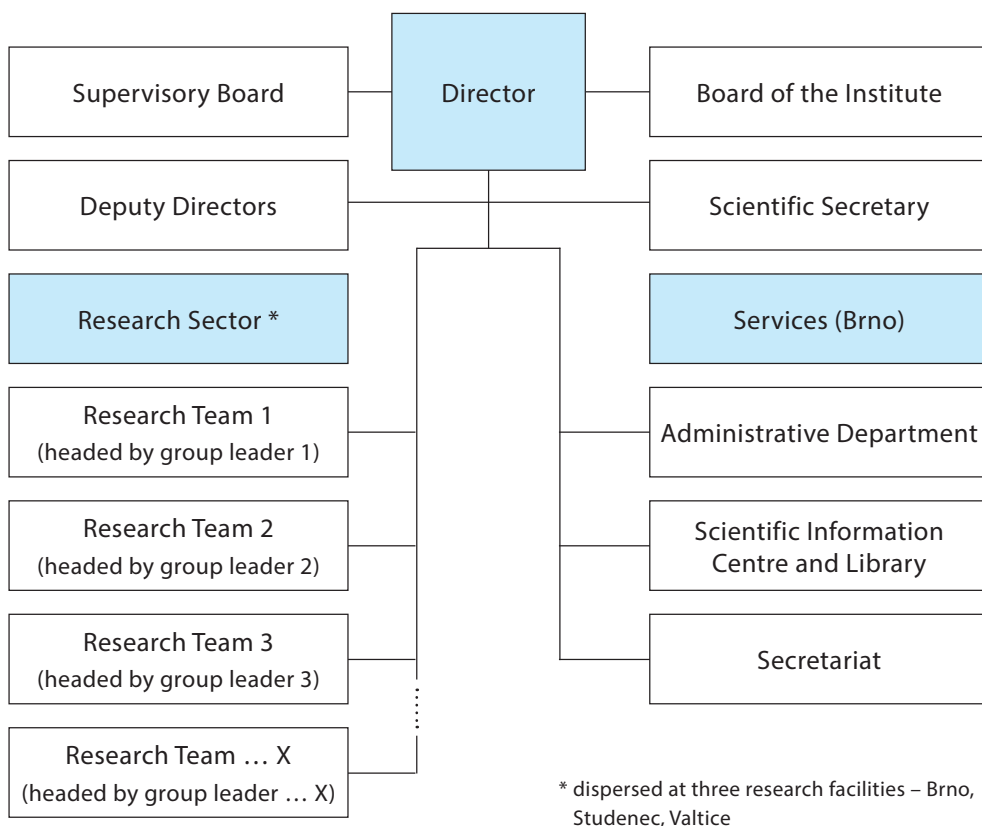
A handwritten signature in black ink, appearing to read 'M. Honza'.

Marcel Honza
Director of the Institute of Vertebrate Biology

April, 2017

1. BASIC FACTS

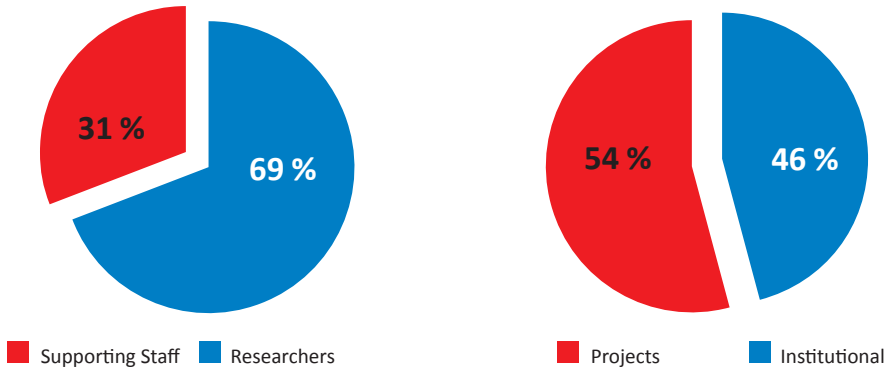
| STRUCTURE OF THE INSTITUTE OF VERTEBRATE BIOLOGY OF THE CAS



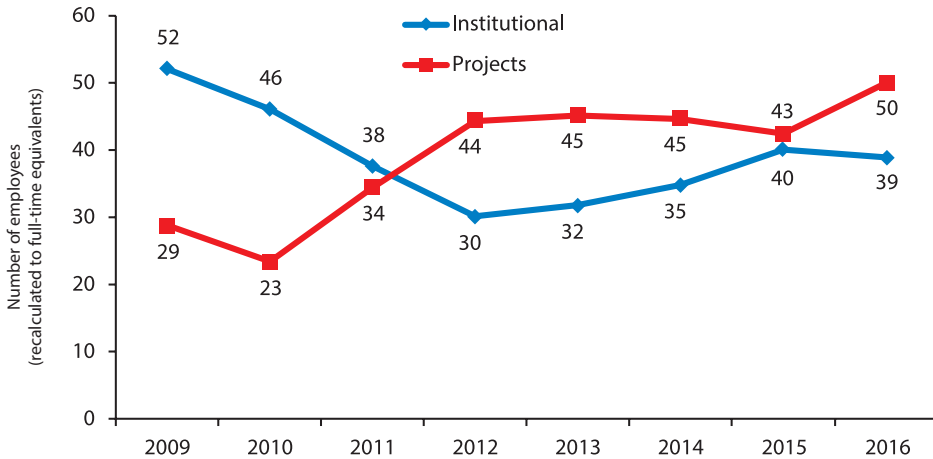
The Institute of Vertebrate Biology (IVB) is a relatively small institute (ca 22-25 permanent researchers) of the Czech Academy of Sciences and, as such, is not structured to separate research departments. Senior researchers are usually the principal investigators of national and international projects and are responsible for creating and maintaining their teams, predominantly from external funds. Principal investigators (group leaders) of projects are directly subordinated to the Director. Research teams are very flexible and are composed of junior researchers, post-doctorates, research assistants, technicians and pre- and post-graduate students (most paid from project grants). Research subjects can be divided into three main domains: evolutionary ecology, biodiversity, and pathogens and diseases (see below). Individual projects, however, can cover more topics and researchers often use interdisciplinary approaches.

| STAFF AND BUDGET

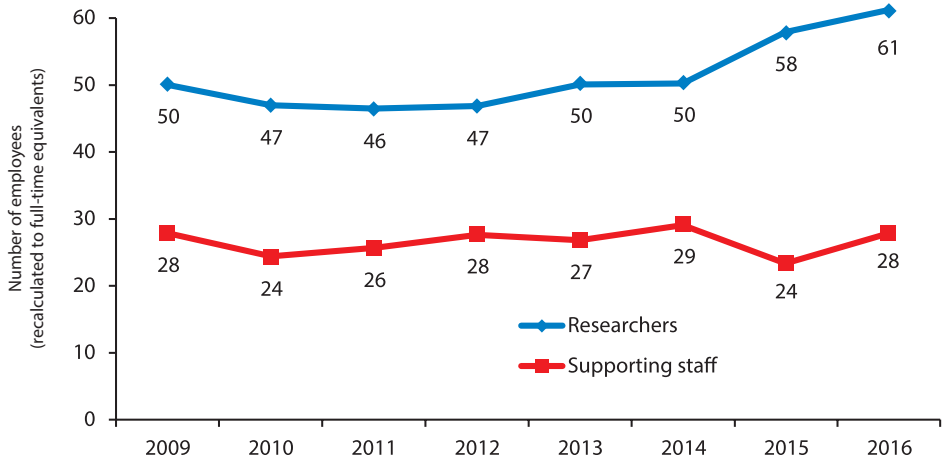
While the IVB is relatively small based on number of employees and budget, it is important as regards scientific output and other activities. Eighty-two people were employed in 2015, a number that rose to 89 in 2016 (full-time equivalents). Staff structure was similar in both years. While a significantly decreasing trend in the number of institutional employees was stopped, the number of people (mainly post-doctorate students, PhD students and technicians) employed on the basis of (unpredictable) external project funding rose to 54%.



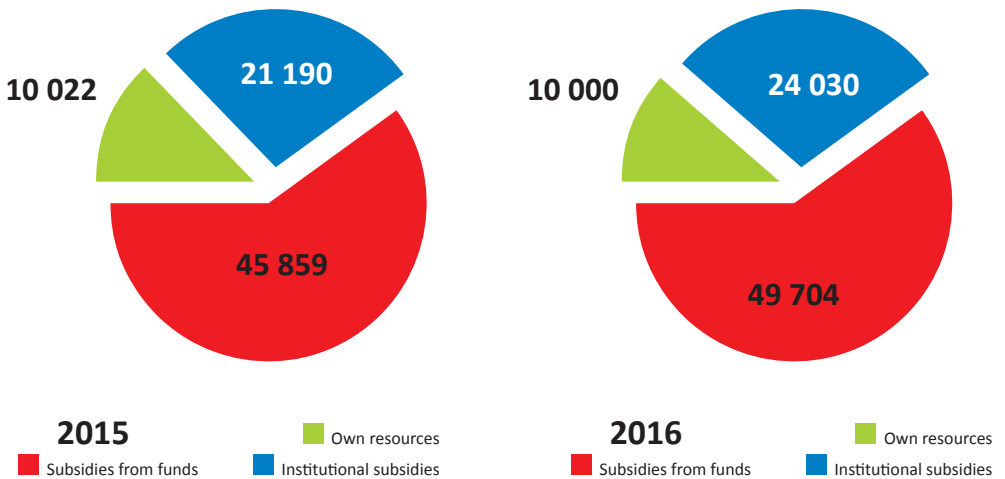
Staff structure of the IVB between 2015 and 2016 (mean values for both years recalculated to full-time jobs).



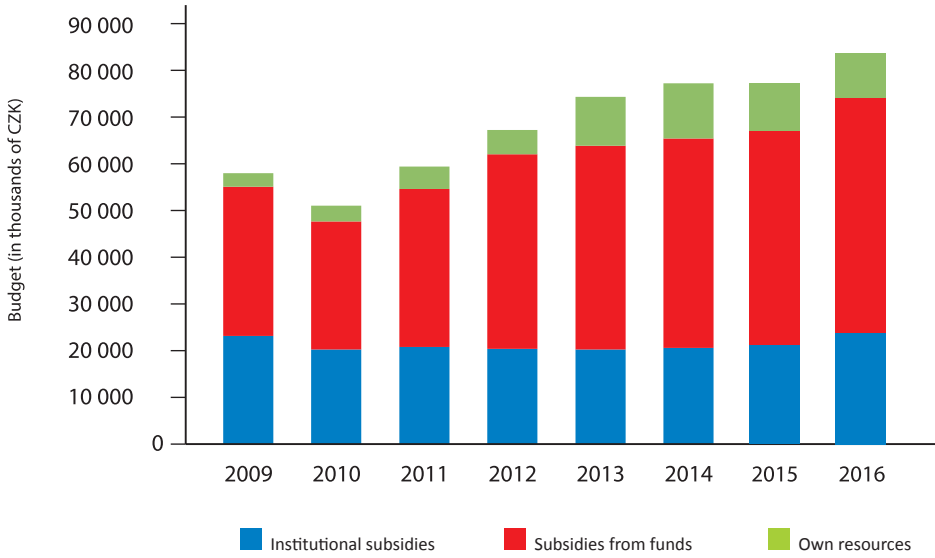
Number of employees has been relatively stable over the last eight years. Thanks to our success in grant competitions, the highest number of people in the Institute’s history were paid from projects in 2016. Despite institutional support improving slightly in 2015-2016, the high proportion of employees dependent on short-term projects may have consequences for long-term planning of research priorities due to the unpredictability of project money.



The number of researchers increased over 2015-2016, owing especially to increased subsidies from funds (i.e. from project competitions).



Budget structure of the IVB over 2015-2016. Numbers are in thousands of Czech crowns.



The total budget of the IVB has been increasing slightly, partly due to an increase in institutional subsidies in 2016.

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| RESEARCH STAFF

Only people with an employment contract are shown, i.e. not all PhD students are listed (for a complete list of PhD students see below). Numerous fellows contracted on the basis of external grant funding have only part-time jobs (the extent not shown here), often limited to short periods.

BRNO RESEARCH FACILITY

The research facilities in Brno include zoological collections, a breeding facility for experimental fish (including facilities for semi-natural experiments), a basic laboratory for molecular genetics studies, a parasitological and ichthyological laboratory and high-quality equipment for field research. Research teams at Brno use model vertebrate groups to study basic questions in the fields of ecology and evolutionary biology, ethology, applied zoology, parasitology, invasion biology and protection and management of freshwater and terrestrial ecosystems.

The main topics studied include:

- reproductive strategies in fishes and birds;
- adaptation and coevolution between parasites and hosts (e.g. cuckoo vs. passerine birds; bitterling vs. bivalves);
- population biology, ecology and biogeography of annual fishes (e.g. *Nothobranchius*, *Cynolebias*);
- relationship between metazoan parasites and their hosts (fish, birds);
- fish communities and populations of key species in various aquatic habitats;

- invasive species in the aquatic environment;
- migration connectivity and seasonal interaction of long-distance migrants;
- ecology and behaviour of bats, especially during hibernation;
- population genetics and interspecies hybridisation in deer;
- ecology and conservation of carnivores in fragmented landscapes;
- food ecology of herbivorous mammals and their impact on the environment;
- diet and parasites of primates.

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VALTICE RESEARCH FACILITY

The Valtice research facility is well equipped with both state-of-the-art molecular equipment and a modern animal rearing facility that fulfils all safety requirements needed for the handling of laboratory animals. Research is mainly focused on ecology and eco-epidemiology of zoonotic microorganisms, with a main emphasis on emerging and re-emerging pathogens. In particular, research focusses on the role of endotherm vertebrates (hosts to pathogenic agents) and haematophagous arthropods (biological vectors) in the circulation of zoonotic pathogens, along with the natural and socio-economic factors driving emergence of particular infections. The main issues addressed include:

- isolation and identification of novel microorganisms, including human pathogens (microbe hunting);
- ecology of arthropod-borne microorganisms (e.g. West Nile and tick-borne encephalitis flaviviruses, spirochaete *Borrelia burgdorferi*, rickettsiae *Anaplasma phagocytophilum*, the spotted fever group rickettsiae and *Babesia* spp. protozoa);
- implementing the 'one health' concept for studying emerging zoonoses;
- risk of introduction and establishment of new mosquito invasive vectors and mosquito-borne diseases into Central Europe;
- providing expert advice regarding prevention and control of zoonoses (contribution to preventive human and veterinary medicine);
- providing expert opinion on emerging infectious diseases.

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STUDENEC RESEARCH FACILITY

The Studenec research facility is a very dynamic part of the IVB that has evolved significantly over recent years. It houses modern, well equipped molecular-genetic, physiological and microscopic laboratories, a breeding facility for small mammals, birds and amphibians (due to re-open following substantial reconstruction in June 2017) and facilities allowing experimentation under semi-natural conditions. Empirical data from observations, laboratory analysis and experiments (supplemented by simulation modelling) are used to investigate important evolutionary questions, mainly at the population level. Research activities are mostly fundamental but may have applications in biomedicine, species conservation and epidemiology. Examples of research topics (model organisms given in parentheses) include:

- hybrid zones as barriers against gene flow and their role in speciation (rodents, amphibians);
- phylogeography, reconstruction of historical colonisation and mechanisms of biodiversity evolution (mainly African rodents and amphibians);
- study of factors affecting population structure, conservation genetics (fish, birds, rodents, carnivores);
- mating systems, analysis of reproductive success and factors affecting fitness (passerine birds);
- immunogenetics, links between adaptive genetic variation and fitness (rodents, passerine birds);
- host-parasite co-evolution, genetic variation in pathogens and their hosts (rodents, bats, pathogenic fungi, helminths, RNA-viruses);
- mechanisms and evolution of thermal physiology traits in ectotherms (newts);
- functional approaches in the study of morphological adaptation (amphibians and reptiles).

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Lucie LABSKÁ

2. RESEARCH PROJECTS

Projects supported by the Czech Science Foundation (GA ČR)

- GA506/11/0112** The evolution and life-history consequences of rapid ageing. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Martin Reichard. *Research years:* 2011-2015.
- GAP505/11/1617** Functional determinants of geographical gradients in avian diversity in sub-Saharan Africa. *Recipient:* Charles University in Prague. *Principal Investigator:* David Hořák. *Subrecipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Co-Investigator:* Petr Procházka. *Research years:* 2011-2015.
- GAP505/11/1768** Non-native goby fishes: exploitation of a free niche or a threat to Central European fishes? *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Pavel Jurajda. *Research years:* 2011-2015.
- GAP505/12/G112** ECIP – European Centre of Ichtyoparasitology. *Recipient:* Masaryk University in Brno. *Principal Investigator:* Milan Gelnar. *Subrecipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Co-Investigator:* Pavel Jurajda. *Research years:* 2012-2018.
- GAP505/12/0375** Evolutionary-immunological and ecological aspects of parasitism in hybrid and polyploid cyprinid fish. *Recipient:* Masaryk University in Brno. *Principal Investigator:* Andrea Vetešnicková Šimková. *Subrecipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Co-Investigator:* Lukáš Vetešník. *Research years:* 2012-2016.
- GAP506/12/1064** Bat adaptations to the fungal disease geomycosis. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Natália Martínková. *Research years:* 2012-2015.
- GAP506/12/2404** Host-parasite interaction as an extreme form of parent-offspring conflict. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Marcel Honza. *Research years:* 2012-2016.
- GAP506/12/2472** Post-copulatory sexual selection and the biology of sperm: within population processes and interspecific patterns in passerine birds. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Tomáš Albrecht. *Research years:* 2012-2016.
- GAP505/13/05872S** The effects of non-native species on host-parasite relationships. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Martin Reichard. *Research years:* 2013-2017.
- GAP505/13/06451S** Linking events through the annual cycle: the importance of carry-over effects for the ecology of migratory birds. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Petr Procházka. *Research years:* 2013-2017.
- GAP506/13/12580S** Which mechanisms affect the diversity of clones and their coexistence with sexual species? European loaches of the genus *Cobitis* as a model. *Recipient:* Institute of Animal Physiology and Genetics CAS, v. v. i., Brno. *Principal Investigator:* Karel Janko. *Subrecipient:* Institute of Vertebrate Biology, CAS, v. v. i., Brno. *Principal Co-Investigator:* Karel Halačka. *Research years:* 2013-2017.

