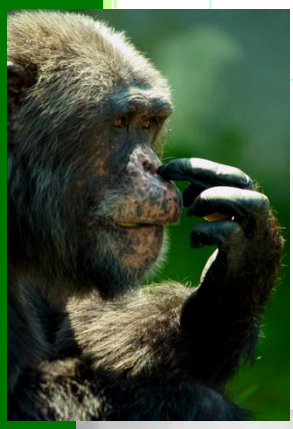
Symposium 2014

12. - 14. 6. 2014

University of Veterinary and Pharmaceutical Sciences; Brno, Czech Republic; www.hpi-lab.com

PRIMATE PARASITOLOGY: Development, Methods and Future



Brno 2014

Conference Proceedings

Edited and revised by Michael Muehlenbein

esf european social fund in the czech republic
EUROPEAN UNION
MINISTRY OF EDUCATION, YOUTH AND SPORTS
OP Education for Competitiveness
INVESTMENTS IN EDUCATION DEVELOPMENT

Organizers:

1) **Laboratory for Infectious Diseases Common to Humans and (non-Human) Primates (HPI-lab)** shared by the **University of Veterinary and Pharmaceutical Sciences** (UVPS), Brno, the Czech Republic and **Institute of Parasitology**, Biological Centre of Academy of Sciences of the Czech Republic (BC ASCR)
2) **Institute of Vertebrate Biology** of the Academy of Sciences of the Czech Republic (IVB ASCR)
3) **Evolutionary Physiology and Ecology Laboratory**, Indiana University, USA (EPE lab)
4) **Durham University,** UK (UDUR)

Venue: Department of Pathology and Parasitology, Faculty of Veterinary Medicine, University of Veterinary and Pharmaceutical Sciences Brno, Palackeho 1-3, 612 42 Brno, Czech Republic

Date: 12. - 14. 6. 2014

This symposium is supported by the operational program "Education for Competitiveness," controlled by the Ministry of Education, Youth and Sports of the Czech Republic, funded by the European Union.

Scientific board:

David Modrý (HPI-lab)
Michael Muehlenbein (EPE lab)
Klára Petrželková (HPI-lab; IVB ASCR)
Joanna M. Setchell (UDUR)

Managing committee:

Lenka Polačiková (HPI-lab)
Veronika Bumbálková (HPI-lab)

Editor: Michael Muehlenbein

Graphical design: Lenka Polačiková

Table of Contents

Thursday 12.6.2014

Programme:

08:00 - 10:00 arrival/ registration

10:00 - 11:00 Keynote talk: Michael Muehlenbein (Indiana University, USA): Primate parasitology: history and methods

11:00 - 12:00 Keynote talk: Joanna M. Setchell (Durham University, UK): Primates and parasites: an editorial perspective

12:00 - 13:00 lunch

Opportunistic protists and helminthes:

13:00 - 14:00 Keynote talk: Jaco Verweij (St. Elisabeth Hospital, NL): Molecular tools to investigate helminths of primates

14:00 - 14:30 Barbora Kalousová (UVPS Brno, CR): Diversity and transmission of strongylid nematodes in CAR

14:30 - 15:00 Rui Sá (UVPS Brno, CR): Molecular phylogeny of *Trichuris* spp. recovered from colobines living in sympatry in Guinea-Bissau

15:00 - 15:30 Jana Petrášová (UVPS Brno, CR): Do we share the same anoplocephalid tapeworms with primates?

15:30 - 16:00 coffee break

16:00 - 17:00 Keynote talk: Lihua Xiao (Centre for Disease Control and Prevention, USA): Advanced molecular detection of enteric protists

17:00 - 17:30 Martin Kváč (Biology Centre AS CR, CR): *Cryptosporidium* and cryptosporidiosis in non-human primates

17:30 - 18:00 Bohumil Sak (Biology Centre AS CR, CR): Microsporidiosis in non-human primates

18:00 - 18:30 Ivan Čepička (Charles University, CR): Trichomonads of African great apes

18:30 - 19:00 Jana Petrášová (UVPS Brno, CR): Diversity of *Blastocystis* sp. infections in captive and free-ranging primates

19:00 - 19:30 Diane Ryu (Emory University, USA): Molecular identification of *Entamoeba spp.* and the differentiation of non-commensal *Entamoeba histolytica* to understand health risks to endangered mountain gorillas in Rwanda

19:30 - 20:00 Liesbeth Frias (Kyoto University, Japan): *Giardia duodenalis* in faunal remains

Friday 13.6.2014

Programme:

Taxonomy and virology:

10:00 - 11:00 Keynote talk: David Modrý (UVPS, Brno): What the names are for: taxonomy in medical parasitology

11:00 - 11:30 Kateřina Pomajbíková, Ilona Pšenková, David Modrý (Biology Centre AS CR, CR): Molecular diversity of intestinal ciliates

11:30 - 12:00 Jana Petrášová (UVPS Brno, CR): New insights into whipworm infections of primates

12:00 - 13:00 lunch

13:00 - 14:00 Keynote talk: Fabian Leendertz (Robert Koch Institute, Germany): Viruses and wild great apes

14:00 - 14:30 Kristýna Hrazdilová (UVPS Brno, CR): Anellovirus infections in primates

14:30 - 15:00 Eva Slaninková (UVPS Brno, CR): Adenovirus infections in Ugalla chimpanzees

