INSTITUTE OF PARASITOLOGY

Biology Centre of the Czech Academy of Sciences, v.v.i.

České Budějovice, Czech Republic

ANNUAL REPORT

A BRIEF SURVEY OF THE INSTITUTE'S ACTIVITIES AND OUTCOMES

2017

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(*As of 1 January 2018*)

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Deputy Director
(***Tomáš Scholz***)

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(***Julius Lukeš***)

Laboratory of Functional Biology of Protists
(*Alena Zíková-Panicucci*)

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Fish Parasitology

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Scientific Council

Miroslav Oborník (Chairman)
Aleš Horák
Petr Kopáček
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External members
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Laboratory of Genomics and Proteomics of Disease Vectors
(*Michail Kotsyfakis*)

Laboratory of Tick Transmitted Diseases
(*Ondřej Hajdušek*)

* Joint research teams of the Institute and Faculty of Science, University of South Bohemia; team leader in bold.

Editorial

Time passes by fast and I am already in the 2nd year of my 2nd term as a director of the Institute of Parasitology (till July 2022), which is part of the Biology Centre, a group of ecologically and evolutionarily directed institutes of the Czech Academy of Sciences, located in the picturesque city of České Budějovice.

I am happy to say that the year 2017 was a very good one for our institute, as we were able to secure substantial funding from several sources, which shall allow us not only to grow but also to provide continuous support to young labs that are still in a sensitive period. Our staff became more international, causing that the lingua franca of the institute is now inevitably English. While the scientific output is at a constant level (but we hope it will get stronger in the upcoming years), I am happy to say that we participated in several high profile publications that appeared in Nature, PLoS Pathogens, Proceedings of the National Academy of Sciences, etc. We also keep publishing our in-house journal Folia Parasitologica that got decent ranking in a recent survey. We have two extensive, increasingly well-equipped supporting facilities, namely the electron microscopy unit and the animal facility, that are run by enthusiastic staff, always willing to engage in challenging projects. As a whole, the institute strives to be a vibrant, flexible, dynamic and competitive group of laboratories, for which parasitology is the common denominator.

Cheers,

Julius Lukeš

Director

Mission statement

The Institute of Parasitology of the Biology Centre is a research institution of the Czech Academy of Sciences performing fundamental research on human and animal parasites at the organismal, cellular and molecular levels. Its mission is to acquire, advance and disseminate knowledge of the biology and host relationships of parasitic protists and related eukaryotic microorganisms, helminths and arthropods. The Institute pursues its mission through research, education and other activities at both the national and international levels. The results obtained have contributed to the prevention and control of human and animal parasitic diseases.

The Institute of Parasitology was established in Prague in 1962, but was relocated to České Budějovice in South Bohemia in 1985. The Institute represents a principal institution devoted exclusively to parasitological research in the Czech Republic. The main research areas encompass protistology, helminthology and medical entomology, including studies on the causative agents of the infections transmitted by arthropods. Investigations into molecular biology of parasitic protists, phylogeny of parasites and their molecular ecology, fish parasites, life-cycles of helminths and parasitic arthropods as vectors of diseases have remained long-term research priorities of the Institute.

Research teams and their activities

1. MOLECULAR PARASITOLOGY

1.1. Laboratory of Molecular Biology of Protists

Research scientists:	Prof. RNDr. **Julius LUKEŠ**, CSc. (*head*) RNDr. **Drahomíra Faktorová**, PhD; Doc. **Mgr. Hassan Hashimi,** Ph.D.; RNDr. **Eva Horáková**, PhD; **Galina Prokopchuk** (Ukrajina); **Priscilla Peña Diaz**, MSc, PhD (Venezuela); **Daria Tashyreva**, PhD (Ukrajina); doc. RNDr. **Jan Votýpka**, PhD; **Vyacheslav Yurchenko**, MSc, PhD
PhD students:	**Paula Andrea Castañeda Londoño** (Colombia), MSc; **Sameer Dixit**, MSc (India); **Ambar Kachale**, MSc (Indie); **Binnypreet Kaur**, MSc (India); **Josef Kaurov**, MSc (Russia); **Anna Nenarokova**, MSc (Russia); RNDr. **Tomáš Skalický**
Research assistants:	Mgr. **Jiří Heller**; Bc. **Sabine Kalterbrunner** (Austria)
Technicians:	**Renata Lukšová** (from June); RNDr. **Eva Stříbrná-Černotíková**
Undergraduate students:	**Anita Baer** (Austria); **Michaela Boudová** (until August); **Lawrence Rudy Cadena** (USA)

Research priorities

We are interested in the studies of various aspects of biology of the kinetoplastid and diplonemid flagellates. These are protists that branched off the main eukaryotic lineage and contain numerous departures from the prototypical eukaryotic cell. In particular their mitochondrion has many unique aspects, which we are exploring by knocking down, tagging, over expressing or knocking in individual genes. In particular we are interested in the following groups of proteins: (i) involved in RNA editing and regulation of stability of mitochondrial transcripts; (ii) that are subunits of respiratory complexes, (iii) involved in iron/sulfur cluster assembly; (iv) participating in processing of imported proteins; (v) involved in heme metabolism, and, finally (vi) that build the mitochondrial cristae.

In diplonemids, we are mainly exploring their evolution, diversity, morphology, metabolism, transcriptome and genome structure. Moreover, we are trying to introduce into culture so far uncultivable representatives of the hyperdiverse marine clade. We have also succeeded in first genetic modification of diplonemids, which should allow their genetic dissection and brings them into the family of model organisms.

Selected publications

- **Dixit S.**, Müller-McNicoll M., **David V.**, Zarnack K., Ule J., **Hashimi H.**, **Lukeš J.** 2017: Differential binding of mitochondrial transcripts by MRB8170 and MRB4160 regulates distinct RNA processing fates in trypanosomes. *mBio* 8: e02288-16. [IF=6.689]
- **Horáková E.**, **Changmai P.**, Vancová M., Sobotka R., Van Den Abbeele J., Vanhollebeke B., **Lukeš J.** 2017: The *Trypanosoma brucei* TbHrg protein is a heme transporter involved in regulation of stage-specific morphological transitions. *Journal of Biological Chemistry* 292: 6998–7010. [IF=2.492]
- **Peña Diaz P.**, Vancová M., Resl C., Field M.C., **Lukeš J.** 2017: A leucine aminopeptidase is involved in kinetoplast DNA segregation in *Trypanosoma brucei*. *PLoS Pathogens* 13: e1006310. [IF=6.158]
- **Skalický T.**, **Dobáková E.**, Wheeler R.J., Tesařová M., **Flegontov P.**, **Jirsová D.**, **Votýpka J.**, **Yurchenko V.**, Ayala F.J., **Lukeš J.** 2017: Extensive flagellar remodeling during the complex life cycle of *Paratrypanosoma*, an early-branching trypanosomatid. *Proceedings of the National Academy of Sciences of the United States of America* 114: 11757–11762. [IF=9.504]
- Zíková A., **Verner Z.**, **Nenarokova A.**, Michels P.A.M., **Lukeš J.** 2017: A paradigm shift: the mitoproteomes of procyclic and bloodstream *Trypanosoma brucei* are comparably complex. *PLoS Pathogens* 13: e1006679. [IF=6.158]

Research projects

- **Integrated Microbial Biodiversity.** Canadian Institute for Advanced Research (CIFAR) (IMB-LUKE-131600; P.I.: J. Lukeš; 2012–2017).
- **Emergence of pathogenicity for vertebrates: insight from ancestral bodonids and insect trypanosomatids.** Czech Science Foundation (14-23986S; P.I.: J. Lukeš; 2014–2016).
- **Diplonemid.** Moore Foundation, USA (GBMF4983; P.I.: J. Lukeš; 2015–2016).
- **Mitochondrial genome-wide studies of RNA-binding proteins in trypanosomes.** Czech Science Foundation (15-21974S; P.I.: J. Lukeš; 2015–2017).
- **Heme: a putative master regulator in trypanosomatids.** Czech Science Foundation (16-18699S; P.I.: J. Lukeš; 2016–2017).
- **Comprehensive study of diplonemids: emerging key players in the oceans.** ERC CZ, Czech Ministry of Education (LL1601)

1.2. Laboratory of Functional Biology of Protists

Research scientists:	RNDr. **Alena ZÍKOVÁ**, PhD (*head*) Mgr. **Eva Doleželová**, PhD; Mgr. **Ondřej Gahura**, PhD
Research assistant:	**Brian Panicucci**, BSc (USA)
PhD students:	**Carolina Hierro Yap**, MSc (Spain); **Gergana Taleva**, MSc (Bulgaria); **Minal Jain**, MSc (India)
Undergraduate students:	Bc. **Michaela Kunzová**; **Mykyta Ielanskyi**; **Leonie Lehmayer**; **Karolína Kubišová, Ana-Marija Andova, Simona Urbanová**

Research priorities

Trypanosoma brucei, a unicellular parasite of humans and livestock, is being extensively studied because of its unique biology, its impact on human health and economy, and because of its readiness to genetic manipulation. It is a digenetic parasite that alternates between an insect vector and a mammalian host. In order to survive within the specialized environments of its hosts, this protist has developed a wide variety of unique physiological functions. One example is its mitochondrion which exhibits many unique features and interesting variations to the mammalian system. Moreover this organelle seems to be flexible and able to respond quickly to different available nutrients. It is our main interest to understand the cellular and molecular mechanisms behind the ability of the parasite to functionally adapt to different tissues of its mammalian and insect hosts.

Mitochondrial bioenergetics of the *Trypanosoma brucei* bloodstream form

In the mammalian bloodstream, *Trypanosoma brucei* relies on the abundant source of glucose for energy production. It is widely considered that the bloodstream form mitochondrion is metabolically idle, does not contribute to glucose and amino acids catabolism and lacks respiratory complexes III and IV. Combining available data we reveal that metabolic flexibility and adaptability of the bloodstream form mitochondrion is much larger than appreciated so far. Further work combining metabolic profiling with functional genomics is needed to get insight into its emerging complexity, which is likely exploited during environmental changes, for example when the parasite migrates to other tissues than blood (e.g. adipose tissue, spinal and cerebral fluids), but also during the differentiation to a stumpy form. We postulate that although the bloodstream parasite is capable of “fine-tuning” its metabolism as a function of varying environmental stimuli, glycolysis remains its predominant pathway. Still, the virtually unexplored array of pathways and enzymes, disclosed recently mostly via mass spectrometry and labelling experiments, begs for attention, as it may have important implications for drug target identification and future novel chemotherapeutics.

Mitochondrion remodeling during *Trypanosoma brucei* differentiation

During Trypanosoma brucei life cycle, the single mitochondrion undergoes dramatic structural and metabolic remodeling while responding to different nutrients in its environment. Until

recently, it was challenging to work with the various intermediate life stages found in the insect vector, tsetse fly, but now each of the insect vector developmental cell types can be created in vitro by simply overexpressing a single RNA binding protein. We aim to study molecular mechanisms underlying mitochondrial metabolic rewiring during the parasite´s development. We also focus on the role of mitochondria in signaling that determines metabolic status of the cell and its fate.

The role of ATP synthase structure in the biogenesis and bioenergetics of *Trypanosoma brucei* mitochondrion

Mitochondrial cristae are inner membrane convolutions where protein factories responsible for bioenergy conversion reside. The cristae exhibit an extremely large variability in their ultrastructure, except for one common attribute - the presence of ATP synthase dimer rows at the crista ridges. Little is known about the role of these arrays in cristae structure and mitochondrial bioenergetics. However, *Trypanosoma brucei* is an excellent model system as the singular mitochondrion of the digenetic parasite is drastically remodeled structurally and metabolically as it progresses through a complex life cycle. Notably, the highly branched, cristae-containing and ATP-producing mitochondrion transitions to a streamlined tubular, cristae-lacking and ATP-consuming organelle. Combining traditional biochemical methods with state-of-art structural approaches (e.g. cryo-EM and cryo-ET), we aim to solve the ATP synthase dimer structure, identify dimer-specific subunits and explore their role in cristae shaping, mt bioenergetics and biogenesis in two major life stages of this parasite.

Selected publications:

- **Panicucci B.**, Gahura O., **Zíková A.** 2017: *Trypanosoma brucei* TbIF1 inhibits the essential F1-ATPase in the infectious form of the parasite. *PLoS Neglected Tropical Diseases* 11:e0005552.[IF=4.367]
- **Zíková A.**, Verner Z., Nenarokova A., Michels P.A.M., Lukeš J. 2017: A paradigm shift: the mitoproteomes of procyclic and bloodstream *Trypanosoma brucei* are comparably complex. *PLoS Pathogens* 13: e1006679. [IF=6.158]

Research projects:

- **Determining the effectors of mitochondrion remodeling during procyclic *Trypanosoma brucei* differentiation.** Grant Agency of Czech Republic (17-22248S; P.I.: A. Zíková, 2017 – 2019)
- **Exploitation of the unique characteristics of the *Trypanosoma brucei* FoF1-ATP synthase complex for future drug development against African sleeping sickness.** Ministry of Education, Youth and Sport of the Czech Republic (ERC CZ LL1205; P.I.: A. Zíková; 2013–2017).

1.3. Laboratory of RNA Biology of Protists

Research scientists:	RNDr. **Zdeněk PARIS**, PhD (*head*) Mgr. **Eva Hegedüsová**, PhD (Slovakia)
PhD student:	**Sneha Sunil Kulkarni**, MSc (India)
Undergraduate students:	Bc. **Veronika Běhálková** (until June 2017); Bc. **Michaela Boudová**; **Helmut Stanzl** (Austria)

Research priorities

Our group (established in February 2014) studies various aspects of RNA biology of the protistan parasite *Trypanosoma brucei* and related flagellates. In those early evolved unicellular organisms most genes are post-transcriptionally regulated. Consequently, post-transcriptional processing of RNA becomes of a great importance to regulate complex life cycles of these pathogens. We are mainly interested in processes such as tRNA modifications, nuclear tRNA export and role of the only intron containing tRNA in trypanosomes. Our long-term goal is an identification of unique mechanisms of RNA metabolism. We believe this will help us reveal new drug targets to combat diseases caused by trypanosomatid parasites.

Queuosine biosynthesis in trypanosomes

Transfer RNAs are typical for the large number of post-transcriptional modifications. Most of the tRNA modifications are present in the anticodon loop and have crucial role in proper translation of proteins. Queuosine is one of the most complex tRNA modifications. Despite its omnipresence among bacteria and eukaryotes, role of queuosine tRNA modification is not clear. The main aim of this project is to evaluate the function and subunit composition of the enzyme responsible for queuosine formation in *T. brucei*. Using the RNAi knock-down strategy, we want to address the principal question regarding the role of queuosine tRNA modification with respect to biology and physiology of this protistan parasite.