- GAP502/14/35009S** Quantifying viral gene capture, and the host's response, during passage across a species barrier: Murine cytomegalovirus in a house mouse hybrid zone. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Joëlle Goüy de Bellocq. *Research years:* 2014-2016.
- GA15-05180S** Genetic diversity and cross-transmissions of strongylid nematodes between African great apes and man. *Recipient:* University of Veterinary and Pharmaceutical Sciences Brno. *Principal Investigator:* David Modrý. *Principal Co-Investigator:* Klára Petrželková. *Subrecipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Research years:* 2015-2017.
- GA15-07140S** Thermal niche: evaluation of current concept in ectothermic vertebrates. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Lumír Gvoždík. *Research years:* 2015-2017.
- GA15-11782S** Biology of ageing: mechanisms and patterns of senescence in free-living birds. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Tomáš Albrecht. *Research years:* 2015-2017.
- GA15-13265S** High resolution genomic analysis of introgression across a species barrier. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Stuart J.E. Baird. *Research years:* 2015-2017.
- GJ15-13415Y** Amphibian species diversification across sky-island and lowland rainforests in a spatial and ecological context: genome-wide and continental transect. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Václav Gvoždík. *Research years:* 2015-2017.
- GA15-20229S** Evolution of rodents and their parasites in open habitats of East Africa. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Josef Bryja. *Research years:* 2015-2017.
- GA16-00291S** Ageing in the wild: from demography to gene expression. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Martin Reichard. *Research years:* 2016-2018.
- GA16-20049S** Hybrid zones: natural laboratories for the study of pathogen emergence. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Joëlle Goüy de Bellocq. *Research years:* 2016-2018.
- GA16-20054S** Advanced studies on West Nile virus infection pathogenesis towards novel therapeutic strategies. *Recipient:* Veterinary Research Institute, CAS. *Principal Investigator:* Daniel Růžek. *Subrecipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Co-Investigator:* Zdeněk Hubálek. *Research years:* 2016-2018.
- GA16-23773S** Phylogeography, selection and mutation rate at genomic level: Inference from mtDNA sequences of the house mouse. *Recipient:* Institute of Animal Physiology and Genetics Czech Academy of Sciences, Brno. *Principal Investigator:* Miloš Macholán. *Subrecipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Co-Investigator:* Jaroslav Piálek. *Research years:* 2016-2018.
- GA16-26714S** Genomic dissection of barriers to gene flow in hybridising fire-bellied toads. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Beate Nürnberger. *Research years:* 2016-2018.

Projects supported by the Technology Agency of the Czech Republic (TA ČR)

TG03010048 Commercialization of results of zoological research – applications for nature conservation. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Jan Zukal. *Research years:* 2016-2018.

Projects supported by the Ministry of Agriculture of the Czech Republic

QJ1510077 Increasing and more efficient production of salmonids in the Czech Republic using their genetic identification. *Recipient:* Mendel University in Brno, *Principal Investigator:* Jan Mareš. *Subrecipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Co-Investigator:* Karel Halačka. *Research years:* 2015-2018.

QJ1620240 Application of “top-down” biomanipulation to reduce eutrophication caused by agriculture in reservoirs. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Karel Halačka. *Research years:* 2016-2018.

Projects supported by the Ministry of Environment of the Czech Republic

CZ.1.02/6.1.00/10.06482 Monitoring and full-area mapping of important European species as a basis of Natura 2000 in Czech Republic. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Karel Halačka. *Research years:* 2012-2015.

MGSII-52 Collection and analysis of available data and literature sources for the decision on Species Action Plan for little owl and ortolan bunting. *Recipient:* Institute of Vertebrate Biology of the Czech Academy of Sciences, Brno. *Principal Investigator:* Martin Šálek. *Research years:* 2015-2016.

MGSII-40 Management plan for Eurasian lynx, grey wolf, and brown bear in the Czech Republic. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Petr Koubek. *Research years:* 2015-2016.

EHP-CZ02-OV-1-029-01-2014 BIOM Mohelský mill Biodiversity education centre. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Josef Bryja. *Research years:* 2015-2016. EEA and Norway Grants. *Managed by:* The Ministry of Finance of the Czech Republic.

Projects supported by the Ministry of Education, Youth and Sport

CZ.1.07/2.3.00/20.0303 Next-generation technologies in evolutionary genetics. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Josef Bryja. *Research years:* 2012-2015.

CZ.1.07/2.3.00/30.0048 Integration of experimental and population biology using novel methods in interdisciplinary research – a route to excellence with young scientists. *Recipient:* Institute of Botany, Czech Academy of Sciences, Brno. *Partner:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Coordinator at IVB:* Martin Reichard. *Research years:* 2012-2015.

International projects

European Union – 7th Framework Programme

EDENext Biology and control of vector-borne diseases in Europe (Coordinated by: Renaud Lanceot, CIRAD-Département Systèmes Biologiques, Campus de Baillarguet, Montpellier, France). *Principal Investigator for the Czech Republic:* Zdeněk Hubálek. *Research years:* 2011–2015.

Bilateral projects (KONTAKT)

KONTAKT USA LH14045 Evolution of sexual ornaments and their information content: a comparative study in isolated populations with divergent signal traits and preferences. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Tomáš Albrecht. *Research years:* 2014–2016. *Managed by:* The Ministry of Education, Youth and Sport of the Czech Republic.

KONTAKT II LH15175 Functional interaction between host gene regulation and the microbiome in the primate gut. *Recipient:* Institute of Vertebrate Biology, Czech Academy of Sciences, Brno. *Principal Investigator:* Klára Petrželková. *Research years:* 2015–2017. *Managed by:* The Ministry of Education, Youth and Sport of the Czech Republic.

Other EU projects

VectorNet European network for sharing data on the geographic distribution of arthropod vectors transmitting human and animal disease agents. *Principal Investigator for the Czech Republic:* Zdeněk Hubálek. *Research years:* 2015–2017.

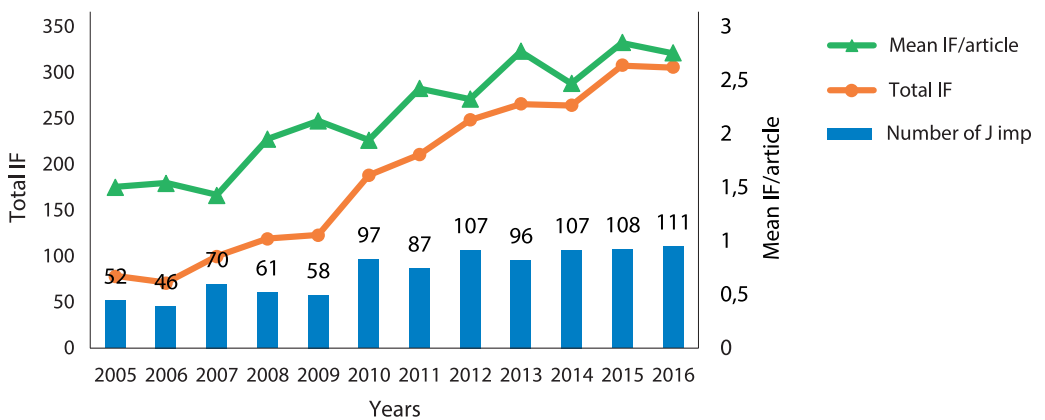
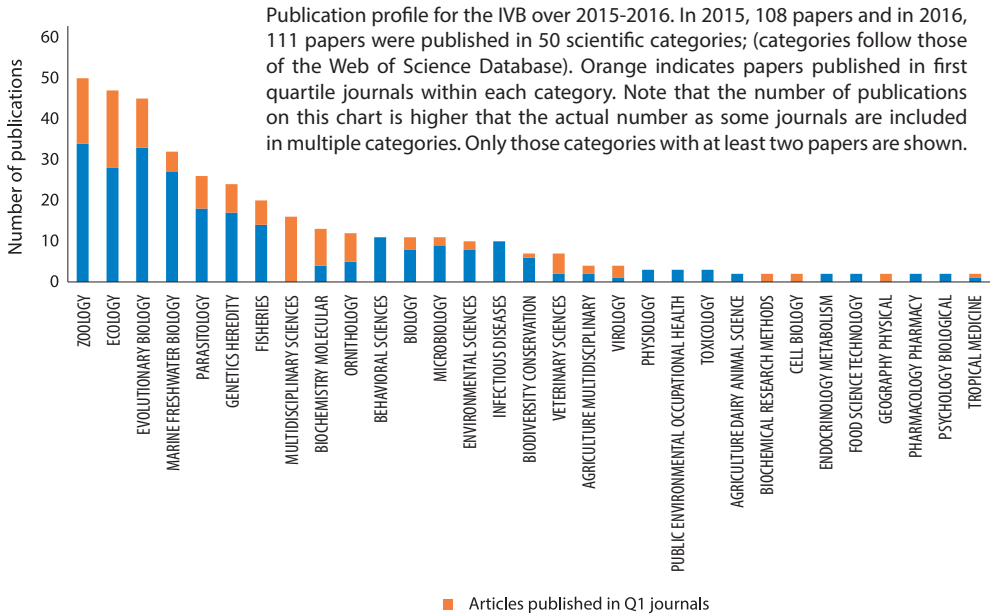
Individual projects

M200931201 The importance of migratory connectivity for the population ecology of long-distance migrants: a model study on the reed warbler (*Acrocephalus scirpaceus*). *Principal Investigator:* Petr Procházka. *Research years:* 2012–2015. Programme of Internal Support for International Cooperation of the Academy of Sciences of the Czech Republic.

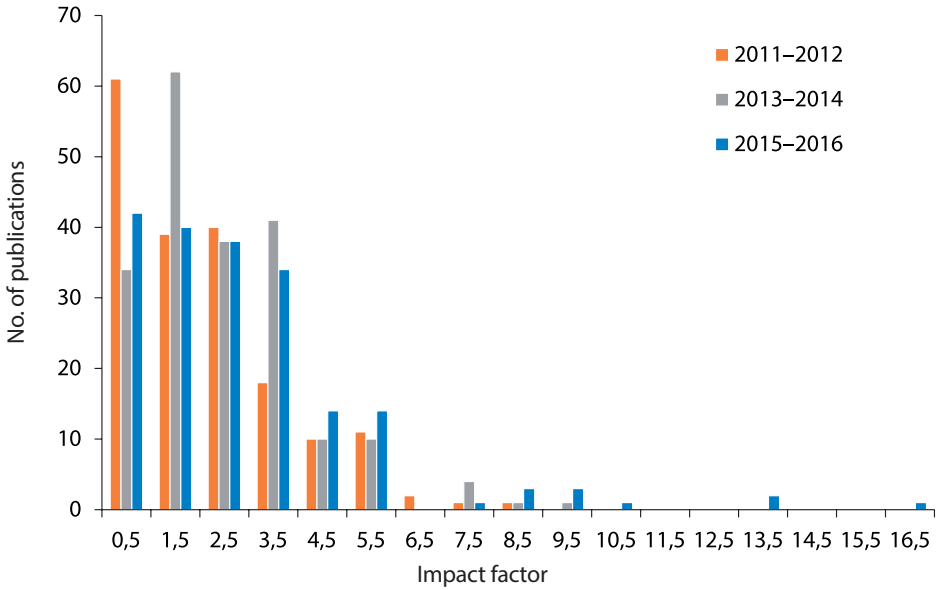
3. SCIENTIFIC RESULTS

| SUMMARY OF PUBLICATION OUTPUT

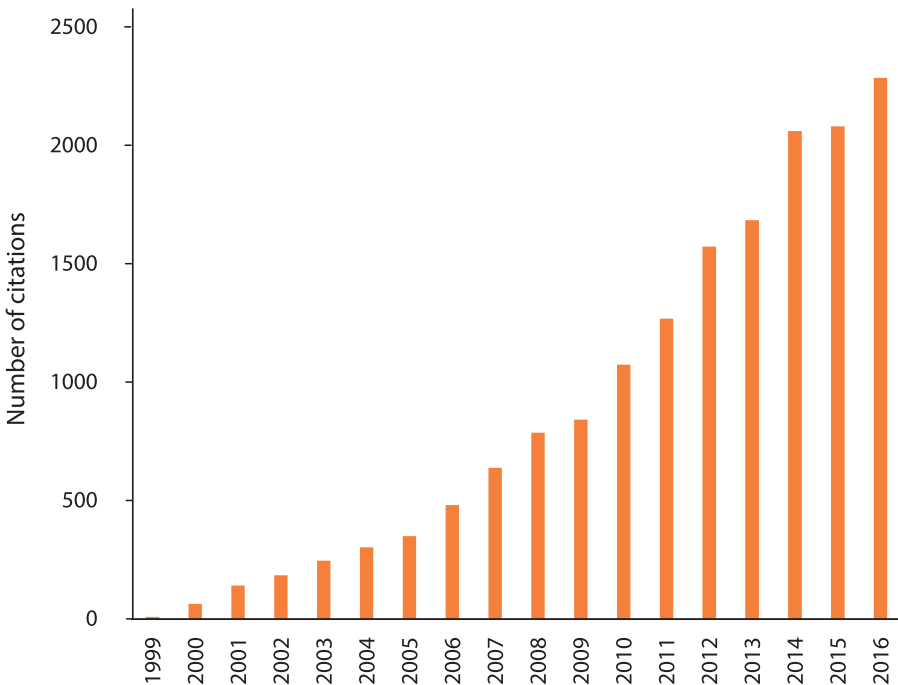
Researchers at the IVB produced numerous scientific publications over 2015-2016, mainly in the form of research articles in international peer-reviewed journals. The publication profile and main scientometric criteria are shown below.



The number of papers published stabilised over 2015-2016, though their quality, as measured by journal impact factor, is increasing (source: ASEP Database, Czech Academy of Sciences and Web of Science).



Distribution of published article impact factors shifted toward higher values once again over 2015-2016.



The IVB was founded in 1998. Since then, the Institute's scientific research output has been cited 16 090 times (source: Web of Knowledge, search limited to research publications from 1998-2016 only).

RESEARCH HIGHLIGHTS

The IVB's various research groups discovered numerous interesting findings in vertebrate biology over 2015-2016 (see COMPLETE LIST OF PUBLICATIONS). As examples of the most important or outstanding scientific achievements, we highlight the following: (a) Two publications (Koleček et al. 2016, *J. Avian. Biol.*; Procházka et al. 2016, *Divers. and Distrib.*) revealed migratory strategies and migratory connectivity in long-distance migrants by using an innovative approach involving light-level geolocators. In doing so, the researchers demonstrated individual flexibility in several migratory species when crossing geographical barriers. They also showed that these mainly nocturnal migrants regularly extended their flights into the day. (b) Genetic drift and low dispersal ability play a significant role in differentiation among populations of annual killifishes inhabiting annually desiccating savanna pools in Mozambique. A detailed genetic study (Bartáková et al. 2015, *J. Biogeogr.*) demonstrated congruence in the unique phylogeographical pattern of three species complexes, combining features of both aquatic and terrestrial taxa. Surprisingly, it was shown that large rivers can play an important role as barriers to gene flow for these freshwater fishes. (c) It was shown that vitamin B2 is a virulence factor in *Pseudogymnoascus destructans* skin infections (the cause of white-nose syndrome) in hibernating bats. This

pathogenic fungus overproduces vitamin B2, leading to high mortality in North America bat species (Flieger et al. 2015, *Sci. Rep.*), while *Eurasian hibernating* bats appear able to tolerate high fungal loads during infection. (d) A series of studies on *African killifish* provided unique data on parasites, fecundity and overall variability in wild populations and revealed intraspecific divergence in aging within the genus as a response to an environmental gradient (Polačik et al. 2016, *Nat. Protoc.*; Cellerino et al. 2016, *Biol. Rev.*; Vrtilík et al. 2016, *Ecol. Evol.*). (e) The results of two phylogeographic studies (Bryja et al. 2017, *J. Biogeogr.*; Mikula et al. 2016, *Zool. Scr.*) show that rodents are an ideal group for studying the role of historical climate change and geomorphology on forming contemporary ecosystems in Africa. Through detailed analysis of small mammal genetic data from widely distributed forest (*Grammomys*) and savannah (*Saccostomus*) taxa, researchers tested alternative evolutionary hypotheses on the history of principal ecosystems in tropical Africa. The results show that, while the evolution of forest taxa primarily mirrors forest fragmentation, savannah taxa evolution is more complex and affected also by other factors. More information regarding these interesting findings (and many others) can be found below in SELECTED SCIENTIFIC ACHIEVEMENTS.



(A) Gerbils of the genus *Gerbilliscus* are typical of the animals living in Sub-Saharan African savannahs. Genetic studies into their evolutionary history can reveal where and when African savannahs have occurred in the past. (B), numerous samples are taken from each rodent specimen for subsequent genetic or epidemiological studies.

(Photo by T. Aghová)

Geographical distribution of selected research activities abroad

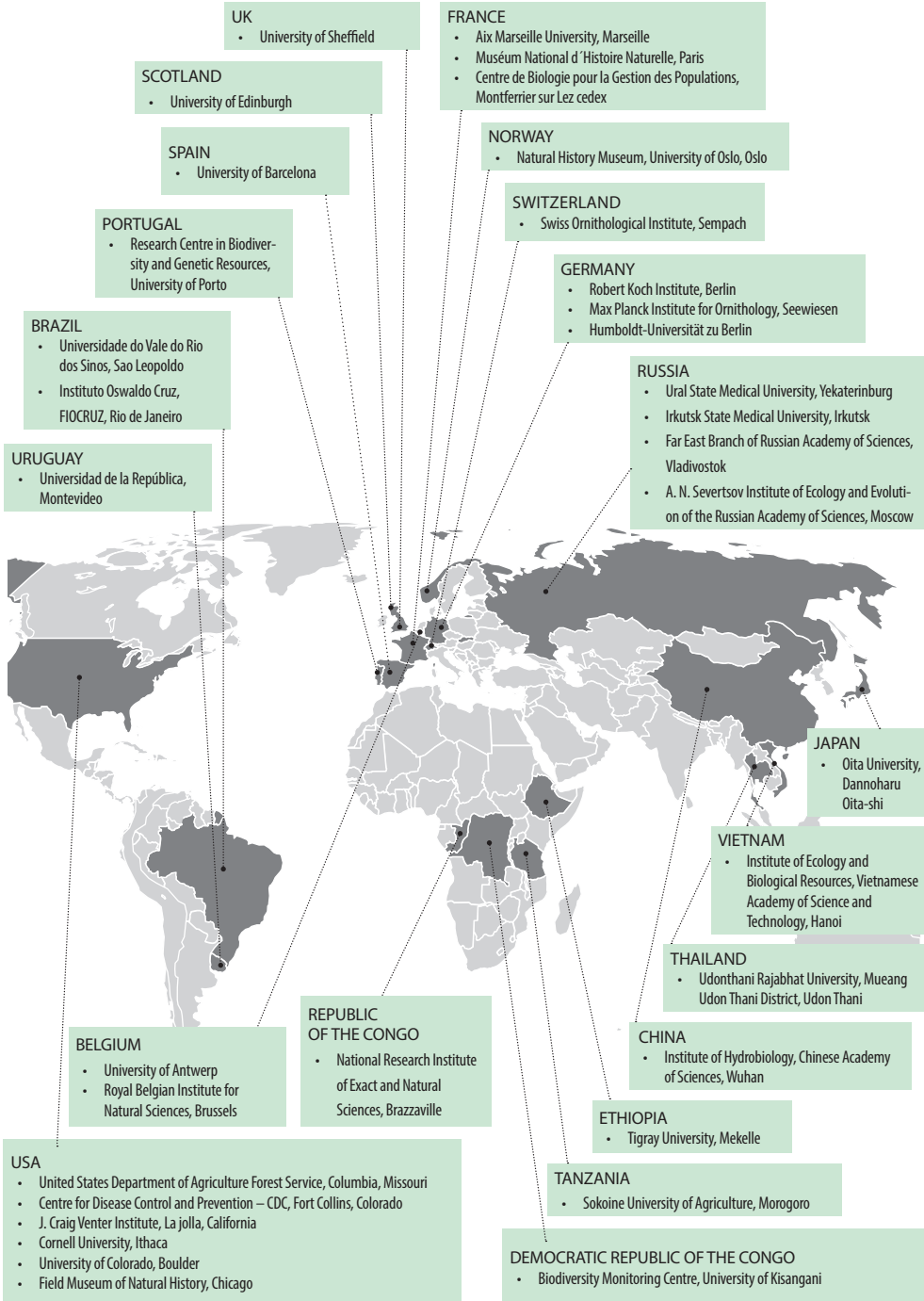


(Photo by P. Procházka, J. Książek, N. Martinková, M. Čapek, M. Reichard)



Publication Output

Most important research collaborations



Publication Output

Complete list of publications

Books, textbooks, edited proceedings

- ALBRECHT J, BUREŠ J, CEPÁK J, ČAPEK M, HAVLÍČEK J, HORA J, KLIMEŠ Z, KLOUBEC B, KUBELKA V, PAKANDL M, PECL K, PELZ P, PYKAL J, ŠŤASTNÝ K, 2015. *Ptáci jižních Čech*. Jihočeský kraj, České Budějovice, 640 pp. ISBN 978-80-87520-12-3.
- ALEXANDER N, ALLEPUZ A, ALTEN B, BÖDKER R, BONNET S, CARPENTER S, CÊTRE-SOSSAH C, CHIROUZE E, DEPAQUIT J, DRESSER K, DUCHEYNE E, DVOŘÁK V, ERISOZ KASAP O, GALL Y, GUEYE FALL A, FARKAS R, FIGUEROLA J, GARROS C, GROSCHUP MH, HALADA P, HENDRICKX G, HENTTONEN H, HLAVÁČKOVÁ K, HORNOK S, HUBÁLEK Z, ILTIS N, KAZIMÍROVÁ M, KLEY N, LAMBERT M-C, LANCELOT R, MIHALCA AD, MIRANDA M, NAPP S, NIEDRIG M, PLANTARD O, PURSE BV, RIZZOLI A, ROGERS DJ, SCHMIDT K, SEARLE KR, SILAGHI C, SIRONEN T, VAYSSIER-TAUSSAT M, VOLF P, VOTÝPKA J, VOURCH G, WHITE S, WINT W, 2015. *The impact of a decade (2004-2015) of research on vector-borne diseases*. CIRAD, 131 pp. ISBN 978-2-87614-707-2.
- BRYJA J, ŘEHÁK Z, ZUKAL J (eds), 2015. *Zoologické dny Brno 2015*. ÚBO AV ČR, Brno, 299 pp. ISBN 978-80-87189-18-4.
- BRYJA J, SEDLÁČEK F, FUCHS R (eds), 2016. *Zoologické dny České Budějovice 2016*. ÚBO AV ČR, Brno, 279 pp. ISBN 978-80-87189-20-7.
- CEPÁK J, ČIHÁK K, HONZA M, HOŘÁK D, HROMÁDKO M, HUDEC K (ed), KLVAŇA P, MUSIL P, MUSILOVÁ Z, SEDLÁČEK O, SITKO J, ŠŤASTNÝ K (ed), ZIMA J, 2016. *Ptáci – Aves*. Díl I. 3. přepracované a doplněné vydání. Fauna ČR, svazek 31. Academia, Praha, 790 pp. ISBN 978-80-200-2575-3.
- ČEPIČKA I, ČERVENÁ B, DOLEŽALOVÁ J, HASEGAWA H, HŮZOVÁ Z, JIRKŮ-POMAJBÍKOVÁ K, JIRSOVÁ D, KALOUSOVÁ B, KVÁČ M, MCEVOY J, MAPUA MI, MODRÝ D, PETRŽELKOVÁ KJ, PŠENKOVÁ I, SAK B, VALLO P, VOTÝPKA J, 2015. *Parasites of African great apes: atlas of coproscopic diagnostics*. University of Veterinary and Pharmaceutical Sciences, Brno, 163 pp.
- ČERVENÝ J, ŠŤASTNÝ K, KOUBEK P, 2016. *Zvěř. Ottova encyklopedie*. Ottovo nakladatelství, Praha, 399 pp. ISBN 978-80-7451-521-7.
- GILARDI KV, GILLESPIE TR, LEENDERTZ FH, MACFIE EJ, TRAVIS DA, WHITTIER CA, WILLIAMSON EA, CAMERON K, CRANFIELD M, GAFFIKIN L, KALEMA-ZIKUSOKA G, KÖNDGEN S, LEENDERTZ S, LONSDORF E, MUEHLENBEIN M, MUGISHA L, NIZEYI JB, NUTTER F, PETRŽELKOVÁ KJ, REED P, RWEGO I, SSEBIDE B, UNWIN S, 2015. *Best practice guidelines for health monitoring and disease control in great ape populations*. IUCN SSC Primate Specialist Group, Gland, 56 pp. Occasional Paper of the IUCN Species Survival Commission, 56. ISBN 978-2-8317-1274-1.
- JURAJDA P, ADÁMEK Z, JANÁČ M, MRKVOVÁ M, ONDRAČKOVÁ M, POLAČIK M, ROCHE K, VALOVÁ Z, VAŠEK M, VŠETIČKOVÁ L, 2015. *Hlaváči v našich vodách*. ÚBO AV ČR, Brno, 16 pp.
- WOOTTON RJ, SMITH C, 2015. *Reproductive biology of teleost fishes*. Wiley-Blackwell, Chichester, 496 pp. ISBN 978-0-632-05426-8.

Chapters in books

- JANÁČ M, REICHARD M, 2016. Use of drift nets to infer fish transport and migration strategies in inland aquatic ecosystems. In Morais P, Daverat F. (eds). *An Introduction to Fish Migration*. CRC Press, Boca Raton: 197-213. ISBN 978-1-4987-1873-8.
- PASSOS C, TASSINO B, ROSENTHAL GG, REICHARD M, 2016. *Reproductive behaviour and sexual selection in annual fishes*. In Berois N, García G, de Sá RO (eds). *Annual fishes: life history strategy, diversity, and evolution*. CRC Press, Boca Raton: 207-229. ISBN 978-1-4822-9971-7.
- POLAČIK M, PODRABSKY JE, 2015. *Temporary environments*. In Riesch R, Tobler M, Plath M (eds). *Extremophile fishes: ecology, evolution, and physiology of Teleosts in extreme environments*. Springer, Cham: 217-245. ISBN 978-3-319-13361-4.
- REICHARD M, 2016. *The evolutionary ecology of African annual fishes*. In Berois N, García G, de Sá RO (eds). *Annual fishes: life history strategy, diversity, and evolution*. CRC Press, Boca Raton: 133-158. ISBN 978-1-4822-9971-7.
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- POLAČIK M, PODRABSKY JE, 2015. *Temporary environments*. In Riesch R, Tobler M, Plath M (eds). *Extremophile fishes: ecology, evolution, and physiology of Teleosts in extreme environments*. Springer, Cham: 217-245. ISBN 978-3-319-13361-4.
- ZIMA J, 2016. *Fylogenetický vývoj a systém ptáků*. Pp. 106-124 in Ptáci – Aves I. Fauna ČR, sv. 31 (K. Šťastný a K. Hudec, red.), Academia, Praha.

Papers in journals included in the databases Web of Science

- ABRAHAM MM, POŽGAYOVÁ M, PROCHÁZKA P, PIÁLKOVÁ R, HONZA M, 2015. Is there a sex-specific difference between parasitic chicks in begging behaviour? *Journal of Ethology* 33: 151-158.
- ADÁMEK Z, KONEČNÁ J, PODHRÁZSKÁ J, VŠETIČKOVÁ L, JURAJDOVÁ Z, 2016. Response of small-stream biota to sudden flow pulses following extreme precipitation events. *Polish Journal of Environmental Studies* 25: 495-501.
- ADÁMEK Z, MRKVOVÁ M, ZUKAL J, ROCHE K, MIKL L, ŠLAPANSKÝ L, JANÁČ M, JURAJDA P, 2016. Environmental quality and natural food performance at feeding sites in a carp (*Cyprinus carpio*) pond. *Aquaculture International* 24: 1591-1606.
- ADAMÍK P, EMMENEGGER T, BRIEDIS M, GUSTAFSSON L, HENSHAW I, KRIST M, LAAKSONEN T, LIECHTI F, PROCHÁZKA P, SALEWSKI V, HAHN S, 2016. Barrier crossing in small avian migrants: individual tracking reveals prolonged nocturnal flights into the day as a common migratory strategy. *Scientific Reports* 6: 21560.
- ARSLAN A, ZIMA J, 2015. Chromosome banding pattern retrieves an independent origin of $2n = 50$ chromosome populations of *Nannospalax xanthodon* from Turkey. *Mammalian Biology* 80: 440-445.
- ARSLAN A, ZIMA J, 2015. Heterochromatin distribution and localization of nucleolar organizing regions in the $2n = 52$ cytotypes of *Nannospalax xanthodon* and *N. ehrenbergi* from Turkey. *Zoological Studies* 54: 6.
- ARSLAN A, ZIMA J, ALBAYRAK I, YORULMAZ T, ARSLAN E, 2015. C-heterochromatin and NORs distribution in karyotypes of three vespertilionid bat species from Turkey. *Biologia* 70: 400-405.
- ARSLAN A, KANKILIC T, YORULMAZ T, KANKILIC T, ZIMA J, 2016. Comparison of the chromosome banding patterns in *Dryomys*

- laniger* and *D. nitedula* from Turkey. *Turkish Journal of Zoology* 40: 363-368.
- ARSLAN A, TOYRAN K, GÖZÜTOK S, YORULMAZ T, ZIMA J, 2016. Comparison of the chromosome banding patterns in three species of social voles (*Microtus irani karamani*, *M. schidlovskii*, *M. anatolicus*) from Turkey. *Turkish Journal of Zoology* 40: 910-916.
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- BAKONYI T, GAYDON GK, SCHWING R, VOGL W, HÄBICH A-C, THALLER D, WEISSENBOCK H, RUDOLF I, HUBÁLEK Z, NOWOTNY N, 2016. Chronic West Nile virus infection in kea (*Nestor notabilis*). *Veterinary Microbiology* 183: 135-139.
- BALOGOVÁ M, GVOŽDÍK L, 2015. Can newts cope with the heat? Disparate thermoregulatory strategies of two sympatric species in water. *PLoS ONE* 10: e0128155.
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SELECTED SCIENTIFIC ACHIEVEMENTS



Evolutionary
Ecology



Biodiversity



Parasites
and diseases

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EVOLUTIONARY ECOLOGY

Mimicry in the coevolutionary arms race between brood parasites and their hosts

The most striking coevolutionary arms race between avian brood parasites and their hosts takes place after the laying of parasitic eggs, when hosts attempt to identify alien eggs in the nest. In the case of the common cuckoo (*Cuculus canorus*), the host faces a tricky challenge as cuckoo eggs are mimetic, i.e. they are very similar to the host's own eggs. Consequently, the more similar the cuckoo egg is to those of the host (i.e. better mimicry), the higher the probability of its acceptance by the host. As birds have very different visual systems than hu-

mans, allowing them to see ultraviolet (UV) light, we focused on the importance of this section of the spectrum in recognition of parasitic eggs by a frequent cuckoo host, the reed warbler (*Acrocephalus scirpaceus*). We found that warblers more often rejected model eggs that had dissimilar UV reflectance than their own; hence, UV signals are likely to be useful to the host for recognising alien eggs in the nest. Moreover, we found that the UV colour of cuckoo and host eggs remained stable during incubation, in contrast with other colours (e.g. green and red), further supporting the importance of UV. On the other hand, we discovered that colour pigments responsible for greenish-brown coloration in cuckoo and great reed warbler (*Acrocephalus arundinaceus*) host eggs faded during incubation. This gradual colour change eventually meant that the quality of cuckoo egg mimicry decreased during the incubation period, suggesting that parasitic egg mimicry may be more dynamic than previously thought.



The great reed warbler *Acrocephalus arundinaceus* is a frequently parasitized host of the common cuckoo *Cuculus canorus* across Europe. To remove foreign eggs from its nest, this species pierces the egg with its bill, a practice known as puncture rejection. Here, we illustrate a great reed warbler removing an egg from its nest.

(Photo by O. Mikulica)

The colour of common cuckoo (*Cuculus canorus*) and great reed warbler (*Acrocephalus arundinaceus*) eggs measured using reflectance spectrometry.

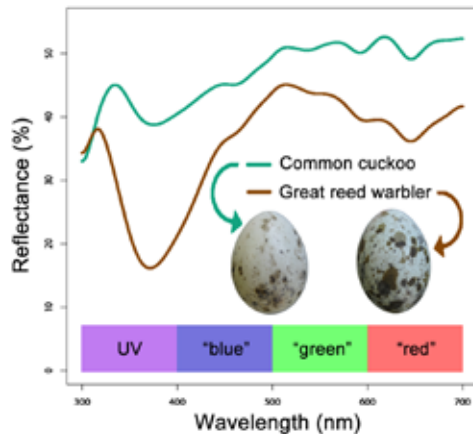
The eggs of both species reflect near ultraviolet radiation between 300–400 nm.

This part of the spectrum could also serve as a signal for recognition of parasitic eggs by hosts.

(Adopted from Šulc and Honza, 2014, *Živa*.)

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Thermal strategies in newts: Implications from a warming world

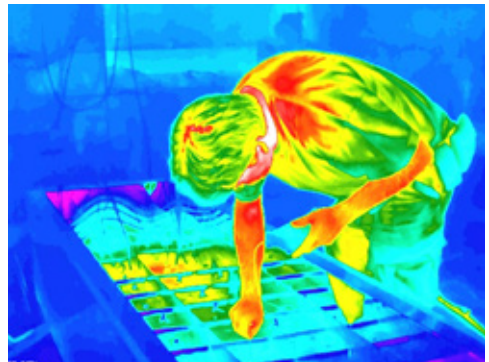
Current climate change poses a serious challenge to ectothermic (cold-blooded) organisms. Their response to changing temperatures involves a combination of behavioural, physiological and evolutionary adjustments, varying greatly in their speed and reversibility. Given the fast pace of current climatic change, it has been assumed that evolutionary adaptation of thermal biology traits in taxa with long generation times will be too slow to follow environmental temperatures closely. Accordingly, the adaptive capacity of ectothermic vertebrates should be largely dependent on behavioural and physiological responses, rather than on evolutionary shifts. We explored these predictions using newts, a threatened group of caudate amphibians, as a study system. Phylogenetic comparative analysis revealed that thermal physiology

traits do indeed evolve very slowly in this group. Results from a mesocosm (semi-natural) experiment showed that predator-induced selection on thermal sensitivity of burst speed is much lower than on body size in newt larvae. In contrast to evolutionary rigidity in thermal physiology, we demonstrated that newts in their aquatic phase employ behavioural thermoregulation to cope with extremely high water temperatures or to provide optimal body temperatures for reproduction. In addition, newts modify metabolic rate thermal sensitivity to reduce energy depletion during the inactive wintering period. Our findings highlight the importance of integrative research on behavioural and physiological adjustments to fully understand the impact of climate change on ectothermic vertebrate population dynamics.



Tuning a respirometer for measuring metabolic rates in newts.

(Photo by M. Polák)



Water temperature measurements over an aquatic thermal gradient, photographed using a thermal imaging camera.

(Photo by M. Polák)

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Annual killifish – a model species group with a range of applications

Annual killifish inhabit seasonal pools in Africa and South America. Their embryos are resistant to drought and hatch soon after the pools fill with water following seasonal rainfall. Young fish quickly mature and spawn to produce the next generation. Annual killifish are small fish that have a naturally short lifespan that is determined by the duration of their pool, which desiccates over the dry season. These fish also live short lives in the laboratory, with some members of the African genus *Nothobranchius* only living for up to 3-6 months. Amongst other factors (e.g. small size and ease of reproduction), this short lifespan makes them especially valuable as a vertebrate model taxon. They are now used for a wide range of biological applications, which we recently reviewed in several synthetic studies. Laboratory ageing research, for example, examines their rapid age-dependent functional decline and expression of cellular and molecular changes comparable to those observed in other vertebrates, including humans.

Due to their unusual life cycle, whereby diapausing eggs are incubated in a non-aquatic environment and show extremely fast metabolism during post-hatching stages, laboratory husbandry of *Nothobranchius* spp. differs in many aspects from that for more traditional fish models, such as the guppy (*Poecilia reticulata*). Consequently, many attempts to maintain laboratory cultures of annual fish have failed. We recently published a manual aimed at helping new researchers establish their own cultures, based on our own long-term husbandry experience with *N. furzeri*, one of the most widely used *Nothobranchius* species. The guide covers all phases of the establishment process,

starting with a description of how to hatch eggs shipped in moist peat, followed by methods of raising and breeding adult fish and suggestions on how to cope with most common problems and diseases.

Nothobranchius fishes also represent a unique model taxon for investigating the evolution of life-history adaptations and their genetic architecture and are an ideal taxon for studying natural genetic variation in a laboratory setting. Distribution ranges of some species span over strong climatic gradients, imposing contrasting selective pressure on different populations. A relatively dry climate translates into shorter pool duration, for example, imposing constraints on maximum survival. We recently utilised this contrast and performed a common garden experiment in which we confirmed that dry climate populations of several *Nothobranchius* species have evolved shorter intrinsic lifespans and an increased rate of aging. These findings demonstrate that variation in life span and age-related functional decline within natural populations are linked and genetically underpinned and, as such, can evolve relatively rapidly.