Role of the only tRNA intron in trypanosomatids

In yeast *Saccharomyces cerevisiae* and other model organisms, 20% of all tRNAs contain introns. Their removal is an essential step in the maturation of tRNA precursors. In *T. brucei*, there is only one intron containing tRNA: $tRNA^{Tyr}_{GUA}$. Since this tRNA is responsible for decoding all tyrosine codons, intron removal is essential for viability. Using molecular and biochemical approaches, several non-canonical editing events were identified within the intron-containing $tRNA^{Tyr}_{GUA}$. The RNA editing involves guanosine-to-adenosine transitions (G to A) and an adenosine-to-uridine transversion (A to U), which are both necessary for proper processing of the intron. We have been obtaining tRNA intron sequences from our collection of newly identified trypanosomatid species. We hope this will help us understand the process of RNA editing and ultimately identify biological function of the presence of the only intron containing tRNA in these organisms.

Nuclear export of tRNAs in trypanosomes

Nuclear tRNA export to the cytoplasm might provide an additional level of regulation of gene expression during the complex life cycle of trypanosomes. However, only a limited set of eukaryotic export factors, conserved in other organisms, can be easily identified in the *T. brucei* genome; thus our knowledge of nuclear tRNA export remains limited. In this project, we employ molecular biological and biochemical approaches to identify and characterise the nuclear tRNA export machinery in trypanosomes and its role in tRNA maturation, with the general idea of tRNA nuclear export as a regulated step.

Selected publications

- Rubio M.A.T., Gaston K.W., McKenney K.M., Fleming I.M.C., **Paris Z.**, Limbach P.A., Alfonzo J.D. 2017: Editing and methylation at a single site by functionally interdependent activities. *Nature* 542: 494–497. [IF=41.577]

Research projects

- **Queuosine: The role of an essential tRNA modification in parasitic protist *Trypanosoma brucei*.** Czech Science Foundation (15-21450Y; P.I.: Z. Paris; 2015–2017).

2. EVOLUTIONARY PARASITOLOGY

2.1. Laboratory of Evolutionary Protistology

Research scientists:	Prof. Ing. **Miroslav OBORNÍK**, PhD (*head*) **Heather Esson**, MSc, PhD (Canada); Mgr. **Zoltán Füssy**, PhD; RNDr. **Aleš Tomčala**, PhD; **Abduallah Sharaf**, MSc, PhD (Egypt)
PhD students:	Mgr. **Jaromír Cihlář**; Mgr. **Jan Michálek**; Mgr. **Jitka Kručinská**; RNDr. Ing. **Pave Poliak**; Ing. **Ivana Schneedorferová** (supervisor Aleš Tomčala)
Research assistant:	Mgr. **Kateřina Jiroutová**, PhD
Undergraduate student:	Bc. **Tereza Faitoá** (supervizor Z. Füssy)

Research priorities

Laboratory of Evolutionary Protistology (LEP) (formerly Laboratory of Molecular Taxonomy) was established in 2000 as a joint laboratory of the Institute of Parasitology and Faculty of Biological Sciences (now Faculty of Science), University of South Bohemia. At present the laboratory is designed to study evolution of protists and algae.

Fatty acid biosynthesis in chromerids

Chromerids are phototrophic algae isolated from Australian corals. Two species have been described so far, *Chromera velia* and *Vitrella brassicaformis*, which have been shown to represent the closest known phototrophic relatives to apicomplexan parasites. We are interested in various metabolic pathways in these algae, including synthesis of fatty acids (FAS). Both types of FAS were found in chromerids, cytosolic FASI as well as plastid located FASII. Evolution of these pathways is studied in context with closely related apicomplexan parasites.

Reduced photosystems in *C. velia* and *V. brassicaformis*

Through investigation of genomic and transcriptomic sequences of chromerid algae and other eukaryotic phototrophs we reconstructed protein compositions of PSI, PSII, cytochrome b6f complex and (plastid) ATP synthase with a special attention to the reductive evolution of photosynthetic complexes in eukaryotes. We documented the highly reduced photosystems in eukaryotic algae, with the highest level of reduction found in chromerids. However, we identified 3 additional protein subunits in *C. velia* with no sequence homology detected.

Investigation of novel bicosoecid

We isolated novel marine bicosoecid (non-photosynthetic stramenopile) as an accompanying organism in yet unspecified pelagophyte alga from Norway. The bicosoesic is grown in the culture without the alga, and is now being characterized in terms of morphology, ultrastructure and genomic sequencing. Preliminary results show unprecedented physical association of mitochondria and nucleus, with a conspicuous pore-like structure between the two cellular organelles.

Selected publications

- **Füssy Z.**, Masařová P., **Kručinská J., Esson H. J., Oborník M.** 2017: Budding of the alveolate alga *Vitrella brassicaformis* resembles sexual and asexual processes in apicomplexan parasites. *Protist* 168: 80–91. [IF=2.702]
- **Füssy Z.**, **Oborník M.** 2017: Chromerids and their plastids. *Advances in Botanical Research* 84: 187–218. [IF=1.387]
- **Füssy Z.**, **Oborník M.** 2017: Reductive Evolution of Apicomplexan Parasites from Phototrophic Ancestors. In: P. Pontarotti (Ed.), Evolutionary Biology: Convergent Evolution, Evolution of Complex Traits, Concepts and Methods. Springer International Publishing, pp. 217–236
- Sobotka R., **Esson H. J.**, Koník P., Trsková E., Moravcová L., Horák A., **Dufková P.**, **Oborník M.** 2017: Extensive gain and loss of photosystem I subunits in chromerid algae, photosynthetic relatives of apicomplexans. *Scientific Reports* 7: 13214. [IF=4.122]
- **Tomčala A.**, **Kyselová V.**, **Schneedorferová I.**, Opekarová I., Moos M., Urajová P., **Kručinská J.**, **Oborník M.** 2017: Separation and identification of lipids in the photosynthetic cousins of Apicomplexa *Chromera velia* and *Vitrella brassicaformis*. *Journal of Separation Science* 40: 3402–3413. [IF=2.415]

Research Projects

- **Photosynthesis Research Centre.** Czech Science Foundation (P501/12/G055; Co-P.I.: M. Oborník; 2012–2018).
- **Search for the origin of exosymbiont.** Czech Science Foundation (15-17643S; P.I.: M. Oborník; 2015–2017).
- ***Chromera velia* as a model organism to study evolution of apicomplexans and chrompodellids.** Czech Science Foundation (16-24027S; P.I. M. Oborník; 2016–2018).

2.2. Laboratory of Environmental Genomics

Research scientists:	Mgr. **Aleš HORÁK**, PhD (*head*)
	Mgr. **Jana Veselá**, PhD
PhD student:	**Olga Flegontova**, MSc (Russia)
Bc student	**Michaela Uhrová**

Research priorities

Study on biodiversity and biology of uncultivable unicellular eukaryotes using next-generation sequencing.

Early stages of evolution of parasitism in Apicomplexa

Apicomplexans are probably the most diverse and successful group of parasitic protists, with millions of dollars spent on the research of the key players (Plasmodium, Toxoplasma, coccidia, etc.). Yet, we know very little about the early phases of their evolution. Therefore, we are characterising the diversity and the genomes of representatives of several enigmatic apicomplexan clades (archigregarines, blastogregarines and agammococcidians) to reveal the evolution of non-photosynthetic plastid (apicoplast) and composition and evolution of the surface proteins associated with the infection of host. Collaboration: Sonja Rueckert, Edinburgh Napier University (UK)

Diversity and ecology of marine diplonemids

Tara Oceans is an international project of unprecedented scale, which aimed to investigate prokaryotic and eukaryotic planktonic diversity of the world oceans. During 2009–2012, almost 28 thousand samples were obtained from 154 locations of the World Ocean. Preliminary analyses of V9 region of the ssu rRNA gene have revealed that some samples, namely from deeper waters are dominated by diplonemid-like excavates. These enigmatic protists were found to be third most diverse and sixth most abundant planktonic organisms of the sunlit oceans. Detailed analysis focused on diplonemids, this time including also samples from mesopelagic zone Diplonemids separate into four major clades, with the vast majority falling into the planktonic DSPD I (deep sea pelagic diplonemid) clade (Lara et al. 2009). Remarkably, diversity of this clade inferred from metabarcoding data surpasses even that of dinoflagellates, metazoans, and rhizarians, qualifying diplonemids as possibly the most diverse group of marine planktonic eukaryotes. Diplonemid communities display no apparent biogeographic structuring, with a few hyper-abundant cosmopolitan operational taxonomic units (OTUs) dominating the communities. Diplonemids display strong vertical separation between the photic and mesopelagic layers, with the majority of their relative abundance and diversity occurring in deeper waters. Our results suggest that the planktonic diplonemids are among the key heterotrophic players in the largest ecosystem of our biosphere. Our ultimate goal is to elucidate the role of these mysterious organisms in the global ocean ecosystem. Compared to diplonemids, kinetoplastids, major human and lifestock pathogens and one of the most studied protozoan group, are much less present in the oceans. The vast majority of kinetoplastid abundance and diversity belong to the neobodonids – mostly

free living bacteriovorous flagellates with *Neobodo* and *Rhynchomonas* as the most prominent genera. Some of the most abundant kinetoplastids have distinct geographical distributions, and three novel putatively parasitic neobodonids were identified, along with their potential hosts.

Collaboration: Tara Oceans Consortium, namely Colomban de Vargas, Station Biologique de Roscoff (France).

Selected publications

- Rueckert S., **Horák A.** 2017: Archigregarines of the English Channel revisited: new molecular data on Selenidium species including early described and new species and the uncertainties of phylogenetic relationships. *PLoS ONE* 12: e0187430. [IF=2.766]
- Sobotka R., Esson H. J., Koník P., Trsková E., Moravcová L., **Horák A.**, Dufková P., Oborník M. 2017: Extensive gain and loss of photosystem I subunits in chromerid algae, photosynthetic relatives of apicomplexans. *Scientific Report*s 7: 13214. [IF=4.122]

2.3. Laboratory of Molecular Ecology and Evolution

Research scientists:	Doc. RNDr. **Jan ŠTEFKA**, PhD (*head*) Prof. RNDr. **Václav Hypša**, CSc.; MVDr. **Jana Kvičerová**, PhD; RNDr. **Eva Nováková**, PhD
PhD students:	RNDr. **Filip Husník**; Mgr. **Marie Krausová**; Mgr. **Anna Mácová**; RNDr. **Jana Martinů**; Mgr. **Jakub Vlček**
Technician:	**Lenka Štifterová**
Undergraduate students:	Bc. **Pavlína Kočová**; Bc. **Lukáš Vejsada**; **Tereza Flegrová**; **Nikola Jachníková**; **Daniela Kotalová**; **Matěj Miláček**; **Stanislava Wolfová**

Research priorities

Our research is mainly focused on population genetic and phylogenetic analysis of the evolution and relationships of parasitic and symbiotic organisms, and their hosts. It involves investigation into their co-evolution, biogeography, intraspecific variability and evolution of adaptations. The research is carried out on several models of parasitic and symbiotic associations.

Coevolution between Galápagos mockingbirds and their ectoparasites

We are studying the character of coevolution between Galápagos mockingbirds and their parasites. The research focuses on determining the factors responsible for formation of population structure, reconciling the mutual evolutionary history and identifying genes under selection in the hosts. With the use of parallel amplicon sequencing of several immune genes (MHC class IIB, TLR) and using the whole genome re-sequencing approach, we are exploring the impact of habitat size on the level of genetic diversity in the populations of mockingbirds and their parasites.

Population genetics, demography and molecular evolution in rodents and their parasites

Adaptive and co-speciation components of host-parasite coevolution are studied in rodents and their parasites. Two rodent groups (voles and wood mice) and their ectoparasites (lice and mites) as well as endoparasites (*Eimeria*) were selected as the model groups. Population structure was analysed using mitochondrial genes and selected nuclear markers. Despite observing lineages with relatively strict degree of host specificity, only limited amount of co-speciation was seen in both parasitic groups. Hence, the adaptive component of evolution seems to be the major driver defining genetic differentiation. Obtained patterns will be validated and explored in further detail using sequences of genes putatively under selection in the hosts (MHC II) and using multilocus and genomic data obtained from both counterparts.

Evolution of symbiotic bacteria associated with arthropods

We are broadly interested in intracellular symbiotic bacteria and their arthropod hosts. The main goal of our research is complex characterisation of symbiotic systems in several model insect groups using microscopical, genomic, transcriptomic, phylogenomic and metagenomic methods.

Our main questions involve genome evolution of both the host and its symbionts, their phylogeny and population structure, and host-symbiont-pathogen interactions.

Selected publications

- **Jirsová D.**, **Štefka J.**, **Jirků M.** 2017: Discordant population histories of host and its parasite: A role for ecological permeability of extreme environment? *PLoS ONE* 12: e0175286. [IF=2.766]
- **Nováková E.**, Woodhams D.C., Rodríguez-Ruano S.M., Brucker R.M., Leff J.W., Maharaj A., Amir A., Knight R., Scott J. 2017: Mosquito Microbiome Dynamics, a Background for Prevalence and Seasonality of West Nile Virus. *Frontiers in Microbiology* 8: 526. [IF=4.019]
- Říhová J., **Nováková E., Husník F., Hypša V.** 2017: *Legionella* becoming a mutualist: adaptive processes shaping the genome of symbiont in the louse *Polyplax serrata*. *Genome Biology and Evolution* 9: 2946–2957. [IF=3.940]
- Thairu M.W., Skidmore I.H., Bansal R., **Nováková E.**, Hansen T.E., Li-Byarlay H., Wickline S.A., Hansen A.K. 2017: Efficacy of RNA interference knockdown using aerosolized short interfering RNAs bound to nanoparticles in three diverse aphid species. *Insect Molecular Biology* 26: 356–368. [IF=2.492]

Research project

- **Genomics and populstion genetics in hodt-parasite system: switches, diversification and adaptation.** (17-19831S; P.I.: V. Hypša; 2017–2019)
- **Phylogenomics and molecular diversity of Mesozoa.** Czech Science Foundation (15-08717S; P.I.: V. Hypša; 2015–2017).
- **Population-genomic analyses on Galapagos mockingbirds.** Swiss Association of Friends of the Galápagos Islands (P.I.: J. Štefka; 2016–2017).

2.4. Laboratory of Genomic and Diversity

Research scientists: Mgr. **Martin Kolísko**, Ph.D. (*head*)

Research Assistants: Mgr. **Serafim Nenarokov**

Bc student: Jessica **Drozdz**

Research Priorities

Current and long-term research in the Laboratory of Genomics and Diversity of Protists revolves around the diversity of microbial eukaryotes and their genomes and transcriptomes. We use methods of comparative genomics and transcriptomics to understand the evolution of parasitism and the interactions between gut microbial parasites and the gut microbiome.