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Nothobranchius furzeri male.
(Photo by M. Polačik)



Fish sampling in an African seasonal pool.
(Photo by M. Polačik)

Carnivores in human-impacted landscapes

Carnivorous top predators are commonly considered sensitive to habitat loss and fragmentation due to their large spatial requirements, low reproduction rate, diet specialisation and/or human persecution. These ecological characteristics make them particularly vulnerable to human activities associated with urbanisation, causing populations to decline and, in some cases, become locally extinct. Responses to urbanisation vary significantly, based on their ability to live in human-impacted habitats, which in turn depends on species-specific ecological or behavioural plasticity and life histories. Despite an increasing

Our results emphasise the remarkable ability of some carnivore species to adapt to novel environments through behavioural flexibility and life history adaptation. On the other hand, carnivores inhabiting human-dominated landscapes are exposed to increased danger, e.g. an increased risk of vehicle collision. Indeed, traffic infrastructure is currently one of the main anthropogenic factors affecting carnivore populations; consequently, an increased understanding of the factors behind spatio-temporal patterns of road mortality is crucial in developing successful conservation measures. In a follow up study, therefore, we in-

The raccoon (*Procyon lotor*) is able to adapt to novel environments through behavioural flexibility and life history adaptation

(Image downloaded from Pixabay, Creative Commons CC0 Public Domain.)



number of studies on urban carnivore ecology, no comprehensive cross-species comparisons have been undertaken to assess the effect of urbanisation on carnivore spatial ecology and population density. Using data from 411 articles, we provided evidence that home range size has decreased in five (red fox [*Vulpes vulpes*], coyote [*Canis latrans*], bobcat [*Lynx rufus*], raccoon [*Procyon lotor*], Eurasian badger [*Meles meles*]) carnivore species, and that population density has increased in three (red fox, coyote, raccoon) carnivore species along the urban-natural habitat gradient. The density dependent pattern of variation in home range size was consistent in all species studied.

investigated the effect of landscape and local characteristics on road mortality in a number of carnivore species. At a landscape scale (1000 m radius), road-kills of habitat generalists (i.e. red fox, stone marten [*Martes foina*], European polecat [*Mustela putorius*], least weasel [*Mustela nivalis*] and stoat [*Mustela erminea*]) were mainly detected in areas with mixture of arable land and human settlements. Road-kills of habitat specialists (pine marten [*Martes martes*], Eurasian badger and European otter [*Lutra lutra*] and non-native species (raccoon dog [*Nyctereutes procyonoides*] and raccoon), on the other hand, were mainly found in areas with a high proportion of forest, grassland

and water bodies. At a local scale (50 m radius), presence of linear habitats (forest edges, corridors) was positively linked to road-kills of European otter, stone marten, Eurasian badger, stoat, least weasel, European polecat and red fox. The presence of watercourses increased mortality risk in European otter and raccoon dog but decreased mortality risk in stone marten, least weasel and

red fox. We documented a significant effect of road topography for raccoons only, with road-kills mostly found along parallel road sections, as opposed to buried and raised roads. Based on our results, we suggest a number of mitigation measures that could reduce carnivore mortality in human-dominated landscapes.

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Extra-pair paternity and post-copulatory sexual selection in passerine birds

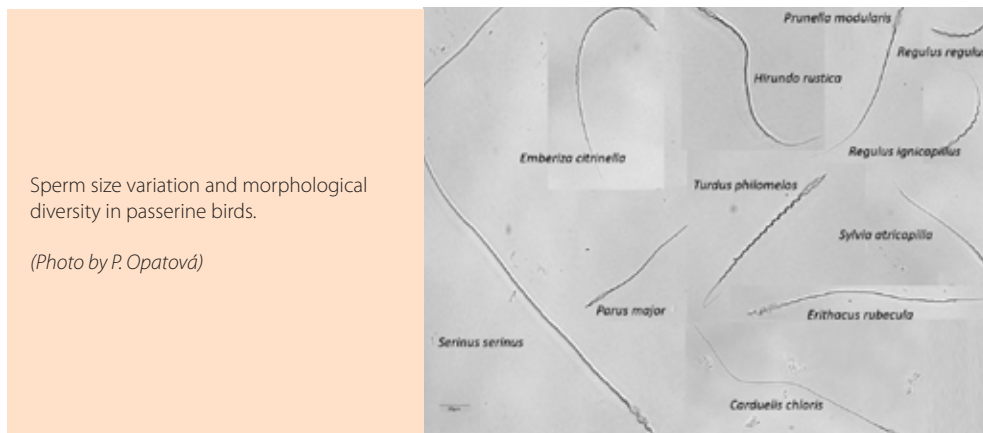
A Post-copulatory sexual selection emerges due to promiscuous female behaviour, i.e. copulating with more than one male. Social monogamy is the prevailing mating system in birds, yet genetic polyandry has been detected in many species. Male reproductive success depends on the ability of sperm to fertilise an egg, which should lead to strong selection on sperm characteristics. We studied the evolution of sperm size and morphology in several passerine clades. Not only did we find that the length of sperm and sperm mitochondria were positively correlated with the risk of sperm competition across passerine species, we were also the first to show an association between the strength of sperm competition and the speed of sperm evolution. Our results suggest that post-copulatory sexual selection promotes rapid evolutionary diversification in sperm morphology and may play an important role in the process of species differentiation in passerine birds. We studied the effects of genetic quality (inbreeding) and oxidative stress on ejaculate quality in zebra finches (*Taeniopygia guttata*) and found that inbreeding led to significantly lower sperm motility and a substantially higher percentage of abnormal spermatozoa in ejaculate. Furthermore, our data suggest that redox homeostasis constrains sperm

morphometry in zebra finches. We also found evidence for a long-term trade-off between ornament expression (pre-copulatory sexual signal) and sperm resistance to oxidative challenge. Interestingly, carotenoid supplementation resulted in fewer sperm abnormalities, in line with the assumption that carotenoids have a beneficial effect on spermatogenesis. Collectively, the results are in line with our previous finding that carotenoids counteract the effect of oxidative challenge on lipophilic (but not hydrophilic) antioxidant capacity in zebra finches, thereby supporting the recently questioned carotenoid antioxidant function in vivo. We also studied how genetic quality and sexual ornamentation affect levels of sexual promiscuity and the occurrence of quasi-parasitism in free-living passerine birds. The latter may occasionally be detected in genetically promiscuous systems where both extra-pair paternity and conspecific brood parasitism occur. Quasi-parasitic eggs are eggs of the parasite fertilised by the resident male, such that all offspring in the nest are progeny of the nest-attending male but not of the nest-attending female. Interestingly, one third of parasitic eggs in our barn swallow (*Hirundo rustica*) population resulted from quasi-parasitism.

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Sperm size variation and morphological diversity in passerine birds.

(Photo by P. Opatová)

Sexual selection and speciation in barn swallows

Mate choice mechanisms have fascinated evolutionary biologists ever since Darwin. Darwin proposed that sexual selection, with its two basic components of male-male competition for access to females (intrasexual selection) and female choice of mate, was the basic concept explaining evolution of elaborate male ornamentation and sexual dimorphism. Recently, we studied the role of natural and sexual selection on population diversification in eight barn swallow (*Hirundo rustica*) populations (four subspecies) by comparing the “isolation by adaptation” scenario (IBA) for population divergence with the complementary and well-known pattern of “isolation by distance”

(IBD). Using statistical approaches to control for spatial autocorrelation of phenotypic variables and geographic distance, we found that divergence in traits related to migratory behaviour and sexual signalling, along with geographic distance, together explained over 70% of genome-wide divergence within populations. Controlling for IBD, we found 42% of genome wide divergence was attributable to IBA through pairwise differences in traits related to migratory behaviour and sexual signalling alone. In a further study, we assessed sexual selection pressure for multiple male visual signals across four barn swallow populations. We demonstrated significant phenotypic differenti-



Hirundo rustica erythro-gaster, a subspecies of North American barn swallow.

(Photo by M. R. Wilkins)

ation in four sexual signalling axes, despite very low genomic divergence and no comparable divergence in an ecological trait. To our knowledge, our study is the first to relate direct measures of the strength and target of sexual selection to phenotypic divergence within closely related wild populations. Our results add to the growing evidence for phenotypic divergence with gene flow. Diverging populations often shift patterns of signal use, a process that could contribute to reproductive isolation and speciation. We tested the hy-

pothesis that the relationship between signal trait elaboration and a central component of organismal health, oxidative stress, differs across closely related populations that have diverged in signal use and preferences, comparing European and North American barn swallow subspecies. Our results suggest that, while some phenotypic traits appear to be capable of conveying similar physiological information regardless of their use as signals, divergence in other phenotypic traits may be associated with shifts in their information content.

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Population-centred perspectives of biological invasions

Understanding biological invasions has major ecological and economic implications; and yet, predicting the impact of invasive species remains challenging. As species populations are genetically and phenotypically variable, the impact of non-native species on local taxa could depend on population-specific traits and adaptations of both native and non-native species. Taking advantage of this unique reciprocal relationship, we demonstrate

that population-specific attributes of invading and native populations do indeed play a critical role in governing the outcome of an invasion. In Europe, the bitterling (*Rhodeus amarus*) is a parasite of freshwater mussels, laying their eggs straight onto its gills. The mussels have their own parasitic stage, termed glochidia, that parasitise fishes in order to complete their larval phase of development. European bitterling are, however, capable of overcom-

ing parasitism by glochidia. A recent invasion of the Chinese pond mussel (*Anodonta woodiana*) has changed this relationship, as the Chinese mussel is capable of escaping parasitism by European bitterling by ejecting its eggs. In addition, *A. woodiana* parasitise European bitterling with its own glochidia, an example of complete host-parasite reversal. Interestingly, there are probably two separate *A. woodiana* populations in Europe, possibly from two independent introductions. Likewise, the European bitterling is represented by two main phylogeographic clades that colonised the continent from separate glacial refugia. We concentrated on understanding inter-population variation in impact of the invasive mussel, using a common garden experiment to measure three key elements in the bitterling-mussel association among two populations of the invasive mussel

and four bitterling populations. We found major differences in the impact of the invasive mussel on geographically distinct bitterling lineages and between local bitterling populations within lineages. The capacity of invasive mussel parasitic larvae to exploit bitterling was higher in the Danubian (Western) bitterling lineage than the Baltic (Eastern) lineage and in populations naïve to the invasive mussel compared with bitterling populations coexisting with the invasive mussel for 5-20 generations. Invasion ecologists have hitherto focused on species-level studies. We suggest that variation in coevolutionary states may predispose different populations to divergent responses to invasive species. Because coevolutionary relationships are ubiquitous, we suggest a conceptual shift from a species-centred to population-centred perspective of the impacts of invasions.

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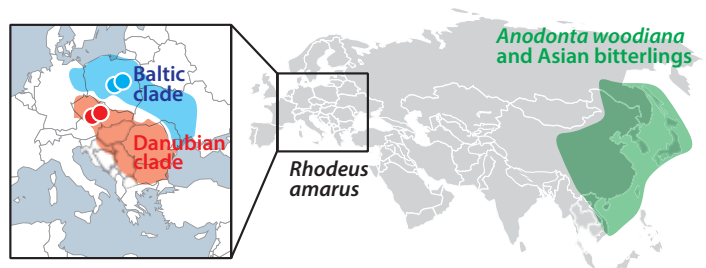
A male European bitterling (*Rhodeus amarus*) approaching a mussel.

(Photo by M. Reichard)



The native range of the Chinese pond mussel (*Anodonta woodiana*) and European bitterling (*Rhodeus amarus*), with an inset illustrating location of Baltic and Danubian populations used in the study and the distribution of two major *R. amarus* clades in Europe.

(Adopted from Reichard et al. 2015, *Proc R Soc Lond B Biol Sci.*)



Cognitive ability affects male reproductive success

The ability to attract mates, acquire resources and outcompete rivals makes demands on a species' cognitive traits, i.e. the mechanisms by which an animal acquires, processes, stores and acts upon information from its environment. While we now have a good understanding of the cognitive abilities of a range of animals, few attempts have been made to relate cognitive traits to reproductive success, and fewer still have examined their genetic basis. Bitterling are fish that spawn in living mussels and, to be reproductively successful, male bitterling must distribute their limited sperm reserves optimally among mussels. Bitterling possess a complex mating system and can display a number of alternative mating tactics. Males may be either territorial or defend a mussel, or reproduce by sneaking into foreign territories to deposit sperm into a mussel.

We measured spatial learning in a group of male and female rose bitterling (*Rhodeus ocellatus*). We found that males were better in solving a maze trial than females. Males were subsequently allowed to play the role of a guarder or a sneaker in competitive mating trials, with reproductive success measured using paternity analysis. While spatial cognitive ability had no effect on reproductive success in a territorial role, the best performing males in maze trials showed greater reproductive success in the sneaker role. We further measured the genetic basis of spatial cognition using a quantitative genetics approach, and found that approximately 30% of variance in the trait is inherited, with significant additive maternal and paternal effects. These findings imply that spatial cognition can undergo sexual selection.

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The rose bitterling (*Rhodeus ocellatus*).

(Photo by C. Smith)

Feeding behaviour of common carp in pond aquaculture

Pond farming with common carp (*Cyprinus carpio*) has a long tradition in the Czech Republic. In recent years, carp stocking densities in ponds have increased considerably and production methods have intensified in order to significantly increase production levels. This has led to dramatic changes in pond conditions. Consequently, current approaches are often aimed at introducing more environmentally friendly technologies into carp pond aquaculture, with greater reliance on

semi-intensive methods that utilise a combination of natural food exploitation supported by supplementary feeding with cereals. While supplementary feeding has been in use for a number of years, there is little information available on how carp respond to this feeding mode and what overall effect it has on the pond environment. Just like other domesticated animals, common carp are able to learn where food can be easily obtained. As a result, carp in semi-intensive polyculture

ponds could conceivably restrict their main activity centres to supplemental feeding sites, leading to lowered exploitation of natural food resources (zooplankton and macrozoobenthos) and localised degradation of environmental conditions. Furthermore, feeding strategies that concentrate fish stocks in restricted areas could increase competition, resulting in less homogenous 'group performance'. In order to investigate some of these phenomena, we undertook a study monitoring the feeding habits and behaviour of two- and three-year old carp in semi-intensive ponds utilising supplementary feeding. At the same time, we monitored environmental conditions and available natural food resources, both at feeding sites and non-feeding sites.

Our results confirmed that carp distribution in such semi-intensive ponds is irregular, with dominant individuals tending to concentrate at feeding sites in densities that could lead to dissolved oxy-

gen concentrations at or below the physiological minimum threshold. Sub-dominant fish tended to be in poorer condition, spent more time near the littoral zone and fed mostly on zooplankton. The areas around feeding sites displayed significantly reduced oxygen concentration and saturation. Likewise, temperature, pH and transparency also decreased significantly, whilst turbidity increased. While there was no significant difference in zooplankton biovolume at feeding and non-feeding sites, zoobenthos density and biomass were significantly lower at feeding sites. Hence, the feeding behaviour of carp in ponds with supplementary feeding led to significant changes in both abiotic and biotic conditions near the supplementary feeding points. These results have been used to formulate proposals for a new supplementary feeding system leading to better-balanced stock, reduced losses and better utilisation of natural food resources.

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Telemetry survey of carp (*Cyprinus carpio*) behaviour in ponds owned by Pohorelice Fisheries a.s.

(Photo by K. Roche)



Geolocators reveal migration strategies and migratory connectivity in long-distance migrants

Animal migration is one of the most exciting fields of animal ecology and evolutionary biology. Regular seasonal movements of animals in space and time represent a complex and widespread biological phenomenon that has shaped many of the migratory species' life history traits. Migrating animals often travel across enormous distances and the different conditions encountered in disparate parts of the world can have far-reaching consequences for individual condition, future reproduction and, in turn, for migratory species' population dynamics. Long-distance migrants also influence distant ecosystems where they may play the role of predator or prey or act as vectors of parasites or transporters of nutrients or propagules. In order to understand such large-scale ecological processes it is important to quantify how many individuals and what biomass moves annually between each ecosystem. Due to their high mobility, however, migratory organisms are notoriously difficult to follow. A major breakthrough in the study of small bird migration was achieved only recently when miniaturised light-level geolocators were successfully applied to passerines. These geolocators enable detailed tracking of migration

and the location of stopover and wintering sites, which are frequently unknown for individual populations. Using geolocators, we demonstrated individual flexibility in several migratory species when crossing major geographical barriers. In contrast to the preferred 'intermittent hypothesis', we convincingly showed for the first time that these otherwise mainly nocturnal migrants regularly extend their nocturnal flights into the day. In addition, we also investigated migration patterns in a trans-Saharan migratory bird, the great reed warbler (*Acrocephalus arundinaceus*), over its wide western Palearctic breeding range. We found moderate migratory connectivity, suggesting that breeding populations mix extensively across the non-breeding grounds and thus any negative effects of adverse local conditions on survival are diffused.

Interestingly, the birds often performed intra-tropical movements between distant parts or the non-breeding grounds, which probably coincided with the onset of the dry season from late October onwards. Our studies clearly demonstrate the great potential of geolocators to provide unrivalled knowledge on small migratory vertebrates.



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An Eurasian reed warbler (*Acrocephalus scirpaceus*) tagged with a light-level geolocators that records light intensity. Light data can be used to ascertain time of local sunset and sunrise, subsequently allowing calculation of latitude and longitude. This enables the study of migration even in small vertebrate species that are difficult to track by other means.