Comparative Genomics of Diplomonads

Some of the microbial eukaryotes are important parasites of humans and animals; however, there are many species that are known to be host-associated, yet their pathogenicity remains unknown. Comparative genomics is a powerful tool for understanding parasitism on a genomic level. Diplomonads are a group of microbial eukaryotes that includes medically and economically important parasites. Additionally, there are several putative secondarily free-living species and host-associated commensalic species. We are performing a taxonomically wide, comparative study of diplomonads, including well-studied parasites, primarily and secondarily free-living species, and commensals. The results will address some of the fundamental questions of biology, including the mechanisms of reversal from free-living to parasitic lifestyle and whether it is possible to predict pathogenicity or host-associated lifestyle based on genomic information.

Diversity of Microbial Eukaryotes in the Gut Microbiome

We study the diversity of microbial eukaryotes in human gut microbiomes using amplicon sequencing by combining several approaches to minimize the presence of host DNA in the results. We will take advantage of a current collaboration with the Institute of Experimental Medicine (IKEM, Prague), giving us access to DNA material from human microbiomes of healthy individuals as well as individuals with a variety of infections and medical conditions. We will also perform DNA sampling from diverse animal hosts.

Microbial Eukaryotes and Their Interactions with the Gut Microbiome

We are using an experimental infection model of a host (mouse or rat) and a microbial eukaryote (Blastocystis) to identify any detectable changes in transcription levels in the metatranscriptome of the microbiome (predominantly the prokaryotic part) as well as changes in transcription in the parasite/commensal and in the host. This will help us to elucidate differences in the interactions between parasites/commensals and their hosts and host microbiomes.

Selected Publications

- Boscaro V., James E.R., Fiorito R., Hehenberger E., Karnkowska A., Del Campo J., **Kolisko M.**, Irwin N.A.T., Mathur V., Scheffrahn R.H., Keeling P.J. 2017: Molecular characterization and phylogeny of four new species of the genus *Trichonympha* (Parabasalia, Trichonymphea) from lower termite hindguts. *International Journal of Systematic and Evolutionary Microbiology* 67: 3570–3575. [IF=1.932]
- Boscaro V., **Kolisko M.**, Felletti M., Vannini C., Lynn D.H., Keeling P.J. 2017: Parallel genome reduction in symbionts descended from closely related free-living bacteria. *Nature Ecology and Evolution* 1: 1160–1167. [IF=0]
- del Campo J., James E.R., Hirakawa Y., Fiorito R., **Kolísko M.**, Irwin N.A.T., Mathur V., Boscaro V., Hehenberger E., Karnkowska A., Scheffrahn R.H., Keeling P.J. 2017: *Pseudotrichonympha leei*, *Pseudotrichonympha lifesoni*, and *Pseudotrichonympha pearti*, new species of parabasalian flagellates and the description of a rotating subcellular structure. *Scientific Reports* 7: 16349. [IF=4.122]
- Hehenberger E., Tikhonenkov D.V., **Kolísko M.**, del Campo J., Esaulov A.S., Mylnikov A.P., Keeling P.J. 2017: Novel Predators Reshape Holozoan Phylogeny and Reveal the Presence of a Two-Component Signaling System in the Ancestor of Animals. *Current Biology* 27: 2043–2050. [IF=9.251]
- Lynn D.H., **Kolísko M.** 2017: Molecules illuminate morphology: phylogenomics confirms convergent evolution among 'oligotrichous' ciliates. International *Journal of Systematic and Evolutionary Microbiology* 67: 3676–3682. [IF=1.932]

3. TICKS AND TICK-BORNE DISEASES

3.1. Laboratory of Molecular Ecology of Vectors and Pathogens

Research scientists:	Prof. RNDr. **Libor GRUBHOFFE**R, CSc., Hon. D.Sc. *(head)* **Nataliia Rudenko**, MSc, PhD (Ukraine) *(deputy head)*; RNDr. **Jiří Černý**, PhD; **Katherina Kotsarenko**, MSc., PhD. (Ukraine); **Dimitrij Loginov**, MSc., PhD. (Russia); **Ryan O.M. Rego**, MSc, PhD (India); RNDr. **Ján Štěrba**, PhD (Slovakia)
PhD students:	Mgr. **Tereza Chrudimská**; Mgr. **Pavlína Kočová**; Mgr. **Martin Selinger**; RNDr. **Jarmila Štěrbová-Dupejová**; Mgr. **Martin Strnad**; Mgr. **Hana Tykalová-Šťastná**; RNDr. **Pavlína Věchtová**
Research assistants:	**Maryna Golovchenko**, MSc (Ukraine); Bc. **Jana Monhartová**; Mgr. **Zuzana Vavrušková**
Undergraduate students:	**Kateřina Vejvodová**; **Joahana Mustacová**; **Hana Pejsová**; **Ida Ramzy** (Austria); Bc. **Jan Černý**; Bc. **Karolína Dostálová**; Bc. **Libor Hejduk**; Bc. **Štěpánka Smolenová**; Bc. **Tomaš Kašpar**; Bc. **Hanka Mašková**; Bc. **Jana Müllerová**; Bc. **Radek Vokurka**; Bc. **Veronika Moravková**; Bc. **Hana Hajková**; Bc. **Hana Slabá**; Bc. **Lisa Hain**, BSc. (Austria); Bc. **Nora Hagleitner**, BSc. (Austria); Bc. **Tereza Liduchová**; Bc. **Katahrina Bottinger**, BSc. (Austria)
Laboratory worker:	**Zuzana Němcová**

Research priorities

Pleomorphism and viability of the Lyme disease spirochete under physiological stress

Cryo-fluorescence and cryo-SEM approach was used in close-to-native analysis of the viability and morphological changes of GFP-expressing spirochetes exposed to physiological stress. Round bodies and blebs were induced *in vitro*, both as a response to human serum. However, blebs are released from microbial cell surfaces as a general response to stress (e.g. after antibiotic treatment, prolonged cultivation, addition of specific antibodies, and complement to culture). Morphological alterations are likely representing stressed viable bacteria that can revert, under some circumstances, back to the motile spiral form. Even though the significance of RBs in Lyme disease remains unclear, we speculate that the presence of atypical morphological forms of in vivo is directly associated with chronic persistent infection in human or animal models and might cause unusual symptoms that last in patients despite antibiotic treatment.

Borrelia afzelii genes required for disseminating within the tick during feeding

Using fluroscently expressing *Borrelia afzelii* we intend on studying unique *Borrelial* genes that play a part in the dissemination within the tick during feeding. We have adapted genetic tools to obtain for the first time such mutants in an european *Borrelia* genospecies. We have published a meta-analysis looking at the presence of *Borrelia* in questing ticks within Europe which is useful in determining the main genospecies that are in circulation within particular geographical areas. It provides help in a better determination of which *Borrelia* infection symptoms a particular patient is presenting within a particular region.

TBEV-induced host response in human cells of neuronal origin

Analysis of response of human medulloblastoma cells derived from cerebellar neurons (DAOY cells) to TBEV (Neudoerfl strain, Western subtype) infection revealed a wide panel of interferon-stimulated genes (ISGs) and pro-inflammatory cytokines, including type III but not type I (or II) interferons (IFNs). The cellular response to TBEV showed only partial overlap with gene expression changes induced by IFN-β treatment - suggesting a virus-specific signature - and we identified a group of ISGs that were highly up-regulated following IFN-β treatment. A high rate of down-regulation was observed for a wide panel of pro-inflammatory cytokines upon IFN-β treatment.

Identification of molecular drivers for tick-borne diseases

The elucidation of the mechanisms involved in tick-pathogen interactions that affect vector competence is essential for the identification of molecular drivers for tick-borne diseases, and exposes paradigms for controlling and preventing these diseases. While vectorial capacity is influenced by behavioral and environmental determinants affecting variables such as vector density, longevity, and competence, vector competence is a component of vectorial capacity that depends on genetic factors affecting the ability of a vector to transmit a pathogen. These genetic determinants affect tick host preferences, duration of tick attachment, tick-host-pathogen, microbiome-pathogen interactions, and susceptibility to pathogen infection. Identification of interactions that promote tick survival, spread, and pathogen transmission provides the opportunity to disrupt these interactions and may assist in development of preventative strategies against multiple tick-borne diseases.

Selected publications

- Cutler S.J., **Rudenko N.**, **Golovchenko M.**, Cramaro W.J., Kirpach J., Savic S., Christova I., Amaro A. 2017: Diagnosing Borreliosis. *Vector Borne and Zoonotic Diseases* 17: 2–11. [IF=2.171]
- Fuente J., Antunes S., Bonnet S., Cabezas-Cruz A., Domingos A., Estrada-Peña A., Johnson N., Kocan K., Mansfield K., Nijhof A., Papa A., **Rudenko N.**, Villar M., Alberdi P., Torina A., Ayllon N., Vancova M., **Golovchenko M.**, **Grubhoffer L.**, Caracappa S., Fooks A., Gortazar C., **Rego R.O.M.** 2017: Tick-pathogen interactions and vector competence: identification of molecular drivers for tick-borne diseases. *Frontiers in Cellular and Infection Microbiology* 7: 114. [IF=3.520]
- **Selinger M.**, Wilkie G.S., Tong L., Gu Q., Schnettler E., **Grubhoffer L.**, Kohl A. 2017: Analysis of tick-borne encephalitis virus-induced host responses in human cells of neuronal origin and interferon-mediated protection. *Journal of General Virology* 98(8): 2043–2060. [IF=2.514]
- **Strnad M., Hönig V., Růžek D., Grubhoffer L., Rego R.O.M.** 2017: Europe-wide meta-analysis of *Borrelia burgdorferi* sensu lato prevalence in questing *Ixodes ricinu*s ticks. *Applied and Environmental Microbiology*, 83(15): e00609-17. [IF=3.633]
- Vancová M., **Rudenko N.**, Vaneček J., **Golovchenko M.**, **Strnad M.**, **Rego R.O.M.**, **Tichá L.**, **Grubhoffer L.**, **Nebesářová J.** 2017: Pleomorphism and viability of the Lyme disease pathogen *Borrelia burgdorferi* exposed to physiological stress conditions: a correlative cryo-fluorescence and cryo-scanning electron microscopy study. *Frontiers in Microbiology* 8: 596. [IF=4.019]

Research projects

- **ANTIDotE (Anti-tick Vaccines to Prevent Tick-borne Diseases in Europe).** FP7 EU-HEALTH project (2013.2.3.4-1; Co-P.I.: L. Grubhoffer; 2013–2018).
- **Novel functions of viral and cellular proteins in tick-borne encephalitis virus infection.** Czech Science Foundation (585410/3220; P.I.: L. Grubhoffer; 2015–2017).
- **Identification of novel antigens/diagnostic markers for the development of diagnostic tests for early diagnosis of Lyme Disease in Europe** - Technology Agency of the Czech Republic (TG02010034; P.I.: R. Rego; 2017–2018).
- **Delineating the role of *Borrelia afzelii* genes required for disseminating within the tick during feeding.** Czech Science Foundation (585410/3238;P.I.: R. Rego; 2017–2019)

3.2. Laboratory of Arbovirology

Research scientists:	Doc. RNDr. **Daniel RŮŽEK**, PhD (*head*) RNDr. **Luděk Eyer**, PhD; Mgr. **Václav Hönig**, PhD; RNDr. **Helena Langhansová-Horká**, PhD (until May 2017); RNDr. **Martin Palus**, Ph.D.**; James Jason Valdés**, PhD
PhD students:	Mgr. **Jana Elsterová**
Research assistant:	Bc. **Veronika Slavíková**
Technicians:	**Jan Erhart**; Bc. **Eva Výletová**
Laboratory worker:	**Lenka Marešová**
Undergraduate students:	**Martina Papajová**; **Veronika Prančlová**

Research priorities

Mechanisms of neuronal injury during tick-borne encephalitis infection in the CNS

Tick-borne encephalitis (TBE), a disease caused by tick-borne encephalitis virus (TBEV), represents one of the most important human neuroinfections in Europe and northeastern Asia. Despite the medical importance of this disease, some crucial steps in the development of encephalitis remain poorly understood. In particular, the mechanisms of TBEV-induced injury to the central nervous system (CNS) are unclear. In our laboratory, we study interactions of TBEV with primary human neurons, mechanisms of their injury and antiviral defence, as well as the interaction of the infected neurons with other key cells in the CNS (astrocytes, pericytes, microglia and brain microvascular epithelial cells). We propose that the innate immune response is an important cause of neuron death during the acute infection. This is in contrast to the prevailing hypothesis that neuron loss is mediated solely by virus. The results of this project should provide new crucial data about the neuropathogenesis of TBE.

Role of the host genetic background in the development of tick-borne encephalitis

In humans, TBEV may produce a variety of clinical symptoms from an asymptomatic disease to a fever and acute or chronic progressive encephalitis. This is influenced by a variety of factors, e.g. inoculation dose and virulence of the virus, age and immune status of the host, but also, as our results strongly suggest, by susceptibility based on host genetic background. Here, we study differences in clinical course of tick-borne encephalitis and its genetical determination. We developed a unique animal model based on BALB/c-c-STS/A (CcS/Dem) recombinant congenic mouse strains showing different severities of the infection in relation to the host genetic background: BALB/c mice showed medium susceptibility to the TBE virus infection, STS mice were resistant and CcS-11 mice were highly susceptible. The resistant STS mice showed lower and delayed viremia, lower virus production in the brain and low cytokine/chemokine mRNA production, but had a strong neutralising antibody response. The most sensitive strain (CcS-11) failed in production of neutralising antibodies, but exhibited strong cytokine/chemokine mRNA production in the brain. We performed transcriptomic profiling that revealed distinct gene-expression patterns in brains of mice differing in susceptibility to TBEV infection. The

susceptible and resistant strains differed in the expression of key cytokines/chemokines, particularly interferon gamma-induced protein 10 (IP-10/CXCL10) and monocyte chemotactic protein-1 (MCP-1/CCL2) in the brain. A linkage analysis of F2 CcS-11 and BALB/c intercross progeny revealed a novel suggestive locus that controls survival after TBEV infection. It is located on chromosome 7 linked to marker D7Nds5. We sequenced whole genomes of strains BALB/c and STS using next generation sequencing. Analysis of segment covering peak of linkage on chromosome 7 from 36.2 Mb to 74.5 Mb for polymorphisms between BALB/c and STS that change RNA stability and gene functions revealed 8 candidate genes of host susceptibility to TBE virus infection.

Development and testing of novel perspective antivirals and their prodrug forms active against tick-borne encephalitis virus

Despite the medical importance of tick-borne encephalitis (TBE), there is no specific treatment of this disease. In our laboratory, we identified nucleoside analogues with high antiviral effect against TBE virus (TBEV) observed *in vitro* as well as in TBEV-infected mice (reduction of viral titres in the brain, reduction of clinical signs of neuroinfection, prolonged mean survival time, lower mortality). The main goal of the current project is to modify these effective molecules into prodrug forms with increased therapeutical potential based on efficient crossing the blood-brain barrier and targeted delivery to the central nervous system. We experimentally combine these antiviral molecules with immunomodulatory therapies with the purpose to maximise viral clearance and minimise immunopathology after TBEV infection in the central nervous system. The results should provide new and important data about the possibilities and directions of antiviral and immunomodulatory therapy of TBE.

Selected publications

- **Eyer L.**, Kondo H., Zouharova D., Hirano M., **Valdés J.J.**, Muto M., Kastl T., Kobayashi S., Haviernik J., Igarashi M., Kariwa H., Vaculovicova M., **Cerny J.**, Kizek R., Kröger A., Lienenklaus S., Dejmek M., Nencka R., **Palus M.**, Salat J., De Clercq E., Yoshii K., **Ruzek D.** 2017: Escape of tick-borne flavivirus from 2'-C-methylated nucleoside antivirals is mediated by a single conservative mutation in NS5 that has a dramatic effect on viral fitness. *Journal of Virology* 91: e01028–17. [IF=4.368]
- **Eyer L.**, Zouharová D., Širmarová J., Fojtíková M., Štefánik M., Haviernik J., Nencka R., de Clercq E., **Růžek D.** 2017: Antiviral activity of the adenosine analogue BCX4430 against West Nile virus and tick-borne flaviviruses. *Antiviral Research* 142: 63–67. [IF=4.307]
- **Palus M.**, **Vancova M.**, **Sirmarova J.**, **Elsterova J.**, **Perner J.**, **Ruzek D.** 2017: Tick-borne encephalitis virus infects human brain microvascular endothelial cells without compromising blood-brain barrier integrity. *Virology* 507: 110–122. [IF=3.374]
- Salat J., Mihalca A.D., Mihaiu M., **Modrý D.**, **Ruzek D.** 2017: Tick-Borne Encephalitis in Sheep, Romania. *Emerging Infectious Diseases* 23: 2065–2067. [IF=7.422]

Research projects

- **Development and testing of novel perspective antivirals and their prodrug forms active against tick-borne encephalitis virus.** Czech Health Research Council (16-34238; P.I.: D. Růžek; 2016–2019).
- **Czech-Austrian Centre for Supracellular Medical Research** (Interreg: ATCZ14 – CAC-SuMeR; Co-P.I.: D. Růžek; 2016–2019).

4. BIOLOGY OF DISEASE VECTORS

4.1. Laboratory of Vector Immunology

Research scientists:	RNDr. **Petr KOPÁČEK**, CSc. (*head*) RNDr. **Lenka Grunclová**, PhD; RNDr. **Marie Jalovecká**, PhD.*; RNDr. **Daniel Sojka**, PhD; **Mgr. Jan Perner**, PhD.; RNDr. **Radek Šíma**, PhD*; RNDr. **Veronika Urbanová-Burešová**, PhD*
Research assistant:	Mgr. **Helena Frantová**
PhD students:	Mgr. **David Hartmann**; Mgr. **Matěj Kučera**
Undergraduate students:	**Tereza Hatalová**; **Barbora Plačková**; Bc. **Pavla Šnebergerová**; **Sára Kropáčková**; Bc. **Tereza Kozelková**; **Dominika Reichensdörferová**

* Also members of the research team of Ondřej Hajdušek.

Research priorities

Molecules involved in the tick innate immunity playing a role in pathogen (*Borrelia* and *Babesia*) transmission. Molecular physiology of blood digestion and haem and iron acquisition. Tick membrane feeding as a tool for the discovery of potential targets for efficient anti-tick intervention.

Interactions of tick complement system with model pathogens

The hard tick Ixodes ricinus possesses components of primordial complement system such as thioester-containing proteins (TEPs), fibrinogen-related lectins (ixoderins) and putative C3 convertases. In the year 2017, we focused mainly on RNAi-based functional characterization of nine TEPs, a putative convertase named IrC2/Bf, and Ixoderins A, B, and C. We found that these molecules play apecific and non-redundant roles in the phagocytosis of model microbes including *B. afzelii* spirochetes by tick haemocytes. However, our findings show that the complement-like reactions within tick hemocoel do not affect the transmission of *B. afzelii* and further support the results achieved in the Ondřej Hajdušek's laboratory denying the salivary route transmission of this spirochete.

Multi-enzyme digestive system of ticks

We have finished and published a characterization of multiple genes encoding tick legumains in the American hard tick *Ixodes scapularis*. Out of the nine homologs, only four are gut-specific. The predominant form is an ortholog of the previously described IrAE1 which is up-regulated by blood-meal uptake of all stages (larvae, nymphs, adults). By contrast, expression of the other prevailing form AE2 is relatively constitutive in all living stages including eggs.

In co-operation with the Institute of Organic Chemistry and Biochemistry, CAS, the comprehensive work on the **molecular structure of the *I. ricinus*** cathepsin D (IrCD1) and the detailed description of novel structural mechanism of allosteric regulation of this enzyme was accomplished and will be published in 2018 in the highly prestigious journal Cell Chemical Biology.

Tick membrane feeding as a tool for the discovery of potential anti-tick targets

Based on our previously published results, we have characterized a **heme-inducible glutathione** S-transferase named IrGST1. We found that this enzyme functions as a potent intracellular heme-binding protein and most likely serves as buffer of labile heme pool to ameliorate its cytotoxic effects upon hemoglobin intracellular hydrolysis in *I. ricinus* digest cells. The results were submitted for publication.

In order to identify **tick salivary molecules induced by host immunity**, we performed, in co-operation with Prof. J.M. Ribeiro (NIH, Bethesda), an extensive RNAseq-based study comparing salivary gland transcriptomes from *I. ricinus* female siblings fed either naturally on rabbits, or artificially on immune-deactivated rabbit blood. The achieved sequencing data are deposited in public databases and the related manuscript was recently submitted.

The static membrane feeding unit for artificial tick feeding was adapted to a continuous flow-system, that markedly reduces the amount of consumed blood, suppresses bacterial grow, increases the capacity of the feeding system and reduces the labor demand. The design of the new feeding system was submitted as a Utility model to the Czech Patent Office

Selected publications

- **Hartmann D.**, **Šíma R.**, **Konvičková J.**, **Perner J.**, **Kopáček P.**, **Sojka D.** 2017: Multiple legumain isoenzymes in ticks. *International Journal for Parasitology* 48: 167–178 [IF=3.078]
- **Honig Mondekova H.**, **Sima R.**, **Urbanova V.**, **Kovar V.**, **Rego R.O.M.**, **Grubhoffer L.**, **Kopacek P.**, **Hajdusek O.** 2017: Characterization of *Ixodes ricinus* Fibrinogen-Related Proteins (Ixoderins) Discloses Their Function in the Tick Innate Immunity. *Frontiers in Cellular and Infection Microbiology* 7: 509. [IF=3.520]
- **Urbanová V.**, **Hajdušek O.**, **Hönig Mondeková H.**, **Šíma R.**, **Kopáček P.** 2017: Tick Thioester-Containing Proteins and Phagocytosis Do Not Affect Transmission of *Borrelia afzelii* from the Competent Vector Ixodes ricinus. *Frontiers in Cellular and Infection Microbiology* 7: 73. [IF=3.520]
- Zavašnik-Bergant T., Vidmar .R, Sekirnik A., Fonović M., **Salát J.**, **Grunclová L.**, **Kopáček P.**, Turk B. 2017: Salivary Tick Cystatin OmC2 Targets Lysosomal Cathepsins S and C in Human Dendritic Cells. *Frontiers in Cellular and Infection Microbiology* 7: 288. [IF=3.520]

Research projects

- **The role of hemoglobin in tick metabolism and transmission of tick-borne pathogens.** Czech Science Foundation (13-110435S; P.I.: P. Kopáček; 2013–2017).
- **ANTIDotE (Anti-tick Vaccines to Prevent Tick-borne Diseases in Europe).** FP7 EU-HEALTH project (602272; Coordinator: J.W. Hovius; 2014–2018).
- **Interraction of tick complement with *Borrelia* and *Babesia*.** Czech Science Foundation (15-12006Y; P.I.: V. Urbanová; 2015–2017).
- **Selective inhibition of babesial proteasomes.** Czech Science Foundation (17-14631S; P.I.: D. Sojka; 2017–2019)

4.2. Laboratory of Genomics and Proteomics of Disease Vectors

Research scientist:	**Michail KOTSYFAKIS**, MSc, PhD (Greece) (*head*)
PhD student:	Mgr. **Jan Kotál**
Undergraduate students:	**Simone Röhrnbacher**; **Marnol Vacarescu-Linder** (both from Austria)
Administration associates:	Bc. **Jana Monhartová**

Research priorities

Our research maximises the public health benefits from the latest technical developments in molecular biology, genetics, genomics and proteomics; we employed the latest next-generation sequencing and quantitative proteomics methodologies with the ultimate goal of improving our understanding of the genetics underlying tick feeding and pathogen transmission. Given the technical difficulties in sequencing tick genomes, our high-throughput transcriptomic studies have provided new insights into how biological processes such as haematophagy and pathogen transmission are regulated by the underlying genetics, and enabled the first quantitative proteomic project on the tick *Ixodes ricinus*. We are currently developing a publicly available platform to host the sequencing data (and the resulting gene annotations) as a key step to support research on *I. ricinus* and to maximise the long-term value of our research results and datasets.

Our work aims to uncover tick proteins that facilitate the transmission of tick-borne pathogens. Tick-borne diseases are a serious public health concern in the Czech Republic (and Europe/the western world in general). Our results shed light on the molecular mechanisms that mediate transmission and pathogenesis of tick-borne diseases. Our group aims to discover novel gene functions, with an emphasis on describing novel tick salivary anti-proteases. We apply our well-established functional and structural analysis approaches to question whether salivary anti-proteases play an important role in the tick life-cycle. This knowledge will be important for the long-term development of improved tools and applications to control tick-borne diseases. Similar to most emerging and re-emerging infections, tick-borne diseases are thought to be vector-borne and transmitted to humans from animal reservoirs, but much remains unknown about the molecular events that take place at the tick-vertebrate host interface. Part of our work is to investigate the potential effects of various tick *I. ricinus* cysteine and serine protease inhibitors in macrophage, neutrophil and monocyte activation.

Our research advances the frontiers of knowledge in the field of tick-borne diseases. We are one of the few groups worldwide that couple high-throughput molecular and cellular techniques/disciplines to address important questions concerning the transmission life-cycle of ticks.

At the same time, our experience in characterising the pharmacological action of salivary anti-proteases in the vertebrate host brings us closer to novel practical applications such as drug and vaccine development that have the potential to better connect science with society (as demonstrated by our patents: 1. Patent number WO2012162611-A1; 2. Patent Number: WO2009017689-A2; WO2009017689-A3; US2010278752-A1).

Selected publications

- Hackenberg M., Langenberger D., **Schwarz A.**, **Erhart J.**, **Kotsyfakis M.** 2017: In silico target network analysis of de novo-discovered, tick saliva-specific microRNAs reveals important combinatorial effects in their interference with vertebrate host physiology. *RNA* 23: 1259–1269. [IF=4.490]
- Chmelař J., **Kotál J.**, **Langhansová H.**, **Kotsyfakis M.** 2017: Protease Inhibitors in Tick Saliva: The Role of Serpins and Cystatins in Tick-host-Pathogen Interaction. *Frontiers in Cellular and infection microbiology.* 7: 216. [IF=3.520]

Research projects

- **The effect of tick salivary serine protease inhibitors on host immune response.** Grant agency of the University of South Bohemia in České Budějovice, grant No. 038/2016/P (Jan Kotál)

4.3. Laboratory of Tick Transmitted Diseases

Research scientists:	RNDr. **Ondřej HAJDUŠEK**, PhD (*head*) RNDr. **Radek Šíma**, PhD*;
PhD students:	RNDr. **Marie Jalovecká***; Mgr. **Sazzad Mahmood**
Undergraduate students:	Mgr. **Tereza Pospíšilová**; **Kamila Bendová**; **Miriama Pekĺanská, Aneta Zemanová**
Technicians:	Ing. **Gabriela Loosová**; **Zuzana Zemanová**

* Also members of the research team of Petr Kopáček.

Research priorities

Laboratory of Tick Transmitted Diseases (founded in 2012) is focused on the molecular interactions between ticks (e.g. iron and heme metabolism pathway, tick immune molecules) and tick-transmitted pathogens and testing of anti-tick vaccines (improvement of the recent vaccine based on Ferritin 2) and vaccines interfering with the pathogen transmission. We have set-up in our laboratory (BSL2) complete transmission model for *Borrelia* infections, which we use for testing the tick candidate genes implicated in the tick-parasite interactions using method of RNA interference (RNAi) and also vaccines blocking the pathogen transmission. Recently, we set-up a system for testing *Babesia* infections and make an effort to set-up a system for *Anaplasma*. We have developed sensitive molecular methods for testing tick-borne diseases in humans and animals. The laboratory works in a close collaboration with the Laboratory of Vector Immunology (head P. Kopáček).

Antigens for a new vaccine against ticks and tick-transmitted diseases

Ticks are blood-feeding parasites and vectors of some of the most devastating viral, bacterial and protozoan diseases of humans and animals. *Ixodes ricinus* is a common tick in Europe including the Czech Republic, transmitting tick-borne encephalitis (TBE), Lyme disease (borreliosis), anaplasmosis and babesiosis. Immunisation of the hosts using recombinant tick proteins reduces tick feeding and, more importantly, blocks transmission of pathogens from the tick into the host. However, available tick antigens still do not reach sufficient efficacy. We use RNA interference (RNAi) to screen genes of *I. ricinus* potentially involved in the tick iron metabolism and heme acquisition in order to find suitable vaccine candidates affecting tick feeding and development. These candidates will be then tested for their potential to inhibit transmission of the pathogens. We believe that vaccination with these proteins may have a great potential as a control strategy to reduce tick feeding and transmission of pathogens.

Lyme disease and babesiosis transmission models

Lyme borreliosis is an emerging vector-borne disease of temperate climates with a concurrent distribution spanning North America and Eurasia. It is caused by spirochetes of the *Borrelia burgdorferi* sensu lato complex, which are transmitted through the *Ixodes* ticks. Although Lyme borreliosis is one of the best studied tick-borne zoonosis, the annual incidence leads over other vector-borne diseases with a continuous increase. There is currently no vaccine available to

prevent Lyme disease in humans. One of the promising strategies to break *Borrelia* transmission development is a vaccine affecting basic tick physiological processes. Development of a promising vaccine against Lyme borreliosis would be greatly facilitated by a reproducible vector-host transmission model. Our aim is to implement such model to find a molecule with proven anti-borrelial effect.