(Photo by P. Procházka)

Biodiversity

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BIODIVERSITY

Habitat preference and population changes in birds

Data obtained by monitoring breeding birds has enabled scientists to relate a species' abundance with its ecological traits. We investigated both short- and long-term interactions between bird populations and local environmental conditions. Over the short-term, we explored abundance and habitat preferences of urban (collared dove [*Streptopelia decaocto*], tree sparrow [*Passer montanus*], house sparrow [*Passer domesticus*]) and farmland (skylark [*Alauda arvensis*]) specialists. We found that for urban species, a mix of built-up areas and city green space was more important for breeding than each habitat individually. Comparison of habitat use and availability revealed that both sparrow species clearly avoided artificial surfaces, though house sparrows showed a preference for built-up areas and tree sparrows showed a similar preference for built-up areas with greenspace. In winter, habitat preferences were similar for both sparrow species and the collared dove. All three species responded positively to the proportion of shrubs/trees, poultry keeping and presence of dairy farms, while avoiding houses, arable land and grassland. Unlike the collared dove, winter occurrence of sparrows was significantly affected by poultry keeping. In farmland, skylarks were

more abundant in Poland than in Germany and the Czech Republic, probably due to less intensive land management. Mean abundance declined with growing sward height during spring and slightly declined with the number of fields surrounding individual sites. Autumn- and spring-sown cereals hosted the highest abundance of skylarks in May, with lower abundance in maize, oilseed rape and meadows. These results indicate that skylark habitat use is somewhat conserved over regions, knowledge that will be of use in management plans throughout Europe. Over the long-term, we found that species breeding in different habitats at higher altitudes had a more negative trend than species breeding at lower altitudes. We also found that species moved upward in response to a warming climate, and that such altitudinal range shifts were associated with more positive population trends at lower altitudes than at higher altitudes. Moreover, long-distance migrants declined more than residents or species migrating for shorter distances. Taken together, these results indicate that climate change, along with other possible environmental changes, is already influencing montane bird populations, with particularly adverse impacts on high-altitude species.



House sparrow (*Passer domesticus*) populations have declined rapidly in breeding habitats throughout the European range, with strongest declines recorded in urban environments. (Photo by M. Šálek)

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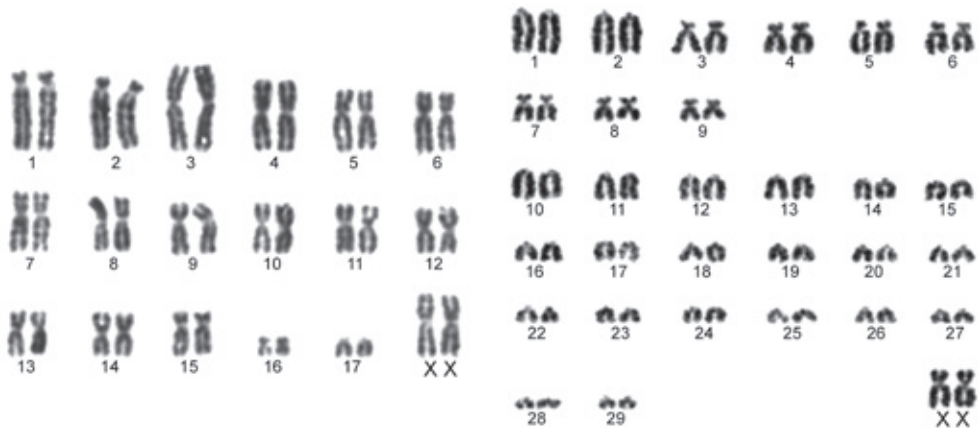
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Amazing chromosomal variation in blind mole rats (Spalacinae)

Blind mole rats (Spalacinae) display fascinating chromosomal variation resulting from complex karyotype re-arrangements. The variation occurs between species, between populations of single species (polytypy) and within populations (polymorphism). We undertook a review of current knowledge on blind mole rat karyotypes and their variation, with special attention paid to karyotype differentiation within species and patterns of chromosomal variation that result in the evolution of distinct chromosomal races (cytotypes). Chromosomal races are defined as groups of geographically contiguous or recently separated populations that share a similar chromosome complement by descent. Our review indicated the existence of 73 distinct blind mole rat chromosome races within the genus *Nannospalax*, along with seven species recognised within the genus *Spalax*. In total, 12 distinct diploid chromosome numbers were re-

ported ($2n = 36-62$). We also observed variation in chromosome morphology between populations with the same number of chromosomes ($NF = 62-124$). Blind mole rats of the genus *Spalax* had a uniform karyotype, both between and within recognised species. Of the species traditionally classified within the genus *Nannospalax*, 25 races could be distinguished within *N. leucodon*, 28 within *N. xanthodon* and 20 within *N. ehrenbergi*. Hybrids between the races were only found exceptionally and were largely absent over extensive areas (Europe, Turkey). This suggests that blind mole rat chromosomal evolution may be related to speciation processes. Definitive phylogenetic and taxonomic conclusions will only be obtained after application of reliable molecular markers and the setting of estimates for genetic distance and gene flow between populations.



Differences in karyotypes between the Xanthodon ($2n = 36$, left) and Vasvarii ($2n = 60$, right) races of blind mole rat. (Photo by A. Arslan)

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African amphibians – diversity, evolution and conservation

Our knowledge of African amphibian diversity is still incomplete, reducing our understanding of the evolution of this group of vertebrates and reducing the effectiveness of conservation management measures. In cooperation with the McMaster University in Hamilton, Canada, we examined the historical biogeography, evolution and systematics of African clawed frogs (*Xenopus*), including that of *Xenopus laevis*, a model species widespread in experimental laboratories around the world. Prior to this study, the evolutionary history of the *X. laevis* species group was unknown within its pan-African range. Analysis of molecular variation indicated population structure and evolutionarily diverged lineages, further contextualising chronology and evolutionary relationships within this group. In addition, the results also shed new light on the taxonomy of the group, with four species recognised within the complex, i.e. *X. laevis*, *X. petersii*, *X. victorianus*

and *X. poweri*. Furthermore, a thorough review of western and central African *Xenopus* sp., utilising genetics, morphology, advertisement calls and historical records, resulted in the description of six new species (*X. calcaratus*, *X. mellotropicalis*, *X. allofraseri*, *X. parafraseri*, *X. eysoole*, *X. kobeli*) and the revalidation of another (*X. fischbergi*).

We focused special attention on the diversity and conservation status of amphibians from Mount Oku in Cameroon. Twenty-five species were recorded for the first time in the region and the proportion of threatened species was found to be 44–48%, more than the global average of 33%. The natural habitats of Mount Oku provide irreplaceable refuges for endemic and restricted-range amphibians, which are under severe pressure elsewhere in their range. Of particular worry is the fact that some species, e.g. the Lake Oku puddle frog (*Phrynobatrachus njiomock*), have not been seen since 2010.

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The Biafran clawed frog (*Xenopus calcaratus*), one of the new species occurring in the Gulf of Guinea region in Central Africa.

(Photo by V. Gvoždík)



Genetic diversity of slow worms and tree frogs in Europe

A comparative phylogeographic study of four slow worm species (*Anguis fragilis*, *A. colchica*, *A. graeca*, *A. cephalonica*) of the Balkan Peninsula revealed the distribution of evolutionary lineages, their contact zones, likely locations of glacial refugia and direction of colonisation after the Ice Age. Phylogeographic patterns were concordant with the 'refugia-within-refugia' model. While slow worm populations from the southern refugia mostly had restricted distributions and had not dispersed much from their refuge areas, populations from extra-Mediterranean refugia in the northern Balkans have colonised vast areas of eastern, central and western Europe. We further found a strong positive correlation between genetic diversity within slow worm populations and

topographic ruggedness of their ranges (mountain systems), areas with more rugged terrain harbouring higher genetic diversity.

We also studied the speciation history of European short-call tree frogs (*Hyla*), a group of morphologically cryptic western Palearctic frogs characterised and genetically differentiated by the short period of their advertisement calls. By inferring genealogical histories and species limits, we showed that gene introgression played an important role in the evolutionary history of short-call tree frogs. Mitochondrial capture upon secondary contact appears to explain the close mtDNA relationship between the geographically remote Iberian *H. molleri* and *H. orientalis* from around the Black Sea.

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The common European slow worm (*Anguis fragilis*; female left, male right).

(Photo by V. Gvoždík)

Extremely low genetic variation and introgressive hybridisation in endangered Tatra chamois

Genetic diversity is a crucial factor affecting the capability of populations to cope with a changing environment, i.e. to evolve and survive. In fragmented and small populations, however, genetic diversity tends to be reduced due to genetic drift and there is a heightened risk of inbreeding, with a consequent decrease in reproduction and survival (i.e. inbreeding depression). Many factors can cause populations to decline, both natural and anthropogenic. The northern chamois (*Rupicapra rupicapra*) is a species of wild goat found only in mountain habitats, and hence living in naturally fragmented populations. Further, as chamois are a game species, their populations have been reduced due to extensive hunting and poaching, while population numbers have been affected by human-mediated translocations and introductions. Using non-invasive genetic sampling (i.e. DNA extracted from faeces) and nuclear microsatellite markers, mtDNA and one adaptive marker (Major histocompatibility complex, MHC), we analysed the impacts of demographic history on the genetic composition of four chamois populations living in isolated area of chamois occurrence in the Western Carpathians (Slovakia and southern Poland). The area is inhabited by two subspecies, the endangered and endemic Tatra chamois (*R. r. tatrica*), which only occurs in the Tatra Mountains (the only native population of the sub-

species) and the Low Tatra Mountains (introduced back-up population), and the non-native Alpine chamois (*R. r. rupicapra*), which were introduced to two adjacent mountain ranges for hunting purposes. We found low genetic variation and a high level of inbreeding in all four populations. The least variable native Tatra population (only one allele of generally highly polymorphic marker on MHC) has probably been affected by several population bottlenecks over the last century, mainly due to hunting and poaching. Introduced Alpine chamois show greater microsatellite and MHC variation, despite originating from just a few founders. The Slovenský raj population, however, founded by just six individuals, also showed highest inbreeding. Further, we detected male-biased introgressive hybridisation between Tatra and Alpine chamois in the Low Tatra mountains. Such hybridisation can be viewed ambiguously as regards conservation in that, though it disrupts the integrity of the unique Tatra chamois genome in the back-up population, it also improves its very low genetic variation and decreases the inbreeding level, with no obvious sign of outbreeding depression. At this time, the unique Tatra chamois genome is probably still sufficiently protected in the Tatra Mountains, with the Podtatranská kotlina basin acting as an impermeable barrier to gene flow to/from other Slovak populations.



Use of droppings for DNA extraction enables the study of rare or endangered species without physical disturbance. (Photo by J. Ksiažek [left & middle] and J. Kormančík [right])

ZEMANOVÁ B, HÁJKOVÁ P, HÁJEK B, MARTÍNKOVÁ N, MIKULÍČEK P, ZIMA J, BRYJA J, 2015. Extremely low genetic variation in endangered Tatra chamois and evidence for hybridization with an introduced Alpine population. *Conservation Genetics* 16: 729-741.

Comparative phylogeography of African small mammals helps to reconstruct history of sub-Saharan biomes

Phylogeography, or the study of the inhabitant's genetic structure, provides powerful tools for understanding the evolutionary history of ecosystems. Genetic studies of European forest animals and plants, for example, have led to the discovery of refugia with suitable conditions for forest organisms during the Pleistocene ice ages and reconstruction of post-glacial colonisation of the western Palaearctic. Similar studies remain scarce for tropical areas, however, despite the fact that an understanding of the evolutionary patterns in the African savannah-forest mosaic, for example, is crucial for understanding the evolution of our own species.

Small terrestrial mammals, such as rodents and shrews, represent an ideal model group for studying the interplay of historical climate change and geomorphology in forming contemporary ecosystems as they have short life spans, rapid reproduction cycles, low dispersal ability and respond quickly to environmental change. Furthermore, they are usually not endangered and, because of their conspicuousness and relatively easy trapability, they are well represented in natural history collections. Despite this, previous studies have often been biased by limited geographic sampling. This is no longer the case as our recent sampling, supplemented by the collections of our collaborators, now allows analysis at a pan-African scale. Using genetic/genomic data, we can now test the respective roles of forest retraction/expansion, rivers, ecological gradients and anthropogenic factors in

explaining the diversification of African rodents and shrews from the late Miocene onward.

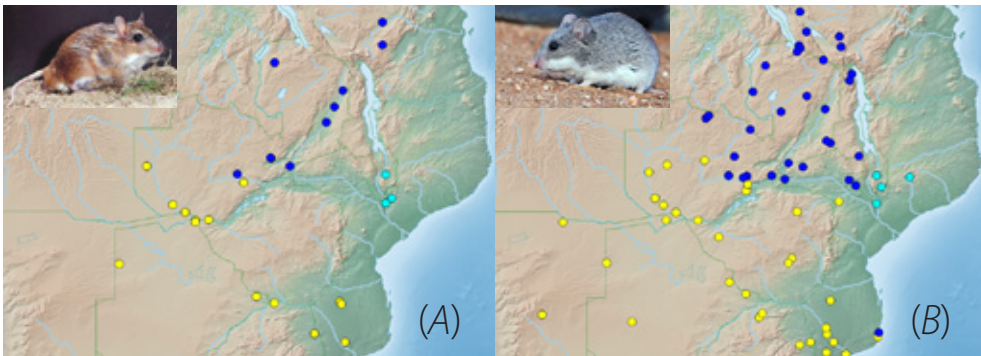
Based on the concept of phylogenetic niche conservatism, we used a phylogeographical approach for both forest- and savannah-dwelling small mammal taxa to investigate evolutionary history and past connections between African biomes. Our results demonstrate the importance of both climatic fluctuation and physiographic vicariance in shaping the distribution of sub-Saharan biodiversity. The evolution of forest taxa (shrews of the *Crocidura olivieri* complex and partly arboreal rodents from the genus *Grammomys*) primarily mirrors fragmentation of forests in the late Miocene, separating Guineo-Congolese forests from East African montane and coastal forests. Later, and particularly in the Pleistocene, climatic oscillations were the most important factor in allopatric diversification of forest taxa in fragmented forest refugia. During the humid Plio-Pleistocene periods, evolution in open habitats was primarily driven by genetic differentiation in fragmented savannahs, though other factors were also involved. In the Zambezian savannahs of East Africa, the most important factor was probably the Zambezi-Kafue river complex, which effectively stopped dispersal following the return of conditions promoting the spread of savannah. These results also have important taxonomic (description of new species) and conservation (defining regions with high phylogenetic diversity) implications.

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The Zambezi-Kafue river system is the most important phylogeographic divide for small mammals living in southeast African savannahs. (A) Genetic structure of the bushveld gerbil (*Gerbilliscus leucogaster*) complex, based on AFLP (amplified fragment length polymorphism) data and mitochondrial sequences (Figure modified from McDonough et al. 2015, *Mol. Ecol.*). (B) Genetic structure of the south African pouched mouse (*Saccostomus campestris*) complex, based on nuclear and mitochondrial gene sequences (Figure modified from Mikula et al. 2016, *Zool. Scripta*)

Rapid diversification of squirrels in the Americas molded by feeding preference

Biological diversity in Central and South American tropical forests is so exceptional that the regions are often referred to as biodiversity hotspots. Tree squirrels of the tribe Sciurini contribute to this tropical biodiversity. Capable of dispersing exceptional distances, these squirrels diversified rapidly after colonising the Central and South American tropics. We compared DNA sequence signals with morphological signals using images of skulls and computational simulations. Genetic data indicated that tree squirrels dispersed gradually across the northern Hemisphere. In Central and South America, however, tree squirrels formed two separate groups that split from a common ancestor. By simulating where the ancestors began to diverge, we identified the tropical forests in the foothills of the Andes in western Amazonia

to be the epicentre of tree squirrel speciation in South America. A comparison of genetic data and morphology revealed one major discrepancy, i.e. species from the genus *Microsciurus* were represented by a single clade morphologically but originated from multiple genetic lineages. The feeding preferences of *Microsciurus* species are unusual among tree squirrels as they glean bark and feed on insects. This feeding strategy is so remarkable that modeling of the morphology-diet relationship indicated that *Microsciurus* sp. were the only species group with a direct link between skull shape and diet. Our findings suggests that the current designation of *Microsciurus* sp. into a genus reflects convergent ecologically-driven changes in morphology, wherein diet has driven skull shape regardless of relatedness.



PEČNEROVÁ P, MORAVEC JC, MARTÍNKOVÁ N, 2015. A skull might lie: modelling ancestral ranges and diet from genes and shape of tree squirrels. *Systematic Biology* 64: 1074-1088.

The Central American variegated squirrel (*Sciurus variegatides*). Tree squirrels that colonised South America show dramatic diversification in feeding specialisation.

(Photo by Tomáš Bartonička, design N. Martínková)

Genomic dissection of barriers to gene flow in hybridising fire-bellied toads

'Proper' biological species are not supposed to interbreed; nevertheless, some occasionally do and, as a result, offer insights into key evolutionary processes. Recombinant hybrids allow us to dissect the genetics underpinning how organisms adapt to different habitats and how such divergent adaptation builds up barriers to gene exchange. The fire-bellied toads *Bombina bombina* and *B. variegata* provide a classic example, with narrow hybrid zones harbouring an abundance of recombinant genotypes forming wherever their distribution ranges adjoin. Despite this, population genetic analysis predicts that such contact zones should act as strong barriers to gene flow. In order to test this prediction, we derived a large, high-confidence set of orthologous genes from *de novo* transcriptome assemblies of the two species. We fitted a range of divergence models to the observed patterns of variation and tested their relative support with analytic likelihood computations. There was clear evidence of gene flow between the two species since the species split about 3.3 million years ago, though the estimate was very low ($M = 4N\mu m = 0.015$ per generation, from *B. bombina* to *B. variegata*). Samples for this study had been collected from either side of the well-studied Kraków transect, at a distance of only a few dozen dispersal ranges. In agreement with theoretical predictions, we found no evidence for recent gene flow via this hybrid zone, which formed about 8,000 years ago. In fact, the rate of gene flow ($m \sim 10^{-6}$) was so low

that adaptive divergence of the taxa should proceed essentially unhindered by the lack of reproductive isolation. We conclude that the extended distribution ranges of *B. bombina* and *B. variegata* not only bolster taxon persistence in the face of small-scale environmental perturbations but also remove the commonly assumed antagonism between gene flow and adaptive divergence. Furthermore, under such para-allopatric conditions, any speciation mechanism can contribute to the build-up of reproductive barriers and the relative contribution from ecological divergence needs to be established empirically. In order to estimate this contribution, we aim to map (a) adaptively diverged traits, and (b) fitness effects disfavouring hybrids or immigrants in the *Bombina* genome. Co-location of these two features would suggest a causal link between ecological divergence and reproductive isolation. As a prerequisite, we are in the process of generating a dense genetic linkage map. We have sequenced the ~7Gb *Bombina* genome to 80x coverage with Illumina short reads and have generated a first-pass assembly that spans 4.6Gb. With the help of the existing orthologous gene sets, we are identifying single-copy genome segments that serve as templates for molecular baits. These will be used to enrich sequencing libraries in an F2 cross (linkage map) which will then be applied to a large archive of existing samples from field collections and laboratory crosses.

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The fire-bellied toads *Bombina bombina* (on the picture) and *B. variegata* commonly hybridise in contact zones.