Babesiosis is a tick-borne, malaria-like disease of mammals. Because of the global environmental changes and continuous expansion of tick range, importance of babesiosis as an emerging zoonosis is increasing. Interplay between the parasite, tick and vertebrate host represents a complex system of multiple molecular interactions. To date, only a limited number of molecules have been identified to play a role in this system. Our research is focused on the identification and characterisation of molecular mechanisms of *Babesia* persistence within the tick vector and its transmission to the vertebrate host. We are currently working on the setting of the *Babesia microti* transmission model in our laboratory and use of this model for testing the tick immune genes in infection with *Babesia* spp. by RNA interference and vaccination.

Selected publications

- **Hönig Mondeková H.**, **Šíma R.**, **Urbanová V.**, **Kovář V.**, **Rego R. O. M.**, **Grubhoffer L.**, **Kopáček P.**, **Hajdušek O.** 2017: Characterization of *Ixodes ricinus* Fibrinogen-Related Proteins (Ixoderins) Discloses Their Function in the Tick Innate Immunity. *Frontiers in Cellular and Infection Microbiology* 7: 509. [IF= 3.520]
- **Urbanová V.**, **Hajdušek O.**, **Hönig-Mondeková H.**, **Šíma R.**, **Kopáček P.** 2017: Tick Thioester-Containing Proteins and Phagocytosis Do Not Affect Transmission of *Borrelia afzelii* from the Competent Vector *Ixodes ricinus*. *Frontiers in Cellular and Infection Microbiology* 7: 73. [IF=3.520]
- Wegener Parfrey L., **Jirků M.**, **Šíma R.**, **Jalovecká M.**, **Sak B.**, Grigore K., **Jirků-Pomajbíková K.** 2017: Abening helminth alters the host immune system and the gut microbiota in a rat model system. *PLoS ONE* 12: e0182205. [IF=2.766]

Research projects

- **ANTIDotE – Anti-tick vaccines to prevent tick-borne diseases in Europe.** FP7 HEALTH project (602272; P.I.: J. Hovius; 2014–2018).
- **Přenosový model Lymeské borreliózy.** Technology Agency of the Czech Republic (TG02010034; P.I.: R. Šíma; 2016–2017).
- **Identification and characterization of the tick salivary glands and midgut molecules involved in the interaction with pathogens.** GAČR (17-27386S; P.I.: O. Hajdušek)
- **Revision of *Borrelia afzelii* transmission cycle: essential step for Lyme disease interventions.** GAČR (17-27393S; P.I.: R. Šíma)

5. FISH PARASITOLOGY

5.1. Laboratory of Helminthology

Research scientists:	Prof. RNDr. **Tomáš SCHOLZ**, CSc. (*head*) RNDr. **František Moravec**, DrSc. (*researcher emeritus*) RNDr. **Jan Brabec**, PhD; RNDr. **Anna Faltýnková**, PhD; **Simona Georgieva**, MSc, PhD (Bulgaria); **Aneta Kostadinova**, MSc, PhD (Bulgaria); RNDr. **Roman Kuchta**, PhD; Mgr. **Miroslava Soldánová**, PhD
Temporary contracts from projects:	
	MVDr. **Daniel BARČÁK**, PhD. (Slovakia); **Ana Born-Torrijos**, MSc, PhD (Spain); **David González-Solís**, MSc, PhD (Mexico); RNDr. **Mikuláš Oros**, PhD (Slovakia); **Jesus Hernández-Orts**, MSc, PhD (Mexico); **Aneta Yoneva**, MSc, PhD (Bulgaria)
PhD students:	**Philippe Vieira Alves** (Brazil); Mgr. **Jana Roháčová** (maternity leave)
Research assistants:	Ing. **Radmila Řepová** (part time); Ing. **Blanka Škoríková**
Technician:	**Martina Borovková**
Laboratory worker:	**Alena Widnerová**
Undergraduate students:	Bc. **Lucie Cibulková**; Bc. **Pavla Heinclová**; Bc. **Hynek Mazanec**; Bc. **Lucie Uhrová**; Bc. **Tereza Vyhlídalová**; **Miroslava Čeňková**

Research priorities

Systematics, phylogeny, life-cycles & ecology of parasitic flatworms, taxonomy of nematodes, diversity of fish helminths, and fish-borne parasitic diseases (broad fish tapeworm).

Diversity of helminths parasitising teleost fish

Using methods of integrative taxonomy, several groups of parasitic flatworms (Cestoda, Digenea and Monogenea) and nematodes (Nematoda), parasites of freshwater and marine fish and other vertebrates, have been revised and new data on their diversity, host associations and interrelations provided. Studies have been focused on hot spots of teleost diversity in freshwaters (Amazonia), and seas off Africa, America and Asia. Several projects are carried out also in Europe.

Systematics and evolution of basal tapeworms (Cestoda)

Based on collaborative effort supported by a NSF-PBI funded project, global diversity of tapeworms has been assessed using morphological and molecular evaluation of newly collected and museum materials. Data on the diversity, morphology, host-associations and phylogenetic relationships of ten cestode orders have been compiled by the lab staff for a monograph that would provides a most comprehensive survey of the current knowledge of this group of helminth parasites.

Integrative taxonomy approaches to trematode diversity and life-cycles

A series of studies focused on species delimitation using integrated molecular, morphological and ecological evidence provided reliable estimates of the diversity and/or information on the life histories of the trematodes in natural host populations. Focus was on eye=flukes, i.e. metacercariae of diplostomid trematodes in freshwater fishes, and trematodes of marine fishes in the Mediterranean Sea.

Selected publications

- Caira J.N., Jensen K., **Georgiev B.B.**, **Kuchta R.**, Littlewood D.T.J., Mariaux J., **Scholz T.**, Tkach V.V., Waeschenbach A. 2017: An overview of the tapeworms of vertebrate bowels of the earth. In: J.N. Caira and K. Jensen (Eds.), Planetary Biodiversity Inventory (2008–2017): Tapeworms from Vertebrate Bowels of the Earth. University of Kansas, Natural History Museum, Special Publication No. 25, USA, pp. 1–20.
- **Kuchta R.**, Oros M., Ferguson J., **Scholz T.** 2017: *Diphyllobothrium nihonkaiense* tapeworm larvae in salmon from North America. *Emerging Infectious Diseases* 23: 351–353. [IF=7.422]
- **Moravec, F.**, Chaabane, A., Neifar, L., Gey, D., Justine, J.-L. 2017: Species of *Philometra* (Nematoda, Philometridae) from fishes off the Mediterranean coast of Africa, with a description of *Philometra rara* n. sp. from *Hyporthodus haifensis* and a molecular analysis of *Philometra saltatrix* from *Pomatomus saltatrix*. *Parasite* 24: 8. [IF=2.069]
- **Soldánová M.**, **Georgieva S.**, **Roháčová J.**, Knudsen R., Kuhn J.A., Henriksen E.H., Siwertsson A., Shaw J.C., Kuris A.M., Amundsen P.-A., **Scholz T.**, Lafferty K.D., **Kostadinova A.** 2017: Molecular analyses reveal high species diversity of trematodes in a sub-Arctic lake. *International Journal for Parasitology* 47: 327–345. [IF=3.078]
- Waeschenbach A., **Brabec J.**, **Scholz T.**, Littlewood D.T.J., **Kuchta R.** 2017: The catholic taste of broad tapeworms - multiple routes to human infection. *International Journal for Parasitology* 47: 831–843. [IF=3.078]

Research projects

- **A Survey of the Tapeworms (Cestoda: Platyhelminthes) from the Vertebrate Bowels of the Earth.** National Science Foundation, USA (Planetary Biodiversity Inventory; Co-P.I.: T. Scholz; P.I.: J.N. Caira, University of Connecticut, Storrs; 2008–2017).
- **ECIP – European Centre of Ichthyoparasitology.** Czech Science Foundation – centres of excellence (P505/12/G112; Co-P.I.: T. Scholz; P.I.: M. Gelnar, Masaryk University, Brno; 2012–2018).
- **Species boundaries and microevolutionary patterns in parasites with high dispersal abilities: a model study of two flatworm systems.** Czech Science Foundation (15-14198S; P.I.: T. Scholz; 2015–2017).

5.2. Laboratory of Fish Protistology

Research scientists:	**Astrid HOLZER**, MSc, PhD (Austria) (head) **Gema Alama-Bermejo**, MSc, PhD (Spain); **Ana Born-Torrijos**, MSc, PhD (Spain); RNDr. **Ivan Fiala**, PhD; RNDr. **Miloslav Jirků**, PhD; Mgr. **Tomáš Korytář**, PhD; **Anush Kosakyan**, MSc, PhD (Armenia/Italy); RNDr. **Alena Lövy** (Kodádková), PhD; RNDr. **Pavla Sojková-Bartošová**, PhD (Slovakia); **Carlos Yanes-Roca**, MSc, PhD (Spain)
PhD students: RNDr.	**Martina Lisnerová**; RNDr. **Jiří Kyslík**
Research assistant:	RNDr. **Hana Pecková**
Technician:	**Marie Fučíková** (part time)
Laboratory worker:	**Ivana Reitingerová**
Undergraduate students:	**Vyara Ganeva** (Bulgaria), BSc; Bc. **Martina Jedličková**; **Ricarda Marko** (Austria); **Anna Tomanová**;

Research priorities

We focus on eukaryotic microorganisms infecting fish and amphibians, including all aspects of their biology, life cycles, host-parasite interactions, their phylogeny and evolution as well as applied reseach based on genomics, proteomics and immunology. The latter aims at the development of functional diets and and vaccines for the aquaculture industry. Our main group of interest is the Myxozoa but we carry out research into a range of other protists, which create economic and health consequences, in collaboration with various academic and commercial partners worldwide.

Biodiversity, phylogeny and evolution

Besides taxonomic descriptions, phylogeny of newly described parasite taxa and the interpretation of evolutinary trends in in different microscopic parasites, our biodiversity research now focusses much on studying parasite population structure in interesting habitats (e.g. South African rock pools) and on obtaining diversity data from aquatic eDNA samples (water filtrates and sediment elutions). Considerable time was invested in designing optimal markers and assays for next generation sequencing, aiming at the detection of Myxozoa and on comparing species richness and diversity in different marine and freshwater habitats. A large evolutionary study elucidated the mechanisms of myxozoan success and vast biodiversity by disentangling the joint evolution of these parasites and their alternate hosts. We demonstrated that myxozoans, despite their indirect life cycle, are extremely successful *de novo* settlers. Myxozoans have the fastest evolutionary rate of eukaryotes and are incredibly flexible with regard to swiching to unrelated host types. Molecular clock analyses demonstrated that they are evolutionary old parasites (588 myrs) which first invaded invertebrate hosts before settling in cartilaginous fish, tetrapods and teleosts, on repeated occasions, hence contradicting previous theories on the evolutionary history of this parasite group.

Functional and applied reseach

Large transcriptomic datasets of the salmon pathogen *Ceratonova shasta* were compared computationally over the last years, identifying important virulence factors in different

genotypes. The presence and expression level of motility-related genes and proteolytic enzymes were determined as the most important factors defining virulence in myxozoans. The evolution and functional characterisation of proteases and protease inhibitors that play a key role in myxozoan-fish host interplay are another main focus. Some of these proteins clearly define the success of myxozoan infections. Much progress was made in establishing our myxozoan model organism, *Sphaerospora molnari*. We are the only laboratory worldwide that centres its research on early proliferative stages of myxozoans in the blood, rather than investigating genes and proteins expressed during spore formation. A large immunological experiment elucidated the whereabouts of the parasites during the first 63 days of infection and the demonstrated the acquisition of specific immunity of carp to *S. molnari*, however host-evasion mechanisms allow the parasite to further proliferate at later stages of infection. These studies are essential for designing antiparasitic strategies, and we are currently testing the effect of immunostimulatory and parasiticidal diets on parasite proliferation rates.

Selected publications

- **Jirsová D.**, **Štefka J.**, **Jirků M.** 2017: Discordant population histories of host and its parasite: A role for ecological permeability of extreme environment? *PLoS ONE* 12: e0175286. [IF=2.766]
- Mulot M., Marcisz K., Grandgirard L., Lara E., **Kosakyan A.,** Robroek B.J.M., Lamentowicz M., Payne R.J., Mitchell, E.A.D. 2017: Genetic Determinism vs. Phenotypic Plasticity in Protist Morphology. *Journal of Eukaryotic Microbiology* 64: 729–739. [IF=2.537]
- **Patra, S.**, **Hartigan A.**, Morris, D.J., **Kodádková A.**, **Holzer A.S.** 2017: Description and experimental transmission of *Tetracapsuloides vermiformis* n. sp. (Cnidaria: Myxozoa) and guidelines for describing malacosporean species including reinstatement of *Buddenbrockia bryozoides* n. comb. (syn. *Tetracapsula bryozoides*). *Parasitology* 144: 497–511. [IF=2.511]
- Tanifuji G., Cenci U., Moog D., Dean S., Nakayama T., **David V.**, **Fiala I.**, Curtis B.A., Sibbald S.J., Onodera N.T., Colp M., **Flegontov P.**, Johnson-MacKinnon J., McPhee M., Inagaki Y., Hashimoto T., Kelly S., Gull K., **Lukeš J.**, Archibald J.M. 2017: Genome sequencing reveals metabolic and cellular interdependence in an amoebakinetoplastid symbiosis. *Scientific Reports* 7: 11688. [IF=4.122]

Research projects

- **ECIP – European Centre Ichthyoparasitology.** Centre of Excellence, Czech Science Foundation (505/12/G112; Coordinator: M. Gelnar, Masaryk University, Brno; I. Co-P.I.: A.S. Holzer; II. Co-P.I.: I. Fiala; 2012–2018).
- **Inhibitors of cysteine proteases crucial for myxozoan pathogenicity and their interaction with the fish host.** Program Inter-Excellence, subprogram Inter-Action (MŠMT; LTAUSA17201; PI: P. Sojková, 2017-2021)
- **Large scale fish and water environment screening to assess the biodiversity of the Myxozoa: a metagenomic approach.** Czech Science Foundation (16-20744S; P.I.: I. Fiala; 2016–2018).
- **Marine Myxozoa and their link to meiofauna: Communities, biodiversity and life cycles.** Swedish Research Council (2016-00541; PI: I. Martinek, 2016-2019).
- **ParaFishControl – Advanced tools and research strategies for parasite control in European farmed fish.** European Commission, RIA – Research and Innovation action, H2020 SFS-2014-2 Sustainable Food Security (634429; Coordinator: A. Sitjá-Bobadilla; 2015–2020).
- **Testing parasiticidal and immunomodulatory substances to combat myxozoan infections in aquaculture using novel *in vitro* and *in vivo* models.** Technology Agency of the Czech Republic (TG02010016; P.I.: A.S. Holzer; 2016–2018).
- **Turn the tide on limited myxozoan phylogeny: using high throughput sequencing to discover new Myxozoa species from the Southwest Atlantic Ocean.** CAS (CR)/ CONICET (Argentina) - Bilateral mobility project (CONICET-16-10, PI: A.S. Holzer, 2017-2018).
- **Transmission strategy and parasitic load of *C. longicollis* hosts in relation to Mediterranean aquaculture.** CAS Programme of Support of Postdoctoral Fellowships (MSM200961706; P.I.: A. Born-Torrijos; 2017-2019)

6. OPPORTUNISTIC DISEASES

6.1. Laboratory of Veterinary and Medical Protistology

Research scientists:	prof. Ing. **Martin KVÁČ**, PhD (*head*) prof. MVDr. **David Modrý**, PhD (part time); RNDr. **Bohumil Sak**, PhD; RNDr. Klára Petrželková, PhD (part time);
PhD students:	Ing. **Šárka Čondlová**; Ing. **Nikola Havrdová**; Ing. **Nikola Holubová;** Ing. **Michaela Horčičková**; RNDr. **Michaela Kotková**, DiS; MVDr. **Jitka Prediger**; Ing. **Veronika Prantlová**
Research assistants:	Ing. **Lenka Hlásková**; RNDr. **Jana Ježková**; RNDr. **Dana Květoňová**;
Undergraduate students:	Bc. **Klára Brdíčková**; **Jan Ferencová**; Bc. **Klára Kellnerová**; **Kristýna Pačesová**; Bc. **Vendula Tomanová**; **Veronika Tomancová**; **Tereza Vecková**; **Gabriela Vlnatá, Veronika Zikmundová**

Research priorities

The focus of this group is to determine the zoonotic sources of emerging parasitic diseases, especially the opportunistic nature of the occurrence of cryptosporidia and microsporidia in immunodeficient (e.g. AIDS) patients and animals.