(Photo by V. Gvoždík)

Non-native gobies in European rivers

Since the 1990s, five Ponto-Caspian gobiid species (round goby [*Neogobius melanostomus*], Western tubenose goby [*Proterorhinus semilunaris*], big-head goby [*Ponticola kessleri*], monkey goby [*N. fluviatilis*], racer goby [*Babka gymnotrachelus*]) have extended their distribution throughout Europe, principally through introduction by shipping ballast water at inland ports followed by establishment and population expansion. Of these, round goby and tubenose goby are now common in the Rivers Morava and Dyje, and a population of round goby has recently been identified in the River Labe/Elbe.

Contrary to expectations, our long-term research strongly suggests that invasive non-native gobiids do not represent any immediate threat to native fish assemblages in Central European rivers, though the outlook for any future impact remains unclear. While gobies have had a negative impact on fish food density (local macrozoobenthos reduced by around 30 %), for example, river productivity in our study area appears high enough to prevent any competition with native species. Diet analysis has shown little or no evidence for predation on eggs or larvae of native fishes, one of the main impacts predicted by North American studies. Analysis of predator diet indicates that gobies have become an important new food source for at least seven native piscivorous fish species. While gobies show high susceptibility to three local parasites, suggesting they may act as parasite reservoirs with the potential to affect local parasite dynamics, they do not appear to represent any danger to native fish assemblages

through introduced parasites or disease. Further, any advantage gained by parasite loss during the initial stages of goby invasion diminishes relatively quickly due to acquisition of local parasite species. Finally, we found no evidence for either a niche shift or a drop in abundance in native fishes after invasion, despite gobies quickly coming to dominate the local fish assemblage. Our results suggest that the successful invasion of (mainly channelised) Czech and Central European rivers by gobiid species is related to exploitation of an under-utilised niche space, i.e. rip-rap bank stabilisation. Increasing boat traffic on navigable European rivers has negatively affected river shoreline habitat for native fishes through wave action, water level instability and reduction of macrophyte cover and habitat diversity. Intensive navigation has also supported the spread of gobies far from their native range through transport in ballast water, while channelisation and rip-rap bank stabilisation have supported their rapid establishment by providing an excess of suitable shelter and spawning sites.

At present, non-native gobies do not appear to pose any major negative threat to native fish assemblages, as previously reported for the Great Lakes of North America, suggesting that different ecological processes may be involved. Further studies are needed to identify these processes, thereby widening our knowledge of the behaviour of these invasive species under different environmental conditions and potentially allowing us to predict and/or prevent any future impacts in European waters.

Since its arrival in 2008, the invasive round goby has become a common species along the lower River Dyje (Czech Republic) and is often caught by anglers.

(Photo by L. Mikl)



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Parasites and diseases

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PARASITES AND DISEASES

Vitamin B2 damages skin during fungal infection of hibernating bats

Hibernating bats infected with the fungal disease commonly known as white nose syndrome (WNS) show enormous differences in survival. Adverse population-level effects differ considerably, both between North American and Eurasian bats and between the species affected. We hypothesised that environmental, behavioural and molecular mechanisms affect the interaction dynamics between host and pathogen, and thus the progress of WNS. We found that *Pseudogymnoascus destructans*, the fungus that causes WNS, also occurs in hibernating Palearctic bats, but that hibernation behaviour (including hibernation pattern, clustering and shelter selection) remains stable in the presence of WNS, thereby potentially helping to ensure lower infection impact. We identified a surprisingly important virulence factor that may

be responsible for the skin damage commonly seen in infected bats: vitamin B2. The pathogenic fungus *P. destructans* produces excess vitamin B2 as a byproduct, which the bats are unable to metabolise while hibernating. This then accumulates in the skin, damaging the cells. Pathogen transmission between hosts can occur through both direct and indirect contact, potentially further exacerbated by ectoparasites. Although prevalence of WNS is high in the Palearctic, mortality is sporadic and Palearctic bat species appear able to tolerate high loading by the fully virulent fungus. This strongly suggests an established evolutionary balance in the host-pathogen system, providing putative hope for Nearctic bat populations following WNS invasion.

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Excessive accumulation of vitamin B2 in lesions damages tissues at high concentrations and causes fluorescence under ultra-violet light. This discovery has shed light on the pathomechanism of white nose syndrome in bats and has unified existing theories.

(Photo by J. Pikula)



Malaria infections in wild great apes

In Africa, the range of non-human primates overlaps with areas where *Plasmodium* infection is endemic in humans. This led to concerns that these primates may represent a source of infection for humans, though supporting data were lacking. The newly introduced method of non-invasive faecal sampling, in combination with molecular diagnostic tools, now allows straightforward detection of circulating *Plasmodium* species and the study of the pathogen's genetic diversity and ecology. We studied the diversity and prevalence of *Plasmodium* sp. in western lowland gorillas (*Gorilla gorilla gorilla*) and human sharing habitats within the Dzanga-Sangha Protected Area (Central African Republic) and in two eastern chimpanzee (*Pan troglodytes schweinfurthii*) populations inhabiting different habitat types in the Kalinzu Forest Reserve in Uganda (forest) and the Issa Valley in Tanzania (savannah). Based on a *cytb* PCR assay, 32% of gorilla faecal samples and 43% of human blood samples were infected

with *Plasmodium* spp. In comparison, while 20% of Kalinzu chimpanzee faecal samples were positive for *Plasmodium* DNA, no positive samples were detected in Issa Valley chimpanzee faecal samples. *Plasmodium praefalciparum* was only present in habituated gorillas, while *P. falciparum* was only detected in human samples. Though a few *P. vivax* and *P. ovale* sequences were obtained from gorillas, evidence for cross-species transmission between humans and gorillas will require more in-depth analysis. Phylogenetic analysis of *cytb* sequences revealed that previously known host-specific *Laverania* species are circulating in Kalinzu chimpanzees and Dzanga-Sangha gorillas. Age was the only factor significantly influencing infection, with younger individuals more susceptible to infection than adults. Sex of individuals had no effect. We observed some evidence of *Plasmodium* spp. switching.

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An eastern chimpanzee (*Pan troglodytes schweinfurthii*) from the Issa community in Uganda, Tanzania.

(Photo by J. Hošek)

Gut microbiome and metabolome of wild gorillas

To improve our understanding of current gut microbiome configurations and diet-microbe co-metabolic fingerprints in primates from an evolutionary perspective, we characterised faecal bacterial communities and metabolomic profiles for lowland and mountain gorillas (*Gorilla gorilla gorilla* and *G. beringei beringei*, respectively). Our results demonstrate that the gut microbiomes and metabolomes of these two species exhibit significantly different patterns. This is supported by the increased abundance of metabolites and bacterial taxa associated with fibre metabolism in mountain gorillas, and enrichment of markers associated with simple sugar, lipid and sterol turnover in the lowland species. Both species' microbiomes

and metabolomes converge, however, when the hosts face similar dietary constraints associated with low fruit availability. We suggest that dietary constraints triggered during their adaptive radiation were potential factors behind the species-specific microbiome patterns observed in primates today. The gut microbiome of a lowland gorilla group under increased anthropogenic pressure should always be distinguishable from that of other lowland groups. We also investigated the effect of antibiotic treatment (cephalosporin) on the microbiome of a wild lowland gorilla group, the results indicating that the antibiotic impacts gut microbiome stability and the relative abundance of bacterial taxa within the colonic ecosystem.

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GOMEZ A, ROTHMAN JM, **PETRŽELKOVÁ K**, YEOMAN CJ, VLČKOVÁ K, UMANA JD, CARR M, MODRÝ D, TODD A, TORRALBA M, NELSON KE, STUMPF RM, WILSON BA, BLEKHMANN R, WHITE BA, LEIGH SR, 2016. Temporal variation selects for diet-microbe co-metabolic traits in the gut of *Gorilla* spp. *The ISME Journal* 10: 514-526.

VLČKOVÁ K, GOMEZ A, **PETRŽELKOVÁ K**, WHITTIER CA, TODD AF, YEOMAN CJ, NELSON KE, WILSON BA, STUMPF RM, MODRÝ D, WHITE BA, LEIGH SR, 2016. Effect of antibiotic treatment on the gastrointestinal microbiome of free-ranging western lowland gorillas (*Gorilla g. gorilla*). *Microbial Ecology* 72: 943-954.

A western lowland gorilla (*Gorilla g. gorilla*) silverback male from the Dzanga Sangha Protected Area in the Central African Republic

(Photo by K. Phillips)



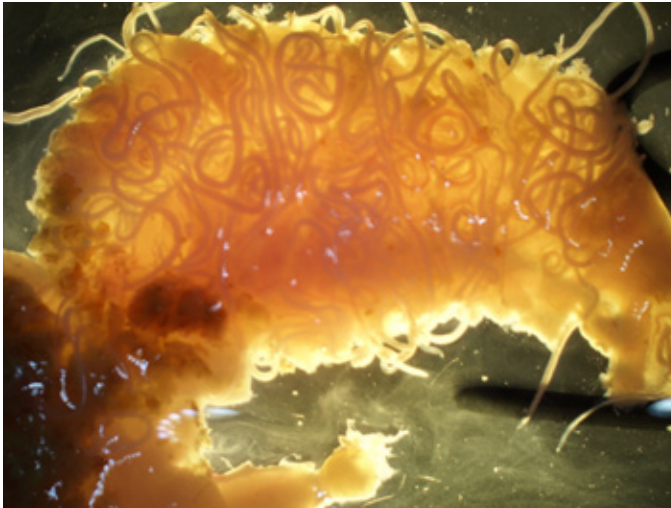
Parasites at host contact zones

When a pair of host taxa become isolated, diverge and then come back into contact, it is likely that intimate parasites, which will have co-evolved with the host during the period of isolation, will also meet and hybridise. Mechanisms determining whether parasites cross their host-species' secondary contact barriers are poorly understood. Parasite traits such as lack of intermediate host or free-living stage have been proposed as 'intimacy' factors, forcing parasites to follow the evolutionary history of their hosts closely. 'Intimately' associated hosts and parasites might then be expected to show similar genetic structure patterns. We compared host-parasite genetic structure

of two mouse parasite species with no intermediate host, a DNA virus, the murine cytomegalovirus (MCMV) and the whipworm *Trichuris muris* across a transect in the European house mouse (*Mus musculus*) hybrid zone. Our results indicate that parasite introgression is correlated with the degree of intimacy, with intimate parasites, such as MCMV, strongly structured with the host while generalist parasites, such as whipworms, show no host-correlated structure. In the latter species, passage through alternate hosts is sufficiently common to erase any genetic structure signal associated with particular host taxa.

GOÛY DE BELLOCQ J, BAIRD SJE, ALBRECHTOVÁ J, SOBEKOVÁ K, PIÁLEK J, 2015. Murine cytomegalovirus is not restricted to the house mouse *Mus musculus domesticus*: prevalence and genetic diversity in the European house mouse hybrid zone. *Journal of Virology* 89: 406-414.

WASIMUDDIN W, BRYJA J, RIBAS A, BAIRD SJE, PIÁLEK J, GOÛY DE BELLOCQ J, 2016. Testing parasite "intimacy": the whipworm *Trichuris muris* in the European house mouse hybrid zone. *Ecology and Evolution* 6: 2688-2701.



A case of hyper-infection with the nematode *Trichuris muris* in the caecum of a wild house mouse in the Bavarian-Bohemian transect of the European house mouse hybrid zone (2009). The caecum has been longitudinal sliced and unfolded revealing the worms with their heads and filamentous anterior portions embedded in the mucosal epithelium of their host.

(Photo by J. G. de Bellocq)

Genomic characterisation of rodent-borne RNA viruses in Africa

Rodents are reservoirs of RNA viruses such as the hantaviruses (family Bunyaviridae) or mammarenaviruses (family Arenaviridae). While some of these are etiologic agents of haemorrhagic fevers and can cause serious health issues in humans, they

have been largely overlooked in the African continent until recently. We screened tissue samples collected under the framework of a small African mammal biogeographic study for the presence of these two viruses types. In doing so, we discovered

a new mammarenavirus, Gairo (GAIV), in Natal multimammate mice (*Mastomys natalensis*) from Tanzania, and a new hantavirus, Tigray, in Ethiopian white-footed mice (*Stenocephalemys albipes*) in Ethiopia. We fully characterised their genomes using high throughput sequencing before performing phylogenetic analyses. Surprisingly, GAIV is not closely related with Morogoro virus, which infects *M. natalensis* only 90 km south of the local-

ity where Gairo virus was discovered, but clusters phylogenetically with the Mobala-like viruses that infect non-*M. natalensis* host species in the Central African Republic and Ethiopia. Phylogenetic analysis of the Tigray virus revealed an original position for this new virus, with its S segment basal to the Murinae-associated hantaviruses but its M and L segments basal to hantaviruses associated with shrews and moles.

GRYSEELS S, RIEGER T, OESTEREICH L, CUYPERS B, BORREMANS B, MAKUNDI R, LEIRS H, GÜNTHER S, GOÛY DE BELLOCQ J, 2015. Gairo virus, a novel arenavirus of the widespread *Mastomys natalensis*: Genetically divergent, but ecologically similar to Lassa and Morogoro viruses. *Virology* 476: 249-256.

GOÛY DE BELLOCQ J, TĚŠÍKOVÁ J, MEHERETU Y, ČÍŽKOVÁ D, BRYJOVÁ A, LEIRS H, BRYJA J, 2016. Complete genome characterisation and phylogenetic position of Tigray hantavirus from the Ethiopian white-footed mouse, *Stenocephalemys albipes*. *Infection, Genetics and Evolution* 45:242-245.

Dissection of rodents in Tanzania.

(Photo by S. Gryseels)



ECIP – European Centre of Ichthyoparasitology

The European Centre of Ichthyoparasitology (ECIP) was instigated as a means of promoting innovation and improved complementarity in ichthyoparasitological research, encouraging new young researchers and increasing mutual collaboration between the Department of Botany and Zoology, Masaryk University; the Institute of Parasitology, Czech Academy of Science Biological

Centre; and the Institute of Vertebrate Biology (IVB), Czech Academy of Science. ECIP's research is organised into four basic modules: (a) parasite diversity and adaptation to parasitism; (b) phylogenetics and molecular taxonomy; (c) host-parasite relationships and molecular interactions, and (d) evolutionary epidemiology and behavioural ecology of parasites. Each module utilises a wide

range of methodological approaches to study eight basic model parasite groups and their host fishes. Over 2015-2016, the IVB team focused on the parasite diversity of invasive European species and monogenean and acanthocephalan parasite diversity in African freshwater fishes. We described a range of new species and new host records from Africa, as well as co-introduction of new parasites into Europe. Our results highlight the importance of fish host ecology and phylogeny for parasite diversity.

We undertook a number of methodological studies to assess the effect of fish sampling method, fish storage method and use of preservation media on the results of fish parasite surveys. The results indicated serious information loss when using gill- or seine-nets (compared with electro-

fishing), when storing live fish for more than three days prior to dissection, or when using preservation media to store fish for later parasitological examination.

We also showed that non-native species represent a potentially significant threat to recipient systems, not only through competition or direct predation but also via parasite interaction. We demonstrated that early life stages of invasive round (*Neogobius melanostomus*) and tubenose (*Proterorhinus semilunaris*) gobies represent a novel, abundant and 'attractive' resource for both native and invasive unionid glochidia. As such, unionids could negatively affect gobiid recruitment through infection-related mortality, with a potential positive effect on unionid populations.

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KVACH Y, JIRKŮ M, SCHOLZ T, 2016. Acanthocephalans of the genus *Megistacantha* Golvan, 1960 (Palaeacanthocephala: Rhadinorhynchidae) in two African mormyrid fishes (Actinopterygii: Mormyridae). *Systematic Parasitology* 93: 927-933.

KVACH Y, ONDRAČKOVÁ M, JANÁČ M, JURAJDA P, 2016. Methodological issues affecting the study of fish parasites. I. Duration of live fish storage prior to dissection. *Diseases of Aquatic Organisms* 119: 107-115.

KVACH Y, ONDRAČKOVÁ M, JANÁČ M, JURAJDA P, 2016. Methodological issues affecting the study of fish parasites. II. Sampling method affects ectoparasite studies. *Diseases of Aquatic Organisms* 121: 59-66.

KVACH Y, ONDRAČKOVÁ M, JURAJDA P, 2016. First report of metacercariae of *Cyathocotyle prussica* parasitising a fish host in the Czech Republic, Central Europe. *Helminthologia* 53: 257-261.

ŠLAPANSKÝ L, JURAJDA P, JANÁČ M, 2016. Early life stages of exotic gobiids as new hosts for unionid glochidia. *Freshwater Biology* 61: 979-990.



Beach seining of fish for the study of host-parasite interactions in a reservoir

(Photo by M. Koničková)

Impact of zoonotic mosquito-borne viruses on human health

Mosquito-borne pathogens such as West Nile virus (WNV), Zika, Yellow fever and Chikungunya virus are now of growing importance due to their rapid and unpredictable spread in many countries worldwide. In Central Europe, mosquito-borne flaviviruses represent a major public health threat, with WNV and Usutu virus (USUV), both belonging to the Japanese encephalitis virus group (Flaviviridae), emerging in the last decade. We have concentrated our studies on WNV, the agent of West Nile fever, which was recently discovered in *Culex modestus* mosquitoes in South Moravia. Our results indicate potential new natural foci for this dangerous virus, along with descriptions of new potential vectors and reservoir hosts. First detected in the Czech Republic in 2014 and now emerging in mosquitoes from the same area, USUV also represents a potential human health threat.

In addition to studying mosquito vectors, we also examined arbovirus circulation in vertebrate hosts. Six captive Nestor kea (*Nestor notabilis*) developed mild to fatal neurological signs after becoming naturally infected with WNV lineage 2 in Vienna (Austria) in 2008. The WNV RNA persisted and the virus evolved in the birds' brains,

as demonstrated by (phylo) genetic analysis of the complete viral genome detected in kea euthanised between 2009 and 2014. Importantly, chronic WNV infection in the brain may contribute to circulation of the virus through oral transmission to predatory birds. We also examined common coots (*Fulica atra*) on Central Moravian fishponds for antibodies against WNV and USUV. Our results indicated that both WNV and USUV infections occur in common coots and that these birds may serve as 'sentinel' species, indicating the presence of these viruses at fishpond and wetland habitats in Central Europe. Concerning human cases of arbovirus infections, the detection of WNV in a blood donation originating from an area with low human WNV prevalence was surprising and emphasises the importance of WNV nucleic acid testing of blood donations, even in such areas. Summing up, epidemiological surveillance of mosquito vectors, reservoir vertebrate hosts and humans for arboviruses represents a sensitive tool for evaluating virus circulation and pathogen emergence and spread, along with an estimation of public health risk.



Ovitraps are important tools for collecting immature stages of invasive mosquito species.

(Photo by I. Rudolf)

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STRAKOVÁ P, ŠIKUTOVÁ S, JEDLIČKOVÁ P, SITKO J, RUDOLF I, HUBÁLEK Z, 2015. The common coot as sentinel species for the presence of West Nile and Usutu flaviviruses in Central Europe. *Research in Veterinary Science* 102: 159-161.

BAKONYI T, GAYDON GK, SCHWING R, VOGL W, HÄBICH A-C, THALLER D, WEISSENBOCK H, RUDOLF I, HUBÁLEK Z, NOWOTNY N, 2016. Chronic West Nile virus infection in kea (*Nestor notabilis*). *Veterinary Microbiology* 183: 135-139.

Emerging tick-borne pathogens on the rise

Ticks, as vectors of several emerging zoonotic pathogens, represent an important and increasing threat for human and animal health in Europe. Appreciation of complex systems (including the tick microbiome) is expanding our understanding of tick-borne pathogens, leading us to evolve a more integrated view that embraces the 'pathobiome'; the pathogenic agent integrated within its abiotic and biotic environments. Of the emerging tick-borne infections, tick-borne rickettsioses increasingly represents a significant human health threat. Consequently, we have focussed our 'tick-borne research' at prevalence studies of human pathogenic bacteria (*Rickettsia* spp., *Babesia* spp., *Neoehrlichia* spp., *Hepatozoon* spp.) in a range of tick vectors (*Ixodes ricinus*, *I. minor*, *Dermacentor reticulatus*, *Amblyomma longirostre* and *A. sabanerae*). In a pooled set of fields in Austria, we collected *Rickettsia raoultii*, the causative agent of tick-borne lymphadenopathy, from *D. reticulatus* ticks for the first time. In similar study, we also provided first evidence for the occurrence of human pathogenic *R. raoultii* in a *D. reticulatus* population in the Czech Republic. In an eco-epidemiological study, we screened 2473 questing and 199 engorged *I. ricinus* ticks for the presence of the neglected *Rickettsia* spp., 'Candidatus *Neoehrlichia mikurensis*', *Anaplasma phagocytophilum* and *Babesia* spp. All species were present at all study sites. Screening for apicomplexan parasites using PCR amplification and sequencing of 18S rRNA gene fragments revealed the presence of *Hepatozoon* DNA in questing *I. ricinus* ticks from south-western Slovakia and the Czech Republic, respectively. *Hepatozoon* DNA was also detected in the spleen and/or lungs of rodents trapped in south-

western Slovakia. Further molecular and ecological studies are necessary to identify the taxonomic status of *Hepatozoon* species parasitising rodents in Europe and host-parasite interactions in natural foci. We also documented first evidence for the occurrence of *B. venatorum* and *B. capreoli* in host-seeking *I. ricinus* ticks in the Czech Republic. Vertebrate serosurveys for zoonotic tick-borne pathogens represent an essential tool for monitoring natural foci of infections.

Infection of humans with tick-borne Crimean-Congo hemorrhagic fever virus can cause severe hemorrhagic fever with fatality rates of up to 80%. Since domestic ruminants play a crucial role in the life cycle of the vector ticks and transmission and amplification of the virus, antibody prevalence in these animals is a good indicator for its presence in the region. Our results highlight the risk of human infection in Bulgaria and Turkey and the importance of investigating prevalence in animals for identification of risk areas. Finally, sera from healthy Czech individuals aged between 10 and 59 were randomly selected from the general population during repeated cross-section surveys in the 1980s and in 2001 and screened for the presence of antibodies against tick-borne encephalitis virus. Age-specific antibody trends in adult age groups during both periods suggest that neither clinically manifested nor non-apparent encephalitis cases induce lifelong immunity, though they are likely to reflect the previous epidemiological situation. In summary, monitoring of neglected tick-borne pathogens, including their tick vector vertebrate hosts, as part of epidemiological surveillance is an important tool for the prevention and control of human tick-borne infections.

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VAYSSIER-TAUSSAT M, KAZIMÍROVÁ M, HUBÁLEK Z, HORNOK S, FARKAS R, COSSON J-F, BONNET S, VOURCH G, GASQUI P, MIHALCA AD, PLANTARD O, SILAGHI C, CUTLER S, RIZZOLI A, 2015. Emerging horizons for tick-borne pathogens: from the "one pathogen-one disease" vision to the pathobiome paradigm. *Future Microbiology* 10: 2033-2043.

VENCLÍKOVÁ K, MENDEL J, BETÁŠOVÁ L, HUBÁLEK Z, RUDOLF I, 2015. First evidence of *Babesia venatorum* and *Babesia capreoli* in questing *Ixodes ricinus* ticks in the Czech Republic. *Annals of Agricultural and Environmental Medicine* 22: 212-214.

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HAMŠÍKOVÁ Z, SILAGHI C, RUDOLF I, VENCLÍKOVÁ K, MAHRÍKOVÁ L, SLOVÁK M, MENDEL J, BLAŽEJOVÁ H, BERTHOVÁ L, KOCIANOVÁ E, HUBÁLEK Z, SCHNITTGER L, KAZIMÍROVÁ M, 2016. Molecular detection and phylogenetic analysis of *Hepatozoon* spp. in questing *Ixodes ricinus* ticks and rodents from Slovakia and Czech Republic. *Parasitology Research* 115: 3897-3904.

RUDOLF I, VENCLÍKOVÁ K, BLAŽEJOVÁ H, BETÁŠOVÁ L, MENDEL J, HUBÁLEK Z, PAROLA P, 2016. First report of *Rickettsia raoultii* and *Rickettsia helvetica* in *Dermacentor reticulatus* ticks from the Czech Republic. *Ticks and Tick-borne Diseases* 7: 1222-1224.

VENCLÍKOVÁ K, MENDEL J, BETÁŠOVÁ L, BLAŽEJOVÁ H, JEDLIČKOVÁ P, STRAKOVÁ P, HUBÁLEK Z, RUDOLF I, 2016. Neglected tick-borne pathogens in the Czech Republic, 2011–2014. *Ticks and Tick-borne Diseases* 7: 107-112.

MERTENS M, SCHUSTER I, SAS MA, VATANSEVER Z, HUBÁLEK Z, GÜVEN E, DENIZ A, GEORGIEV G, PESHEV R, GROSCUP MH, 2016. Crimean-Congo hemorrhagic fever virus in Bulgaria and Turkey. *Vector-Borne and Zoonotic Diseases* 16: 619-623.

Tick collection is an essential tool for monitoring tick-borne infections.

(Photo from archive of I. Rudolf)



4. OTHER ACTIVITIES

| POPULARISATION ACTIVITIES AND COLLABORATION WITH UNIVERSITIES AND HIGH SCHOOLS

BIOM: Mohelský mill Biodiversity education centre



The BIOM project, supported through EEA Grants 2009-2014, helps facilitate collaboration between the IVB and universities, high schools, nature conservation organisations and the public.

The BIOM project focuses on biodiversity education and improving networking between scientific researchers, nature protection management and conservation policy makers. The IVB facilitates such networking activities through its extensive experience in research and education, and by putting scientific results into conservation practice. The National Animal Genetic Bank (see below), which is being created within the framework of this project, also relies on good co-operation between the various zoological and conservation organisations. Most of the project activities are held at the Mohelský Mill Field Station. This site is ideal for hosting a wide range of educational programs, which are individually prepared for different target groups in accordance with the Strategy for Sustainable Development and the Concept of Environmental Education and Public Awareness in the Highlands Region.

A main aim of the BIOM project has been to establish a regional educational centre for the study of biodiversity dynamics, with the aim of increasing biodiversity awareness in students of all educational levels, conservation professionals and the general public. An interactive approach is used to increase motivation and awaken interest in biodiversity conservation.

Over 2015-2016, 848 people attended around 32 activity sessions organised by the project, including seminars, field excursions and workshops. A public educational trail has been constructed around Mohelský mill, as well as a field game and a map of regional producers of food.



An ornithological excursion at the Mohelno field station in April 2015.

(Photo from IVB archive)



Spring terrain excursion at the Mohelno field station in May 2015.

(Photo from IVB archive)



Spring terrain excursion at the Mohelno field station in May 2015.

(Photo from IVB archive)



Field excursion for the public at the Mohelenská Serpentine Steppe National Nature Reserve in June 2016.

(Photo from IVB archive)

Foundation of the National Animal Genetic Bank – a useful tool for zoological research and species conservation



National Animal Genetic Bank • CZ

The National Animal Genetic Bank (NAGB) was established in 2015 by the IVB and the Department of Zoology (Faculty of Science) of Charles University in order to provide genetic material for research and present genetic data publicly. Prior to this, there had been no collection of wild animal genomic material in the Czech Republic, despite the increasing importance of genetics and genomics in zoological research over recent decades. The NAGB represents a network of organisations that share an interest in the long-term preservation of animal genomic material and the presentation of associated data. It seeks to contribute to the development of member collections by sharing experience and jointly addressing technical, legal and financial issues related to the long-term storage of genomic material. At present, in addition to the two founder organisations, the NAGB has three additional full members (Mendel University in Brno, NaturaServis Ltd., and the Comenius

Museum Ornithological station in Přerov) and ten supporting organisations providing genomic samples. Other organisations storing genetic samples are encouraged to become base members and individual researchers, animal rescue station workers, museum and state nature conservation zoologists and hunters are invited to contribute material to the bank by providing samples from either completed research projects or from vertebrate carcasses. The Institute of Vertebrate Biology provides support to the NAGB secretariat, which provides administrative support and communication services for current and prospective members and cooperates closely with the Global Genome Biodiversity Network, an international biobanking initiative. At the end of 2016, data on the first 1500 samples was presented through the NAGB Data Portal, accessible from the NAGB website (<http://www.ngbz.cz/>), with thousands more samples waiting to be processed. The NAGB aims to contribute to the development of zoological research in the Czech Republic by making the largest possible number of existing animal genomic samples available. Further, it aims to benefit Czech species conservation by continuously collecting new samples from the Czech fauna, thus enabling monitoring of changes in species and population genetic diversity over time.

The NAGB was established with financial support from EEA Grants 2009-2014, the Vysočina Region and Strategy AV21 of the Czech Academy of Sciences, and the Diversity of Life and Health of Ecosystems Research Programme (ROZE).



Several seminars focused on the role of biobanking in zoological research and species conservation were organised for Czech zoologists, conservationists and policy makers from a range of organisations such as natural history museums, research institutions, state nature conservation and nature conservation NGOs and animal rescue stations, with the aim of building a National Animal Genetic Bank network of sample providers.

(Photo by P. Hájková)



Animals killed on the roads, that die in rescue stations or are found dead in the wild are a valuable source of material for genetic analysis. Tissue sample sent to the genetic bank can facilitate future zoological research.

(Photo by J. Roleček)



A pinhead sized piece of animal tissue is sufficient for DNA extraction. Consequently, samples at the genetic bank can be used for dozens of DNA extractions.

(Photo by B. Zemanová)

The Institute of Vertebrate Biology and Strategy AV21



The Czech Academy
of Sciences

Strategy AV21

Top research in the public interest

The IVB is an active institute within Strategy AV21, a new research strategy of the Academy of Sciences aimed at increasing direct contact and collaboration between the Czech Academy of Sciences and the wider application sector. As part of these efforts, several activities were performed over 2015-2016, or are planned for 2017, within the Diversity of Life and Health of Ecosystems Research Programme (= ROZE).

Besides the foundation of the National Animal Genetic Bank supported also by Strategy AV21 (see above), two popular science brochures for the public were published:

- (1) *Non-native species of fish in Czech waters*. Authors: P. Jurajda, Z. Adámek, Academia Publishing House, 2016. The aim of the guide is to briefly introduce the most important non-native fish presently found in Czech rivers, lakes and fishponds and to describe their influence on native species and the ecological functioning of aquatic ecosystems. In particular, the brochure presents some of the results of our ongoing research into the current spread of these non-native species, with examples of the potential hazards they pose.
- (2) *Invasive mosquito species as a potential risk for biodiversity and transmission of dangerous diseases*. Author: I. Rudolf, Academia Publishing House, 2017. The aim of this brochure is to create a platform for subsequent cooperation between the Academy of Sciences, the South Moravian Regional Hygiene Station, the State Health Institute, the City of Brěclav and the Regional Authority of the South Moravian Region. These bodies will coordinate activities aimed at reducing the occurrence of dangerous invasive mosquito species (especially *Aedes albopictus*) and introducing measures to reduce the risk of transmission of dangerous diseases.

Other activities planned for 2017:

- Field excursions for members of the public and primary and secondary school students. These field excursions are designed to explain the role and relevance of biological research for society at large.
- Breeding of unique domestic and related mouse strains. The aim of this project is to combine two large collections of inbred house mouse (*Mus musculus*) strains, along with other closely related species of the genus *Mus*, in order to preserve as many as 60 wild-derived strains representing genetic variability comparable to that found in wild populations.



For several years now, the non-native round goby (*Neogobius melanostomus*) has been a common catch of fishermen in the lower stretches of the Rivers Dyje and Moravia.

(Photo by P. Jurajda)

| MEETINGS ORGANISED BY THE INSTITUTE

“Zoological Days” Conference 2015 (Brno) and 2016 (České Budějovice)

As in previous years, the IVB was the main organiser of the ‘Zoological days’ conferences in 2015 and 2016. The “Zoological days” conferences are a traditional and very popular meeting place for Czech and Slovak zoologists, organised in Brno since 1969. Since 2008, the conference has only been held in Brno every second year, and in other Czech university towns every other year.

In 2015, the conference was organised in collaboration with the Institute of Botany and Zoology of Masaryk University’s Faculty of Science. The conference took place at Masaryk University’s Faculty of Economics and Administration, which is an ideal site situated just next to the the IVB’s headquarters and provides a fine location for such a large and important conference. We welcomed a total of 482 zoologists to Brno in 2015. In 2016, the overall quality of the conference was again improved by organising it in partnership with the University of South Bohemia (Faculty of Science) in České Budějovice. In total, 504 people visited the 2016 conference.

In both years, before the two-day conference there was a pre-conference workshop focused on zoological research methodology (supported by the Education for Competitiveness Operational Programme). Both the number of participants and the number and quality of presentations unequivocally shows that the Zoological days have become a serious scientific event of importance to the whole Czech and Slovak zoological community.

For more information, please see: <http://zoo.ivb.cz/>



Students in the Institute’s library preparing conference materials used during the registration of participants for Zoological Days 2015.

(Photo by Z. Hladlovská)



Borja Jiménez-Alfaro (*Department of Botany and Zoology, Masaryk University*) during his lecture on the “Theory of statistical methods for ecological niche modeling and practicalities about general assumptions, methods and tools” presented at the 2015 pre-conference workshop in Brno.

(Photo by Z. Hladlovská).

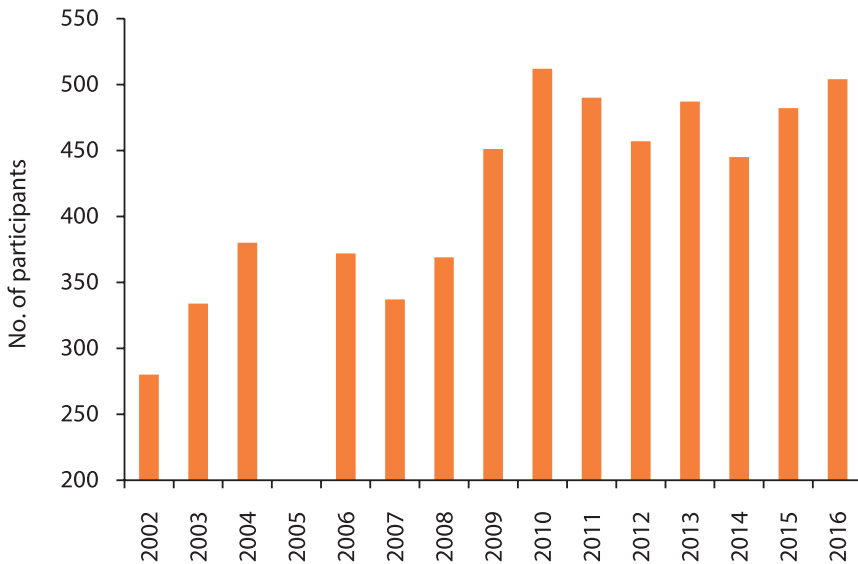
One day pre-conference student workshop in České Budějovice, focused mainly on approaches to studying animal behaviour in nature. The workshop was introduced by Radim Šumbera (Faculty of Science, University of South Bohemia).

(Photo by Z. Hladlovská)

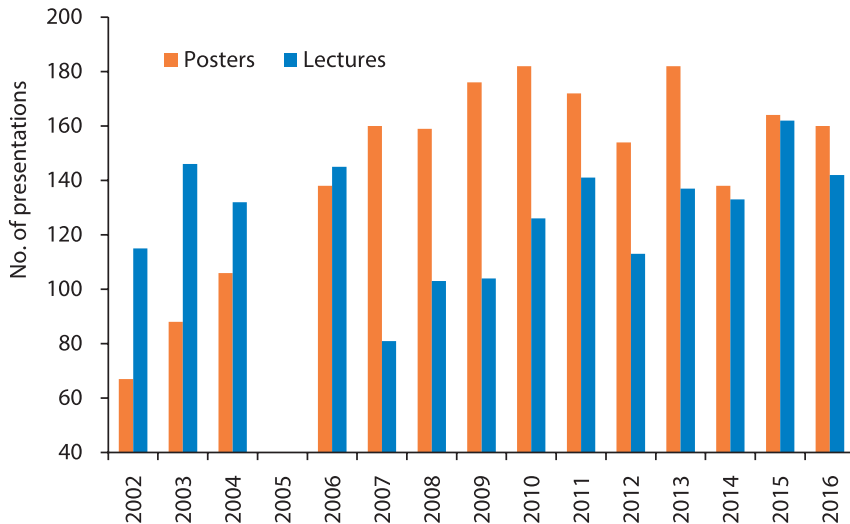


Zoological days 2016 at the Faculty of Science, University of South Bohemia, České Budějovice

(Photo by F. Sedláček)



The number of registered participants at the Zoological days has reached a plateau of 450-500 individuals. No conference was organised in 2005.



The Zoological days conference offers a unique opportunity to see hundreds of presentations covering all areas of zoological research performed in the Czech Republic and Slovakia over two days.