Cryptosporidium in cricetids from North America and Europe

We reported an occurrence of *Cryptosporidium* in wild cricetid rodents. The isolates were characterized by sequence and phylogenetic analyses of the small subunit ribosomal RNA and actin genes. A phylogeny and principal coordinate analysis showed that closely related cricetid hosts in Europe and North America are infected with closely related *Cryptosporidium* genotypes. Additionally more at least nine novel cryptosporidia characterized by different host specificity has been reported.

Cryptosporidium infections in native and introduced squirrels in Europe

The occurrence of *Cryptosporidium* infection in population of naive and introduced squirrels was studied. Despite the overlapping ranges of native and introduced tree squirrel species in the study area, they host different *Cryptosporidium* spp. Based on the result of the study was proposed that *Cryptosporidium* skunk genotype and possibly *C. ubiquitum* subtype XIIb were introduced to Europe with eastern grey squirrels. C*ryptosporidium* chipmunk genotype I and ferret genotype were associated with high intensity infections, but not with diarrhea.

Infection of different *Encephalitozoon cuniculi* genotypes in a host with different immune status

Although the primary sites of infection caused by *E. cuniculi* are the small intestine and respiratory tract, it can cause disseminated infection, particularly in hosts with impaired immune

function. It has been shown that *Encephalitozoon* persists in immunocompetent hosts for a long time and can be re-activated. Contrast to encephalitozoonosis caused by *E. cuniculi* II, that caused by *E. cuniculi* III had very progressive spreading into all organs within first week post inoculation. The experimental treatment with albendazole of immunocompetent mice infected with *E. cuniculi* III has shown a very weak effect compared to treated animals infected with *E. cuniculi* II.

Selected publications

- **Kotková M.**, **Sak B.**, **Hlásková L.**, **Kváč M.** 2017: The course of infection caused *by Encephalitozoon cuniculi* genotype III in immunocompetent and immunodeficient mice. *Experimental Parasitology* 182: 16–21. [IF=1.821]
- Piekarska J., Kicia M., Wesołowska M., Kopacz Z., Gorczykowskia M., Szczepankiewicza B., **Kváč M.**, **Sak B.** 2017: Zoonotic microsporidia in dogs and cats in Poland. *Veterinary Parasitology* 246: 108–111. [IF=2.422]
- **Prediger J.**, **Horčičková M.**, Hofmannová L., **Sak B.**, Ferrari N., Mazzamuto M.V., Romeo C., Wauters L.A., McEvoy J., **Kváč M.** 2017: Native and introduced squirrels in Italy host different *Cryptosporidium* spp. *European Journal of Protistology* 61: 64–75. [IF=2.430]
- **Sak B.**, **Kotková M.**, **Hlásková L.**, **Kváč M.** 2017: Limited effect of adaptive immune response to control encephalitozoonosis. *Parasite Immunology* 39: e12496. [IF=2.836]

Research projects

- **The application of molecular methods to identify and characterize microsporidia in immunocompetent and immunosuppressed patients with kidney disease and evaluating the impact of selected drugs on the process of microsporidia invasion in *in vitro* research.** National Science Centre, Poland (P.I. Kicia; Contractor: M. Kváč; 2013–2017).
- **Revealing *Cryptosporidium* diversity: linking genetic variation to parasite biology.** Czech Science Foundation (15-01090S; P.I.: M. Kváč; 2015–2017).
- **Elucidation of different virulence and drug resistance of genotypes of *Encephalitozoon cuniculi* using murine model.** Czech Science Foundation (17-12871S; P.I.: B. Sak; 2017–2019).
- **Diversity and co-evolution of *Cryptosporidium* parasiting in rodents: Linking genetic variation to parasite biology.** The Ministry of Education, Youth and Sports (LTAUSA17165; P.I.: M. Kváč; 2017–2020).

6.2. Laboratory of Parasitic Therapy

Research scientists:	MVDr. **Kateřina JIRKŮ-POMAJBÍKOVÁ**, PhD (*head*)
	RNDr. **Milan Jirků**; Mgr. **Kateřina Sobotková**, PhD;
Technicians:	RNDr. **Blanka Macháčková**; Bc. **Oldřiška Hložková**
Undergraduate students:	**Oldřiška Hložková**; **Jana Levá**; **Zuzana Lhotská**; **Lucie Řežábková**; **Jiřina Růžková**; **Kristýna Brožová**

Research priorities

Main lines of this laboratory are focused on investigation of an impact of the commensal gut eukaryotes (protists and helminths) on some immune-mediated diseases (IMD). The incidence and prevalence of IMD has increased in Western countries over the past decades. IMDs continue to emerge in new countries as they develop and adopt to Western life-styles and is becoming a global disease. Abundant evidence now suggests that the dysbiosis of gut microbiome (including viruses, bacteria, archaea, fungi and eukaryotes) is one of the main risk factors for developing some IMD (e.g. Inflammatory Bowel Diseases). The increase in IMD incidence is also associated with loss of helminth infection. Very recently, the research has shown that helminths, gut bacterial communities and even commensal protist inhabiting gut may positively influence the health status of individuals suffering from some IMD.

When the Laboratory of Parasitic Therapy opened at the Institute of Parasitology (in October 2013), it was obvious that the fulfilling of the early promise of helminth therapy likely requires widening the scope of investigation to its influence on the gut bacterial microflora and additional organisms (more suitable helminth candidates and protists) and novel therapeutic strategies. We have identified two candidates of gut eukaryotes for our research - one helminth and protist. Our results showed that helminth candidate is able to ameliorate chemically induced colitiis. However, we need to indetified the imunological mechanisms reponsible for supression of inflammation. In case of helminth, we also test the effect of its extract on inflammation. Our preliminary data from the pilot study focused on the protist candidate also suggest its anti-inflammatory effect on the cheminically induced colitis.

Characterisation of the diversity and functional changes of the bacterial microbiota in the intestine using next-generation sequencing is conducted in the collaborative laboratory headed by Laura Wegener Parfrey at the University of British Columbia, Vancouver, Canada.

Selected publications

- Červená B., Vallo P., Pafčo B., **Jirků K.**, **Jirků M.**, Petrželková K.J., Todd A., Turkalo A.K., Modrý D. 2017: Host specificity and basic ecology of Mammomonogamus (Nematoda, Syngamidae) from lowland gorillas and forest elephants in Central African Republic. *Parasitol* 144: 1016–1025. [IF= 2.511]
- Jirků-Pomajbíková K., Stensvold C.R. 2017: *Balantioides coli* (Formerly *Balantidium coli*). In: S.S. Long, Ch. G. Prober, M. Fischer (Eds.), Principles and Practice of Pediatric Infectious Diseases, 5th Edition. Elsevier Inc., USA, pp. 1303–1305.
- Parfrey W. L., **Jirků M.**, **Šíma R.**, **Jalovecká M.**, **Sak B.**, Grigore K., **Jirků-Pomajbíková K.** 2017: A benign helminth alters the host immune system and the gut microbiota in a rat model system. *PLoS ONE* 12: e0182205. [IF= 2.766]
- Ponce-Gordo F., Jirků-Pomajbíková K. 2017: *Balantidium coli,* PART III – Specific excreted pathogens: Environmental and epidemiology aspects. In: J.B. Rose, B. Jiménez-Cisneros (Eds.), UNESCO - Global Water Pathogens Project, http://www.waterpathogens.org. (online book)

Research projects

- **Interplay of eukaryotic symbionts with gut microbiome and influence on immune-mediated disorders.** Young investigator category, agency: Human Frontiers Science Program Organization (RGY0078/2015; P.I.: K. Jirků-Pomajbíková; 2015–2019)

Supporting facility

Laboratory of Electron Microscopy

Research scientists:	Ing. **Jana NEBESÁŘOVÁ**, CSc. (*head*) RNDr. **Marie Vancová**, PhD; Ing. **Zdenko Gardian**, PhD (part-time job)
PhD students:	Mgr. **Tomáš Bílý**; Mgr. **Martin Strnad**
Technicians:	Mgr. **Jan Langhans**; **Petra Masařová**; Mgr. **Martina Tesařová**; **Jiří Vaněček**
Undergraduate students:	Bc. **Ayya Tashlieva**; **Dominik Bauman** (Austria); **Johannes Grahammer** (Austria)

Research priorities

Electron microscopy is used to image the structure of molecules, cells and tissues at sub-nanometer resolution. Transmission electron microscopy (TEM) is dedicated for the examination of samples cut into ultrathin sections with the thickness 80–100 nm so that the electron beam can pass through the sample and form an image on the detector. In scanning electron microscopy (SEM), the electron beam is scanned over the small sample area to produce secondary signals carrying information about the specimen surface topography or composition. The team of the Laboratory of Electron Microscopy (LEM) works closely with several research groups of the Biology Centre but also from other institutions to plan, optimise and implement experiments, producing images that allow scientists to understand their samples at the subcellular level. Members of LEM are experts in preparing, imaging and interpreting a wide range of biological samples. They use a broad spectrum of traditional and novel preparation techniques for optimum preservation of sample morphology and localisation of proteins. Since 2016 LEM has been involved in a distributed national research infrastructure Czech-BioImaging (https://www.czech-bioimaging.cz/), which provides an open access to a wide range of imaging technologies and expertise to all scientists in the Czech Republic and from abroad by a unified and coordinated logistics approach.

Technical equipment

Transmission electron microscopes

- JEOL 2100F (2012) equipped for electron tomography, STEM and image recording with CCD camera Orius SC1000 (Gatan)
- JEOL 1010 (1996) equipped with SSC camera MegaView 3
- Low voltage electron microscope LV EM 5 (2002), Delong Instruments, Inc.

Scanning electron microscopes

- JEOL 7401F (2005) with cryo-attachment ALTO 2500 GATAN
- JEOL 6300 (1993)

Ultramicrotomes Leica with and without cryo-chamber.

High Pressure Freezer Leica EM Pact2 – a system for vitrifying samples up to 200 μm in thickness without the artifacts of chemical fixation.

Automatic freeze substitution system Leica EM AFS for substitution and low temperature embedding after cryofixation and for the PLT technique.

Selected results

- Peña-Diaz P, **Vancová M**, Resl C, Field MC, Lukeš J. 2017: A leucine aminopeptidase is involved in kinetoplast DNA segregation in *Trypanosoma brucei*. *PLoS Pathogens* 13: e1006310. [IF = 6.158]
- Sytnyk M., Jakešová M., Litviňuková M., Mashkov O., Kriegner D., Strangl J., **Nebesářová J**., Fecher F.W., Schöfberger, Sariciftci N.S., Schindl R., Heiss W., Glowacki E.D. 2017: Cellular interfaces with hydrogen-bonded organic semiconductor hierarchical nanocrystals. *Nature Communications* 8: 91. [IF=12.353]
- **Vancová M.**, Rudenko N**., Vaneček J.**, Golovchenko M**., Strnad M.**, Rego R.O.M**.,** Tichá L., Grubhoffer L., **Nebesářová J.** 2017: Pleomorphism and viability of the Lyme disease pathogen *Borrelia burgdorferi* exposed to physiological stress conditions: a correlative cryo-fluorescence and cryo-scanning electron microscopy study. *Frontiers in Microbiology* 8: 596. [IF=4.019]

Research projects

- **Electron Microscopy.** Programme of the Technology Agency of the Czech Republic to support the development of long-term collaboration of the public and private sectors on research, development and innovations. The project is managed by a consortium of representatives of eight participating organisations – Thermo Fisher Scientific, Delong Instruments, Crytour, Institute of Macromolecular Chemistry of the Czech Agency of Sciences (CAS), Institute of Molecular Genetics of CAS, Institute of Scientific Instruments of CAS, Biology Centre of CAS (LEM), Research and Testing Institute Plzeň (2012–2019).
- **National Infrastructure for Biological and Medical Imaging – Czech-BioImaging.** Project is supported by the Ministry of Education, Youth and Sports. Programme of Large Research Infrastructure (LM2015062; Main coordinator: Institute of Molecular Genetics of CAS; 2016–2022).
- **Modernization and support of research activities of the national infrastructure for biological anmedical imaging Czech-BioImaging.** Project is supported by Ministry of Education, Youth and Sports, project n. CZ. 02.1.01/0.0/0.0/16_013/0001775. Main coordinator: Institute of Molecular Genetics, 2017–2020.

Special activities

Collections of parasitic organisms

An extensive collection of helminths (curator Tomáš Scholz) is available for comparative studies. It comprises more than 3,000 species from around the world, including numerous type specimens. A collection of holotypes and paratypes of about 300 species of parasitic arthropods, on 430 microscopic slides, is deposited at the Institute, as well as a large collection of several thousand specimens of parasitic mites and fleas from mammals, birds and reptiles, and a small collection of ticks in alcohol. The Institute maintains laboratory colonies of ticks (8 species), mosquitoes (4 species, 5 lines) and arboviruses (33 species and strains). A collection of cryopreserved cultures of blood flagellates and amphizoic amoebae is maintained at the Laboratory of Fish Protistology. More information can be found at http://www.paru.cas.cz/en/collections/.