The BIOM Spring Camp

In April 2016, a five-day workshop for Czech Masters and PhD students was organised at the IVB's Studenec Research Facility focused on next-generation sequencing (NGS) methods and their application in conservation biology. Students were trained in the practical analysis of NGS data (e.g. metabarcoding, restriction site associated DNA [RAD] sequencing) under the supervision of experienced lecturers from both the Czech Republic and abroad (Stuart Baird, Reto Burri, Dagmar Čížková, Sophie Gryseels, Jakub Kreisinger, Michael Matschiner, Beate Nürnberger, Lubomír Piálek, Alexander Suh, Emiliano Trucchi). As part of the workshop, a number of presentations were given based on actual studies using NGS methods for conservation work, e.g. the use of metabarcoding in studies of environmental DNA by Pierre Taberlet from the University of Grenoble.

Forty-six students attended the event, with student accommodation provided by the Mohel'ský mill field station. The official language of the workshop was English.



Professor Pierre Taberlet (*on the left*), from the Université Joseph Fourier, Grenoble, presented outstanding examples of studies using environmental DNA for monitoring biodiversity.

(Photo by A. Bryjová)



Associate Professor Stuart J. E. Baird explained how to effectively analyse NGS data.

(Photo by A. Bryjová)

Open door days

Over the course of the Czech Republic 'Science and technology Week' (4-6/11/2015; 2-5/11/2016; 17-21/4/2016), the Czech Academy of Sciences opens its doors to the public in a series of open house events. All the research facilities of the IVB participate in the event and welcome a wide selection of the general public through their doors. Visitors gain an insight into the research taking place and the normal functioning of the laboratories and breeding facilities. In addition, talks are given on some of the more interesting foreign research expeditions undertaken by fellows of the Institute.

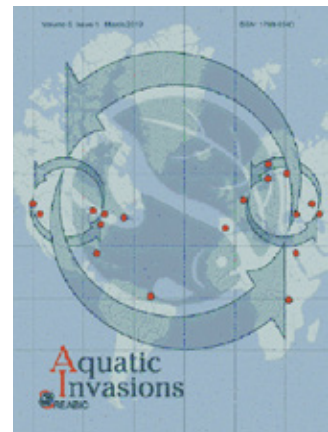


Photo by A. Bryjová

Photo by M. Čapek

MEMBERSHIP IN EDITORIAL BOARDS

A number of researchers at the IVB are members of the editorial boards of international peer-reviewed journals (e.g. Herpetology Notes, Cryobiology, International Journal of Primatology, Zoology and Ecology, Folia Zoologica, Comparative Cytogenetics, Mammal Research, Acta Zoologica Bulgarica, Archives of Biological Science...). Of particular note has been the appointment of research fellows to the important position of Associate Editor in such well-known journals as Evolutionary Ecology (M. Reichard), Evolution (S. J. E. Baird) and Aquatic Invasions (M. Janáč).

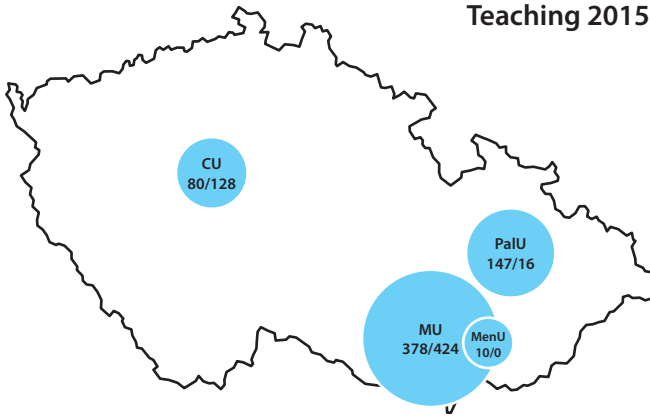


EDUCATION AND TEACHING ACTIVITIES

Teaching at universities

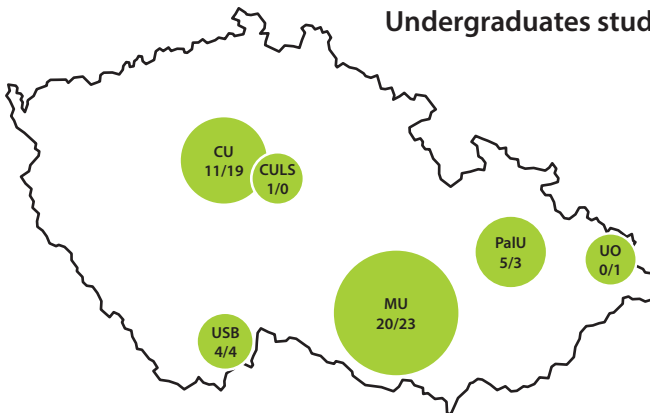
Employees of the IVB are very active in lecturing at five universities around the country, providing a total of 651 hours lecturing in 2015, and 556 hours in 2016. Many gradual students are also involved in research programs. In total, the Institute’s researchers supervised 41 Bachelor and 50 Masters students over 2015-2016. Seventeen students graduated in 2015 (nine Bachelors and eight Masters) and 16 students graduated in 2016 (nine Bachelors and seven Masters).

Teaching 2015/2016 (in hours)



MU = Masaryk University, Brno; MenU = Mendel University in Brno; PaU = Palacký University, Olomouc; CU = Charles University, Prague. Numbers in the circles indicate hours of lecturing in 2015/2016, respectively.

Undergraduates students 2015/2016



MU = Masaryk University, Brno; CU = Charles University, Prague; CULS = Czech University of Life Sciences, Prague; USB = University of South Bohemia, České Budějovice; UO = University of Ostrava; PaU = Palacký University, Olomouc. Numbers in circles indicate number of Bachelors/Masters students supervised at particular universities.

PhD students working at the Institute and/or supervised by the Institute's fellows

Over 2015-2016, researchers at the IVB supervised 54 PhD students, eight of which successfully defended their theses during that period.

Student	Supervisor or Consultant *	Start of the study	Defended the thesis	Faculty**
ABRAHAM Marek Mihai	Honza	2011		1
ADÁMKOVÁ Marie	Albrecht/Tomášek*	2013		1
AGHOVÁ Tatiana	Bryja	2012		1
ALBRECHTOVÁ Jana	Piálek	2007		2
BAINOVÁ Hana	Albrecht*	2011		2
BARTÁKOVÁ Veronika	Bryja/Reichard	2013		1
BARTOŇOVÁ-Marešová Eva	Mendel	2007		1
BENDOVÁ Martina	Tkadlec	2013		8
BETÁŠOVÁ Lenka	Rudolf	2016		1
BLAŽKOVÁ Barbora	Albrecht	2015		1
BOBEK Lukáš	Albrecht/Tomášek*	2013		1
BURGUNDER Jade	Petrželková	2013		1
ČEPELKA Ladislav	Heroldová*	2010	2015	4
ČÍŽKOVÁ Dagmar	Bryja	2006	2015	1
DAMUGI, Emmanuel Ira Dali	Tkadlec	2014		8
DOLINAY Matej	Gvoždík V	2015		1
ELFEKI Mohamed	Tkadlec	2011		8
GARCÍA Daniel	Reichard	2015		7
GAST Oliver	Baird*/Piálek*	2015		1
HÁNOVÁ Alexandra	Bryja*	2016		1
HLAVÁČ David	Adámek	2011	2015	6
CHRENKOVÁ Monika	Šálek	2011		5
JABLONSKI Daniel	Gvoždík V*	2013		11
JANČA Martin	Albrecht	2013		1
JELÍNEK Václav	Procházka	2010		2
KALOUSOVÁ Barbora	Petrželková*	2013		9
KLITSCH Marek	Koubek	2011		10
KRÁLOVÁ Tereza	Bryja/Albrecht*	2012		1
KRÁSOVÁ Jarmila	Bryja*	2015		5
KRISTIN Peter	Gvoždík L	2011	2015	1

Student	Supervisor or Consultant *	Start of the study	Defended the thesis	Faculty**
KRKAVCOVÁ Eva	Javůrková*	2012		2
MARTINCOVÁ IVA	Piálek	2012		1
MAZOCH Vladimír	Bryja*	2009		5
MICHÁLKOVÁ Romana	Albrecht	2012		2
MICHÁLKOVÁ Veronika	Ondračková/Reichard*	2012		1
MIKL Libor	Adámek	2012		1
MIKULA Peter	Albrecht	2015		2
OPATOVÁ Pavlína	Albrecht	2012		1
PAVLISKA Petr	Šálek	2015		5
PAVLUVČÍK Petr	Tkadlec	2010		8
PRAVDOVÁ Markéta	Ondračková	2015		1
RYBNIKÁR Juraj	Prokeš*	2010	2016	3
SCHULZ Doreen	Petrželková	2013		1
SOSNOVCOVÁ Kateřina	Procházka/Koleček*	2015		2
SOUDKOVÁ Martina	Albrecht	2011		2
STRAKOVÁ Petra	Hubálek	2013		1
ŠLAPANSKÝ Luděk	Jurajda	2012		1
ŠULC Michal	Honza	2012	2016	2
TĚŠÍKOVÁ Jana	Goüy de Bellocq/Bryja*	2014		1
TOMÁŠEK Oldřich	Albrecht	2009		2
TURBAKOVÁ Barbora	Bryja/Krojerová*	2015		1
URBÁNKOVÁ-Stierandová Soňa	Mendel	2010	2016	1
VENCLÍKOVÁ Kristýna	Rudolf	2011	2015	1
VLČKOVÁ Klára	Petrželková	2012		9
Total 54			8	

** 1 = Faculty of Science, Masaryk University, Brno; 2 = Faculty of Science, Charles University, Prague; 3 = Faculty of Agronomy, Mendel University in Brno; 4 = Faculty of Forestry and Wood Technology, Mendel University in Brno; 5 = Faculty of Science, University of South Bohemia, České Budějovice; 6 = Faculty of Fisheries and Protection of Waters, University of South Bohemia, České Budějovice; 7 = Universidad de la República, Montevideo, Uruguay; 8 = Faculty of Science, Palacký University in Olomouc; 9 = Faculty of Veterinary Medicine, University of Veterinary and Pharmaceutical Sciences, Brno; 10 = Faculty of Forestry, Wildlife and Wood Sciences, Czech University of Life Sciences, Prague; 11 = Faculty of Natural Sciences, Comenius University in Bratislava, Slovakia.

PhD theses defended over 2015–2016 and supervised by the Institute's fellows

- ČEPELKA Ladislav, 2015: *Selected aspects of small mammal ecology in relation to the variability of forest habitats*. [In Czech; Vybrané aspekty ekologie drobných savců ve vztahu k variabilitě lesních stanovišť]. Faculty of Forestry and Wood Technology, Mendel University in Brno. Supervisor: M. Heroldová.
- ČÍŽKOVÁ Dagmar, 2015: *Diversity and evolution of two MHC class II genes in wild populations of a model species, the house mouse*. Faculty of Science, Masaryk University, Brno. Supervisor: J. Bryja.
- HLAVÁČ David, 2015: *Influence of modified feed components on carp ponds on water quality in containers* [In Czech; Vliv příkrmování upravenými krmnými komponenty na kaprových rybnících na kvalitu vody v recipientech] Faculty of Fisheries and Protection of Waters, University of South Bohemia, České Budějovice. Supervisor: Z. Adámek.
- KRISTIN Peter, 2015: *Sources of variation in standard metabolic rate in newts* [In Czech; Význam metabolismu v termální ekologii ektotermů]. Faculty of Science, Masaryk University, Brno. Supervisor: L. Gvoždík.
- RYBNÍKÁR Juraj, 2016: *Breeding of sterlet (Acipenser ruthenus) in the Czech Republic* [In Czech; Chov jesetera malého (Acipenser ruthenus) v České republice.]. Faculty of Agronomy, Mendel University in Brno; Co-supervisor: M. Prokeš.
- ŠULC Michal, 2016: *Visual cues in the coevolution between brood parasites and their hosts* [In Czech; Optické podněty v koevoluci hnízdního parazita a jeho hostitelů]. Faculty of Science, Charles University, Prague. Supervisor: M. Honza.
- URBÁNKOVÁ-STIERANDOVÁ Soňa, 2016: *Molecular biodiversity inventory of selected fish species from families Cyprinidae and Umbridae* [In Czech; Inventarizace molekulární biodiverzity vybraných druhů ryb čeledi Cyprinidae a Umbridae]. Faculty of Science, Masaryk University, Brno. Supervisor: J. Mendel.
- VENCLÍKOVÁ Kristýna, 2015: *Ecology of tick-borne zoonotic microorganisms* [In Czech; Ekologie zoonotických mikroorganismů v klíšťatech]. Faculty of Science, Masaryk University, Brno. Supervisor: I. Rudolf.

| EDITORIAL ACTIVITIES

The Institute publishes the international journal *Folia Zoologica* jointly with the Faculty of Environmental Sciences of the Czech University of Life Sciences in Prague. The journal has a publishing tradition going back more than 80 years and is currently covered by many reference journals, including the Elsevier Bibliographic Database (Scopus) and the ISI Web of Knowledge by Thomson Reuters. Eight regular issues were published over 2015 and 2016. Altogether, 75 full papers appeared in the two previous volumes of *Folia Zoologica*, covering various areas of mammalogy, ornithology, herpetology and ichthyology.

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Aims & Scope

Folia Zoologica publishes articles containing original insights into various aspects of vertebrate zoology that have not previously been published and are not presently under consideration for publication elsewhere. The journal welcomes significant papers presenting new and original data of more than regional significance. Studies testing explicitly formulated hypotheses are preferred to those presenting primarily descriptive results. Review papers are particularly welcomed and should deal with topics of general interest or of current importance, being synthetic rather than comprehensive in emphasis. Authors should consult with the editors before submitting reviews.

The journal is published quarterly and one volume usually consists of four issues. However, additional issues may be published occasionally. There is no page charge except for colour pages and other extras.

Full papers published in *Folia Zoologica* are available on <http://www.ivb.cz/pubseren.htm> one year after publishing. *Folia Zoologica* is indexed by CAB Abstracts, Elsevier Bibliographic Databases incl. Scopus, the ISI Web of Knowledge by Thomson Reuters and the NISC Bibliographic databases. The Journal is distributed by EBSCO Publishing.

Submission of manuscripts

All manuscripts should be submitted online at http://mc.manuscriptcentral.com/fozia_zool. Correspondence concerning editorial matters should be addressed to the Editorial Office. A comprehensive version of the 'Instructions to Authors' is available on www.ivb.cz/pubser_en.htm.

Folia Zoologica offers authors:

- expert and thorough peer review
- no page charges

- a free pdf copy of the published article
- on-line distribution of abstracts on Scopus and the ISI Web of Science, and full texts on EBSCO products

| AWARDS

SCIAP award for the popularisation of science

The SCIAP (SCIENCE APProach) Competition was established in 2011 as an initiative of the Department for the Popularisation of Science and Marketing of the Centre for Administration and Operations of the Czech Academy of Sciences. The aim of the competition is to evaluate and reward the most successful popularisation activities implemented in the Czech Republic (or in the Czech language), and the popularisation and presentation of science by the Czech Academy of Sciences. The competition winners are announced by the Centre for Administration and Operations of the Czech Academy of Sciences. The competition is open to all entities dealing with science and the popularisation of science.

A series of ten popular documentaries produced by the IVB entitled ‘Tales of curious biologists’ won 2nd place in the Audio/video/film category in 2015. These films formed part of the ‘Science by all senses’ project, supported by the European Social Fund via the Education for Competitiveness Operational Programme. These short (ca. 20 min) documentaries presented not only the most impressive research topics of the Institute but also brought to the forefront the scientist’s personalities, their motivation and general principles of the scientific work undertaken. The films were produced by J. Hošek (Director) and M. Polák (camera) and broadcast by the Czech television station CT2.

The programmes can be viewed here: <http://www.ceskatelevize.cz/porady/11015147646-tribe-hy-zvedavych-prirodovedcu/dily/>



Filmmakers were involved in numerous field work expeditions with the Institute's scientists.

(Photo from archive of M. Polák and J. Hošek)



A series of ten popular documentaries produced by the IVB entitled 'Tales of curious biologists' won 2nd place in the Audio/video/film category of SCIAP competition in 2015.

(Photo from archive of M. Polák and J. Hošek)





All the prizewinners at the SCIAP awards ceremony.

(Photo from archive of SCIAP)

The Otto Wichterle Award

The Otto Wichterle Award is an honour given by the Czech Academy of Sciences to exceptional young scientists (not older than 35) working with the Academy for their remarkable contribution to the advancement of knowledge in a given area of science in order to stimulate and encourage their future work.

The winner of the Otto Wichterle Award in 2016 was Martin Šálek. Martin's main interests at present are the ecology of birds and mammals in fragmented agricultural landscapes, behavioural ecology and genetic variability in little owl (*Athene noctua*) populations, spatial and roosting ecology of bats, and the return of large herbivores as a high priority in biodiversity conservation (rewilding projects).



M. Šálek (right) receiving the Otto Wichterle Award from the President of the Czech Academy of Sciences, Prof. J. Drahoš (left).

(Photo from archive of M. Šálek).

The NEURON Fund for the Support of Science

The Neuron Fund for the Support of Science promotes philanthropic support of science and research in the Czech Republic. The Neuron Expedition Project is intended to recall the famous era of Czech scientific expeditions by supporting and enabling research expeditions that make a significant contribution to contemporary knowledge.

For the year 2016, the competition jury selected the project (the mysterious crocodile of the Congo) of Václav Gvoždík from the IVB to receive that year's award. The Congo dwarf crocodile, as Václav has temporarily named it, is not widely accepted by experts and the scientific community still confuses it with the West African dwarf crocodile (*Osteolaemus tetraspis*).

The expedition to the Republic of Congo took place in January 2017 and lasted two-months. Members of the expedition team included Matej Dolinay from the IVB and Masaryk University in Brno, Jérémy Thomas from France, and Ange Zassi-Boulou from the Congo, along with their local assistants. The data acquired from the field expedition supports the initial hypothesis that there is indeed an unrecognised crocodile species in the Congo. Tissue samples that will confirm this are now awaiting DNA analysis. Václav expects his research will soon bring definitive recognition of the Congo dwarf crocodile as a valid species. Only a proper understanding of species diversity can lead to adequate protection and the preservation of fauna and flora for future generations. This is essential for the future of the Congo dwarf crocodile, such that it can be seen not only in photographs but also in Central African rainforests.



Václav Gvoždík with a Congo dwarf crocodile and whole team of “crocodile hunters” in Congo during The Neuron Expedition supported by the Neuron Fund.

(Photo by M. Dolinay)