Publishing and editorial activities

FOLIA PARASITOLOGICA – an international journal

Editor-in-Chief: **Tomáš Scholz**

Assistant Editors: **Ivan Fiala** (parasitic protists & myxozoans; molecular phylogenetics)
Jan Štefka (ecology of parasites & parasitic arthropods) (from January)
Tomáš Scholz (helminths)

Editorial Assistant: **Petra Rozkošná**

Folia Parasitologica is an international journal for parasitology, publishing articles written in English. It was founded in 1953 as an annual edition; from 1966 until 2014, it was published four times a year. Since January 2015, the journal has been moved to an Open Access mode, without any hard copies published. Editor-in-Chief and three Assistant Editors from the Institute of Parasitology are aided by an international Board of Editorial Advisors, consisting of 23 highly regarded scientists, overwhelming majority of them being foreign parasitologists. The rejection rate is more than 60%. *Folia* has a wide international authorship. The Impact Factor of *Folia* was 1.505 in 2017; five-year Impact Factor is 1.342.

CzechoSlovak virology conference 2017, České Budějovice, 16–17th February 2017

Dedicated in memory of deceased Dr. Dimitrij Slonim to tribute his merit in research, development and production of polio, smallpox, rabies, measles and mumps vaccines as well as other outstanding achievements in the area of viral infectious diseases of human.

Our goal is to bring together scientists working on all fields of virology research from basic to applied and clinical science. We hope that this conference increase the overall awareness of the cutting edge virology research and will serve to stimulate scientific exchange and create opportunities for new collaborations among the participants.

Publication activities

Published in 2017

Authors explicitly affiliated to the Institute of Parasitology are enboldened

1. ACOSTA A.A., FRANCESCHINI L., ZAGO A.C., **SCHOLZ T.**, DA SILVA R.J. 2017: Six new species of *Heteropriapulus* (Monogenea: Dactylogyridae) from South American fishes with an amended diagnosis to the genus. *Zootaxa* 4290: 459–482. [IF=0.931]
2. ACOSTA A.A., **GONZÁLEZ-SOLÍS D.**, DA SILVA R.J. 2017: *Spinitectus aguapeiensis* n. sp. (Nematoda: Cystidicolidae) from *Pimelodella avanhandavae* Eigenmann (Siluriformes: Heptapteridae) in the River Aguapeí, Upper Paraná River Basin, Brazil. *Systematic Parasitology* 94: 649–656. [IF=1.273]
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137. **TÝČ J.**, NOVOTNÁ L., **PEÑA-DIAZ P.**, MASLOV D.A., **LUKEŠ J.** 2017: RSM22, mtYsxC and PNKD-like proteins are required for mitochondrial translation in *Trypanosoma brucei*. *Mitochondrion* 34: 67–74. [IF=3.226]

138. **URBANOVÁ V., HAJDUŠEK O., HÖNIG MONDEKOVÁ H., ŠÍMA R., KOPÁČEK P.** 2017: Tick Thioester-Containing Proteins and Phagocytosis Do Not Affect Transmission of *Borrelia afzelii* from the Competent Vector *Ixodes ricinus*. *Frontiers in Cellular and Infection Microbiology* 7: 73. [IF=3.520]

139. **VALDÉS J.J., BUTTERILL P.T., RŮŽEK D.** 2017: *Flaviviridae* viruses use a common molecular mechanism to escape nucleoside analogue inhibitors. *Biochemical and Biophysical Research Communications* 492: 652–658. [IF=2.559]

140. **VANCOVÁ M., RUDENKO N., VANEČEK J., GOLOVCHENKO M., STRNAD M., REGO R.O., TICHÁ L., GRUBHOFFER L., NEBESÁŘOVÁ J.** 2017: Pleomorphism and viability of the Lyme disease pathogen *Borrelia burgdorferi* exposed to physiological stress conditions: a correlative cryo-fluorescence and cryo-scanning electron microscopy study. *Frontiers in Microbiology* 8: 596. [IF=4.019]

141. **VÁVRA J.**, HYLIŠ M., **FIALA I.**, SACHEROVÁ V., VOSSBRINCK C.R. 2017: Microsporidian genus *Berwaldia* (Opisthosporidia, Microsporidia), infecting daphnids (Crustacea, Branchiopoda): Biology, structure, molecular phylogeny and description of two new species. *European Journal of Protistology* 61: 1–12. [IF=2.430]

142. VIDAL O., DRÖGEMÜLLER C., OBEXER-RUFF G., REBER I., JORDANA J., MARTÍNEZ A., BÂLTEANU V.A., DELGADO J.V., EGHBALSAIED S., LANDI V., GOYACHE F., TRAORÉ A., PAZZOLA M., VACCA G.M., BADAOUI B., PILLA F., D'ANDREA M., ÁLVAREZ I., CAPOTE J., **SHARAF A.**, PONS A., AMILLS M. 2017: Differential distribution of Y-chromosome haplotypes in Swiss and Southern European goat breeds. *Scientific Reports* 7: 16161. [IF=4.122]

143. WAESCHENBACH A., **BRABEC J.**, **SCHOLZ T.**, LITTLEWOOD D.T.J., **KUCHTA R.** 2017: The catholic taste of broad tapeworms - multiple routes to human infection. *International Journal for Parasitology* 47: 831–843. [IF=3.078]

144. WEGNER PARFREY L., **JIRKŮ M.**, **ŠÍMA R.**, **JALOVECKÁ M.**, **SAK B.**, GRIGORE K., **JIRKŮ POMAJBÍKOVÁ K.** 2017: A bening helminth alters the host immune system and the gut microbiota in a rat model system. *PLoS ONE* 12: e0182205. [IF=2.766]

145. **YONEVA A.**, **KUCHTA R.**, MARIAUX J., GEORGIEV B.B. 2017: The first data on the vitellogenesis of paruterinid tapeworms: an ultrastructural study of *Dictyterina cholodkowskii* (Cestoda: Cyclophyllidea). *Parasitology Research* 116: 327–334. [IF=2.558]

146. YOUNG C., MILLER M.A., **KUCHTA R.**, **BRABEC J.**, NEWSOME S.D., DAILEY M. 2017: First Report of an Adult Tapeworm (Cestoda: Diphyllobothriidea) in a Southern Sea Otter (*Enhydra lutris nereis*). *Journal of Wildlife Diseases* 53: 934–937. [IF=1.247]

147. ZAVAŠNIK-BERGANTT., VIDMARR., SEKIRNIKA., FONOVIĆM., **SALÁTJ.**, **GRUNCLOVÁL.**, **KOPÁČEK P.**, TURK B. 2017: Salivary tick cystatin OmC2 targets lysosomal cathepsins S and C in human dendritic cells. *Frontiers in Cellular and Infection Microbiology* 7: 288. [IF=3.520]

148. **ZÍKOVÁ A.**, **VERNER Z.**, **NENAROKOVA A.**, MICHELS P.A.M., **LUKEŠ J.** 2017: A paradigm shift: the mitoproteomes of procyclic and bloodstream *Trypanosoma brucei* are comparably complex. *PLoS Pathogens* 13: e1006679. [IF=6.158]

Papers in peer-reviewed journals (not yet with impact factor)

1. BOSCARO V., **KOLÍSKO M.**, FELLETTI M., VANNINI C., LYNN D.H., KEELING P.J. 2017: Parallel genome reduction in symbionts descended from closely related free-living bacteria. *Nature Ecology & Evolution* 1: 1160–1167.

2. FERNÁNDEZ DE MERA I.G., CHALIGIANNIS I., HERNÁNDEZ-JARGUÍN A., VILLAR M., MATEOS-HERNÁNDEZ L., PAPA A., SOTIRAKI S., RUIZ-FONS F., **CABEZAS-CRUZ A.**, GORTÁZAR C., DE LA FUENTE J. 2017: Combination of RT-PCR and proteomics for the identification of Crimean-Congo hemorrhagic fever virus in ticks. *Heliyon* 3: e00353.

3. GONZÁLEZ-ÁLVAREZ V H., FERNÁNDEZ DE MERA I G., **CABEZAS-CRUZ A.**, DE LA FUENTE J., ORTGA-MORALES A.I., ALMAZAN C. 2017: Molecular survey of *Rickettsial organisms* in ectoparasites from a dog shelter in Northern Mexico. Veterinary *Parasitology: Regional Studies and Reports* 10: 143–148.

4. MATEOS-HERNÁNDEZ L., VILLAR M., MORAL A., RODRÍGUEZ C. G., ARIAS T.A., DE LA OSA V., BRITO F.F., FERNÁNDEZ DE MERA I.G., ALBERDI P., RUIZ-FONS F., **CABEZAS-CRUZ A.**, ESTRADA-PEÑA A., DE LA FUENTE J. 2017: Tick-host conflict: immunoglobulin E antibodies to tick proteinsin patients with anaphylaxis to tick bite. *Oncotarget* 8: 20630–20644.

5. STEJSKALOVA K., BAYEROVA Z., FUTAS J., HRAZDILOVA K., KLUMPLEROVA M, OPPELT J, SPLICHALOVA P, DI GUARDO G, MAZZARIOL S, DI FRANCESCO CE, DI FRANCESCO G, TERRACCIANO G, PAIU RM, URSACHE TD, **MODRY D.**, HORIN P 2017: Candidate gene molecular markers as tools for analyzing genetic susceptibility to morbillivirus infection in stranded Cetaceans. *HLA (Human leukocyte antigens)* 90: 343–353.

Cooperation with foreign research institutions

Research area: Molecular biology of parasitic protists and nematodes & Molecular taxonomy and phylogeny of parasites

- Berkeley Lab – Biosciences, Berkeley, USA (K.M. Davies)
- Boston University, Boston, USA (R. Aphasizhev)
- CNRS, Ecole Normale Supérieure, Paris, France (C. Bowler)
- Comenius University, Bratislava, Slovakia (A. Horváth)
- Edinburgh Napier University, Edinburgh, UK (S. Rueckert)
- Mitochondrial Biology Unit, Cambridge, UK (J.E. Walker)
- Natural History Museum, London, UK (V. Smith)
- Ohio State University, Columbus, Ohio, USA (J. Alfonzo)
- Station Biologique de Roscoff, Roscoff, France (C. de Vargas)
- Staten Serum Institute, Copenhagen, Denmark (C.R. Stensvold)
- The State University of New York at Buffalo, Buffalo, New York, USA (L. Read)
- University of Bordeaux, Bordeaux, France (F. Bringaud)
- University of British Columbia, Vancouver, Canada (P.J. Keeling, L.W. Parfrey)
- University of California, Riverside, California, USA (D.A. Maslov)
- University of Edinburgh, UK (A. Schnaufer)
- University of Glasgow, Glasgow, UK (H. de Koning)
- University of Huddersfield, Huddersfield, UK (M.L. Ginger)
- University of Montreal, Québec, Canada (G. Burger)
- University of Zurich, Zurich, Switzerland (L. Keller)

Research area: Biology of disease vectors

- Academic Medical Center, Amsterdam, The Netherlands (J.W.R. Hovius)
- Barcelona Supercomputing Center, Barcelona, Spain (V. Guallar)
- Catholic University Leuven, Belgium (E. de Clercq)
- Dresden University of Technology & University Clinic Carl Gustav Carus, Dresden, Germany (T. Chavakis)
- Hokkaido University, Sapporo, Hokkaido, Japan (K. Yoshii)
- Institute for Systems Biology, Seattle, USA (M. Brunkow, Ch. Lausted, N. Jabbari)
- Institute of Bioorganic Chemistry and Fundamental Medicine, Novosibirsk, Russia (S. Tkachev)
- Institute of Virology, Slovak Academy of Sciences, Bratislava, Slovakia (B. Klempa)
- Institute of Zoology, Slovak Academy of Sciences, Bratislava, Slovakia (D. Žítňan, M. Kazimírová)
- Johannes Gutenberg University of Mainz, Mainz, Germany (E. Schmitt, S. Tenzer)
- Mount Allison University, New Brunswick, Canada (V. Lloyd)
- National Institutes of Health, Rockville, Maryland USA (J. Valenzuela, J. Ribeiro)
- National Institute of Public Health and Environment (RIVM), Bilthoven, The Netherlands (H. Sprong, K. Takumi)
- Norwegian Institute of Public Health, Oslo, Norway (A. Aase)
- Oklahoma State University, Stillwater, Oklahoma, USA & Instituto de Investigación en Recursos Cinégeticos, Ciudad Real, Spain (J. de la Fuente)
- Parasitological Institute, Slovak Academy of Sciences, Košice, Slovakia (B. Peťko)
- State University of New York, Stony Brook, USA (B.J. Luft)

- University of Arizona, Tucson, Arizona, USA (C. Bender, J. Winzerling)
- University of Glasgow (A. Kohl)
- University of Granada, Granada, Spain (M. Hackenberg)
- University of Neuchâtel, Neuchâtel, USA (P. Guerin)
- University of Rome La Sapienza, Roma, Italy (B. Arca)
- University of Southern Mississippi, Hattiesburg, Mississippi (S. Karim)
- University of Strasbourg, Illkirch, France (N. Boulanger)
- The Pirbright Institute, Surrey, UK (L. Bell-Sakyi)

Research area: Parasites of fish

- ECOSUR, Chetumal, Mexico (D. González-Solís)
- Fish and Wildlife Research Institute, St. Petersburg, Florida, USA (M. Bakenhaster)
- Hungarian Academy of Sciences, Budapest, Hungary (E. Eszterbauer)
- Mote Marine Laboratory, Sarasota, Florida, USA (K. Main, C. Yanes-Roca)
- Muséum d'Histoire Naturelle, Genève, Switzerland (A. de Chambrier)
- Muséum National d'Histoire Naturelle, Paris, France (J.-L. Justine)
- Natural History Museum, London, UK (D.T.J. Littlewood, A. Waeschenbach)
- Oregon State University, Corvallis, Oregon, USA (J. Bartholomew, S. Atkinson)
- Ross University School of Veterinary Medicine, St. Kitts, West Indies (M. Freeman)
- Parasitological Institute, Slovak Academy of Sciences, Košice, Slovakia (M. Oros, I. Hromadová)
- Skretting Aquaculture Research Centre, Stavanger, Norway (C. McGurk)
- University of Cape Town, Cape Town, South Africa (C.C. Reed)
- University of Geneva, Switzerland (D. Soldati-Favre)
- University of Haifa, Israel (T. Lothan)
- University of Iceland, Reykjavik, Iceland (K. Skirnisson)
- University of Tasmania, School of Aquaculture, Launceston, Tasmania, Australia (B. Nowak)
- University of Valencia, Valencia, Spain (F. Montero, A. Pérez del Olmo)
- University of Oran, Algeria (D. Marzoug)
- Federal Rural University of Rio de Janeiro, Brazil (J. Luque)
- Wageningen University and Research, Wageningen, Netherlands (G. Wiegertjes)

Research area: Parasitic protists of man and animals with special reference to opportunistic parasites

- Canadian Institute for Advanced Research, University of Ottawa, Ottawa, Ontario, Canada (N. Corradi)
- CDC, Division of Parasitic Diseases, Atlanta, Georgia, USA (L. Xiao, V. Cama, E.W. Secor)
- Center for Food Safety, University of Georgia, Griffin, Georgia, USA (Y. Ortega)
- Christchurch Science Centre, Christchurch, New Zealand (E. Moriarty)
- Higher National School of Veterinary, EL Harrach, Algiers, Algeria (A.E. Laatamna, M. Aissi)
- North Dakota State University, Fargo, North Dakota, USA (J. McEvoy)
- Parasitological Institute of Slovak Academy of Sciences, Košice, Slovakia (M. Stanko)
- Wroclaw Medical University, Wrocław, Poland (M. Wesolowska, M. Kicia)
- Wroclaw University, Institute of Genetics and Microbiology, Wrocław, Poland (A. Perec-Matysiak)
- University of Kent, School of Biosciences, Canterbury, UK (Anastasios D. Tsaousis)

Membership in international organisations

Maryna Golovchenko
- Member of the European Study Group for Lyme Borreliosis

Libor Grubhoffer
- Member of General Assembly of the International Union of Biochemistry and Molecular Biology
- President of the Czech Society for Biochemistry and Molecular Biology

Astrid Holzer
- Member of the British Society for Parasitology
- Member of the Fisheries Society of the British Isles

Petr Kopáček
- International Society of Developmental and Comparative Immunology

Michail Kotsyfakis
- Member of the International Proteolysis Society
- Member of the American Society of Biochemistry and Molecular Biology

Julius Lukeš
- Fellow of the American Academy for Microbiology
- Member of the Faculty of 1000
- President of the International Society for Evolutionary Protistology
- Senior Fellow of the Canadian Institute for Advanced Research
- Vice-President of the International Society of Protistologists

František Moravec
- Honorary Member of the American Society of Parasitologists
- Honorary Member of the Slovak Society of Parasitologists

Jana Nebesářová
- Member of the European Microscopy Society
- President of the Czechoslovak Microscopy Society

Miroslav Oborník
- Member of the International Society for Evolutionary Protistology

Ryan O. M. Rego
- Member of American Society for Microbiology
- Member of European Society of Clinical Microbiology and Infectious Diseases

Nataliia Rudenko
- Member of the European Study Group for Lyme Borreliosis
- Member of the American Society for Microbiology
- Member of the European Society of Clinical Microbiology and Infection

Daniel Růžek
- Member of the International Scientific Working Group on Tick-Borne Encephalitis
- National Representative at the International Committee for Taxonomy of Viruses
- Member of the American Society for Microbiology
- Member of the Czechoslovak Society for Microbiology

Tomáš Scholz
- Corresponding member of the Natural History Museum, Geneva, Switzerland

Jan Štefka
- Member of the International Society of Phthirapterists

Jiří Vávra
- Member of the International Society of Protistologists

Membership on editorial boards

Acta Parasitologica (Poland): ***F. Moravec***
Acta Protozoologica (Poland): ***J. Vávra***
Acta Virologica (Slovakia): ***D. Růžek***
American Journal of Blood Research (USA): ***M. Kotsyfakis***
Antiviral Chemistry and Chemotherapy (USA): ***D. Růžek***
BMC Genomics (UK): ***M. Kotsyfakis*** (Associate Editor)
Clinical and Vaccine Immunology (USA): ***D. Růžek***
Developmental & Comparative Immunology (UK): ***P. Kopáček***
Epidemiology and Vaccinal Prevention – Scientific and Practical Journal (Russia): ***D. Růžek***
Folia Parasitologica (Czech Republic): ***I. Fiala*** (Associate Editor), ***F. Moravec***, ***T. Scholz*** (Editor-in-Chief), ***J. Štefka*** (Associate Editor), ***J. Vávra***, ***V. Yurchenko***
Helminthologia (Slovakia): ***F. Moravec***
Journal of Agrobiology (Czech Republic): ***M. Kváč***
Journal of Applied Biomedicine ***L. Grubhoffer***
Parasite (France): ***F. Moravec***, ***T. Scholz***
Parasite & Vectors (UK): ***A. Kostadinova*** (Editor-in-Chief), ***M. Kotsyfakis*** (Associate Editor)
Scientific Reports (UK): D. Růžek
Systematic Parasitology (UK): ***A. Kostadinova*** (Editor-in-Chief), ***F. Moravec***, ***T. Scholz***
Scientific World Journal (UK, USA, Egypt): ***D. Růžek***
Ticks and Tick-Borne Diseases (Germany): ***D. Růžek*** (Section Editor)
World Journal of Virology (China): ***D. Růžek***

Teaching activities

The principal mission of the Institute of Parasitology is to perform basic research. However, participation of the staff in teaching is an integral part of their activities and is essential for further development of the Institute. Therefore, most of the key scientists participate in teaching, both by giving lectures and supervising graduate and undergraduate students.

The students actively participate in research projects of the Institute and all graduate students and selected undergraduates have part-time contracts at the Institute. Most students are from the University of South Bohemia in České Budějovice, especially its Faculty of Science, but also from other faculties (Faculty of Agriculture; Faculty of Health and Social Studies) and universities, such as Charles University in Prague, Masaryk University in Brno and the University of Veterinary and Pharmaceutical Sciences in Brno.

To facilitate scientific cooperation and participation of students in the research performed at the Institute, the Laboratory of Molecular Ecology of Vectors and Pathogens (head *L. Grubhoffer*) and the Laboratory of Evolutionary Protistology (head *M. Oborník*) have been established jointly with the University of South Bohemia.

List of PhD theses

(Faculty of Science, University of South Bohemia unless otherwise stated)

- **FLEGONTOVA (BUTYRSKAYA) Olga**: Diversity and biogeography of diplonemid and kinetoplastid protists in global marine plankton
  Supervisor: Horák Aleš
- **JALOVECKÁ Marie**: Establishment of Babesia laboratory model and its experimental application
  Supervisor: Hajdušek Ondřej, Malandrin Laurence
- **JIRSOVÁ Dagmar**: Population genetics of the fish tapeworm Wenyonia virilis (Caryophyllidea: Caryophyllaeidae) and its fish host Synodontis schall
  Supervisor: Jirků Miloslav
- **KOČOVÁ Pavlína**: Sledování exprese proteinů v savčích buňkách infikovaných virem klíšťové encefalitidy / Monitoring of protein expression in mammalian cells during tick-borne encephalitis infection
  Supervisor: Štěrba Ján
- **ONDRUŠ Jaroslav:** Význam sialovaných glykoproteinů pro klíště *Ixodes ricinus*/ The importance of the sialylated glycoproteins for the tick *Ixodes ricinus*
  Supervisor: Štěrba Ján
- **PATRA Sneha**: Malacosporea and Sphaerospora sensu stricto: Myxozoan clades with unique biology and evolution
  Supervisor: Holzer Astrid S.
- **PERNER Jan**: Nutritional requirements of ticks.
  Supervisor: Kopáček Petr
- **SKALICKÝ Tomáš**: Insight into insect trypanosomatid biology via whole genome sequencing
  Supervisor: Lukeš Julius

List of Master of Science theses

- **CIBULKOVÁ Lucie**: Trematode diversity in freshwater pulmonate snails from the St Lawrence Wetlands, Canada
  Supervisor: Georgieva Simona
- **HÁJKOVÁ Hana**: Patogeny v klíšťatech získaných ze psů a koček v Českých Budějovicích a okolí
  Supervisor: Rudenko Nataliia
- **HEJDOVÁ Barbora**: Vliv klíštěcích slin na žírné buňky na úrovni signálních drah
  Supervisor: Lieskovská Jaroslava
- **JEŽKOVÁ Jana**: Diverzita kryptosporidií volně žijících hlodavců rodu *Rattus*
  Supervisor: Kváč Martin
- **KALTENBRUNNER Sabine**: Characterization of TbPH1, a kinetoplastid-specific pleckstrin homology domain containing kinesin-like protein
  Supervisor: Hassan Hashimi
- **LISNEROVÁ (JEDLIČKOVÁ) Martina**: Lokalizace a kvantifikace rybomorky *Sphaerospora molnari* (Myxozoa) u kapra obecného
  Supervisor: Fiala Ivan
- **MARŠÁLKOVÁ Eliška**: Vliv klíštěcích slin na fagocytózu borelií dendritickými buňkami
  Supervisor: Lieskovská Jaroslava
- **SLABÁ Hana**: Characterisation of novel serpin TILIr and its relatives from the superfamily of serine protease inhibitors from *Ixodes ricinus* tick
  Supervisor: Rudenko Nataliia
- **ŠOLCOVÁ Lucie**: Analýza invazivní schopnosti a infekčního potenciálu nově popsaných druhů borelie z komplexu *Borrelia burgdorferi* sensu lato, *B. americana* a *B. carolinensis* na laboratoním modelu infikovaných savců
  Supervisor: Rudenko Nataliia
- **TOMANOVÁ Vendula**: Přítomnost specifické DNA a koproantigenu kryptosporidií jako indikátor probíhající infekce
  Supervisor: Kváč Martin

List of Bachelor of Science theses

- **BĚHÁLKOVÁ Veronika**: Elucidating the subunit composition of tRNA-guanine transglycosylase in *Trypanosoma brucei*
  Supervisor: Paris Zdeněk
- **BROŽ Marek: Střevní paraziti savců introdukovaných na Svalbard**
  Supervisor: Ditrich Oleg
- **DOSTÁLOVÁ Karolína**: Interakce *Borrelia burgdorferi* s. s. a *Borrelia afzelii* s buněčnými liniemi klíšťat *Ixodes ricinus* a *Ixodes scapularis*
  Supervisor: Rego Ryan
- **HONEDER Sophie**: Construction and use of GFP and DsRed expressing vectors and transformation in Borrelia afzelii 2017
  Supervisor: Rego Ryan
- **JUHAŇÁKOVÁ Eliška**: Mikrobiomy komářích hostitelů**:** metodologická revize dosavadní praxe s využitím amplikonového sekvenování na Illumina platformách
  Supervisor: Nováková Eva
- **KŘEPELKOVÁ Simona**: Diverzita mikrobiomů vybraných druhů ovádů (Diptera: Tabanidae) a její vliv na přenos trypanosom (Trypanosoma sp.)
  Supervisor: Nováková Eva
- **LEVÁ Jana**: Sledování změn genové exprese interleukinu 10 u potkana jako modelového organizmu v průběhu infekce tasemnicí *Hymenolepis diminuta*
  Supervisor: Jirků-Pomajbíková Kateřina

- **RADOS Anda**: OASL protein isoforms in human neural cell lines infected by tick-borne encephalitis
  Supervisor: Štěrba Ján
- **ŘEŽÁBKOVÁ Lucie:** Molekulárně-fylogenetická charakteristika izolátu Hymenolepis diminuta udržovaného v laboratorních podmínkách
  Supervisor: Jirků-Pomajbíková Kateřina
- **ŠKOCHOVÁ Veronika:** Mikrobiomy krevsajících ploštic podčeledi Triatominae**.**
  Supervisor: Nováková Eva
- **VESELÁ Dominika:** Vliv klíštěcích slin na myší neutrofilní granulocyty aktivované virem klíšťové encefalitidy
  Supervisor: Lieskovská Jaroslava
- **VOKURKA Radomír**: Potenciální antivirotické účinky derivátů přírodních látek proti viru klíšťové encefalitidy /Potential antiviral effects of derivatives of natural compounds against tick-borne encephalitis virus
  Supervisor: Štěrba Ján
- **VYHLÍDALOVÁ Tereza:** Složení společenstev larválních stádií motolic (Digenea) u vybraných zástupců plicnatých plžů čeledi Planorbidae
  Supervisor: Soldánová Miroslava
- **ŽIŽKOVÁ Kateřina:** Diverzita a populační struktura bakteriálních symbiontů vší rodu Polyplax
  Supervisor: Nováková Eva

Survey of lectures and courses[1]

Name	Course
I. Fiala	Field Parasitology
I. Fiala	Protistology
L. Grubhoffer	Biochemistry 1; 2 (CB + Linz)*
L. Grubhoffer	Glycobiochemistry (CB+Linz)
L. Grubhoffer	Development & Comparative Biochemistry (CB+Linz)
L. Grubhoffer	Advanced Seminar in Biological Chemistry (CB+Linz)
L. Grubhoffer	Bachelor Seminar in Biological Chemistry (CB+Linz)
	H. Hashimi Cell Regulation and Signalling
H. Hashimi	Seminar in molecular biology
A. Horák	Introduction to Bioinformatics
A. Horák	Introduction to Genomics
A. Horák	Seminar of Master´s courses - Genetics
V. Hypša	Biology of Parasitism
V. Hypša	Molecular Phylogenetics
V. Hypša	Molecular Ecology
V. Hypša	Seminar of Master´s courses - Parasitology
V. Hypša	Biology of parasitic arthropods
V. Hypša	Molecular phylogenetics
R. Kuchta	Practical Course of Invertebrate Zoology
R. Kuchta	Field Course of Marine Organisms
R. Kuchta	Introduction to Parasitology[4]
M. Kváč	Zoohygiene and Prevention of Diseases of Farm Animals[6]
M. Kváč	Animal Health[6]
M. Kváč	Veterinary Parasitology[6]
M. Kváč	Breeding and Use of Laboratory Animals[6]
J. Lukeš	Cell Biology
J. Nebesářová	Electron Microscopy for Biologists[1+5]
J. Nebesářová	Electron Microscopy[1+2]
J. Nebesářová	Natural bioactive substances
J. Nebesářová	Analytical Methods in Biochemistry
M. Oborník	Introduction to Bioinformatics
M. Oborník	Molecular Taxonomy[6]
M. Oborník	Bioinformatics Project
Z. Paris	Epigenetics and regulation of gene expression
D. Růžek	Medical Virology
D. Růžek	Pathogenesis of Viral Infections[3]
T. Scholz	Fish Cytology and Histology
T. Scholz	Parasite Diseases in Fish
T. Sholz	Field Parasitology
J. Štefka	Conservation Genetics
J. Štefka	Molecular Phylogenetics
J. Štefka	Molecular Ecology
J. Štefka	Population and Evolutionary Genetics
J. Štěrba	Advanced Biochemistry Laboratory
J. Štěrba	Biochemistry Laboratory [1+](CB + Linz)
J. Štěrba	Xenobiochemistry and Toxicology (CB + Linz)
J. Štěrba	Chemistry Seminar for 2 year
J. Štěrba	Instrumental Methods in Biochemistry and Biophysics
J. Štěrba	Glycobiochemistry
J. Štěrba	Pharmacology and toxicology

J. Štěrba	Practice in biochemistry (Praktikum z biochemie)
J. Štěrba	Biochemical Practice for Biology and the Environment
J. Štěrba	Experimental methods - practice
A. Zíková	Molecular Biology

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