15:00 - 15:30 Kristýna Brožová (UVPS Brno, CR): Widespread infection of parvoviruses in Ugalla chimpanzees

15:30 - 16:00 coffee break

Bacteriology, NGS:

16:00 - 17:00 Keynote talk: Andres Gomez (Illinois University, USA): A Meta-"OMICS" systems approach to microbial community studies in non-human primates

17:00 - 17:30 Klára Vlčková (UVPS Brno, CR): Effects of antibiotic treatment on the gastrointestinal microbiota of free-ranging western lowland gorillas (*Gorilla g. gorilla*)

Programme:

Saturday 14.6.2014

Blood parasites seen through "brown glass"

08:30 - 09:30 **Keynote talk: Ananias Escalante (Arizona State University, USA): Phylogenetic systematic analyses of nonhuman primate malarias**

09:30 - 10:30 **Keynote talk: Julius Lukeš (Biology Centre, CZ): Trypanosome infections in primates**

10:30 - 11:00 Mwanahamissi Issa Mapua (UVPS Brno, CR): Ecology of the western lowland gorillas malaria parasite in Dzanga Sangha Protected Areas, Central African Republic

11:00 - 11:30 Helene De Nys (Robert Koch Institute, Germany): Non-invasive investigation of epidemiological aspects of malaria infection in wild chimpanzees: effects of age and pregnancy

11:30 - 12:00 Erhan Yalcindag (Masaryk University, CR): *Plasmodium* species in monkeys: a look from out of Hominidae family

12:00 - 13:00 **lunch**

13:00 - 14:00 **Keynote talk: Christopher Whittier (Tufts Cummings School of Veterinary Medicine, USA): Managing primate health in the wild: philosophy and practice**

14:00 - 15:00 **Keynote talk: Thomas Gillespie (Emory University, USA): Ecological and anthropogenic drivers of zoonotic disease transmission in primates**

15:00 - 15:30 **coffee break**

15:30 - 16:00 **departure**

Michael Muehlenbein: "Primate parasitology: history and methods"

Michael P. Muehlenbein[1], Michael A. Huffman[2], Charles L. Nunn[3]

[1]*Evolutionary Physiology and Ecology Laboratory, Indiana University, USA*
[2]*Primate Research Institute, Kyoto University, Japan*
[3]*Department of Evolutionary Anthropology, Duke University, USA*

Research in parasitological analyses of wild primate populations has a rich history. As our closest living relatives, nonhuman primates serve as both sources and sinks of human infections. Because more than half of primate species are threatened, it is imperative to continue concentrated efforts focusing on field epidemiology of wild primates. In just a few decades, we have seen several shifts in such research: from a biomedical focus to more ecological approaches and theoretical questions involving the roles of anthropogenic factors, from inductive to deductive reasoning in study designs, from microscopy to genomics, and so on. Arguably, there has also been a change in methodological standards, with an increasing number of publications produced by non-specialists with less intensive training in parasitology. Cursory analyses of manuscript submissions to the American Journal of Primatology and the International Journal of Primatology reveal relatively high rejection rates for such manuscripts. Analyses utilizing the Global Mammal Primate Database reveal a relative *lack* of studies that utilize multiple diagnostic methods, that utilize multiple samples collected from known animals, and that sample across age groups, sex and seasons. Additional analyses illustrate how studies that use samples from unidentified individual animals (i.e., sample prevalence) provide larger estimates of prevalence than do studies that use samples from identified individuals. Sources of sample, detection and publication biases should receive more attention by scholars in this field. More sampling must take place in arboreal species as well as all species in Southeast Asia, South America and West Africa. We need to understand the effects of the most common intestinal parasites on survivorship and reproduction in wild primate hosts. Continued use of comparative phylogenetic analyses, meta-analyses and agent-based modeling will prove important. We must also continue to identify ecological factors that promote spill-over events as well as the socioecological factors associated with spread of disease within and between groups. Critically, we must remain cautious in assigning causality in these complex systems.

Joanna M. Setchell: „Primates and parasites: an editorial perspective”

Department of Anthropology, Durham University, UK

My interest in primate parasitology stems from my research interests in parasite-mediated sexual selection theory, on the one hand, and my editorial interests in improving the quality of primatology as an integrative field of enquiry, on the other. Robust tests of parasite-mediated sexual selection theory require the integration of expertise in behavioural ecology and in parasitology, and require a multidisciplinary approach. I argue that an interdisciplinary approach is far more productive, and that we must train students in both host and parasite ecology if we are to make progress.

Jaco Verweij: “Molecular tools to investigate helminths of primates”

St. Elisabeth Hospital, the Netherlands

Human oesophagostomiasis has long been considered a rare zoonotic disease. Haaf and Van Soest (1964) reported nine cases of human *Oesophagostomum* infections in the northern region of Ghana, and Gigase and others (1987) reported fifty-four cases in the northern region of Togo. Following these initial studies, further analyses reveal a higher than expected frequency of human oesophagostomiasis of zoonotic origin in this region of West Africa. The molecular methods used to answer questions on human *Oesophagostomum* epidemiology and biology, particularly in relation to infections in wild primates, are discussed.

Lihua Xiao: "Advanced molecular detection of enteric protists"

National Center for Emerging and Zoonotic Infectious Diseases, Centers for Disease Control and Prevention, USA

Molecular diagnostic tools have played a major role in improving understandings of the transmission of enteric parasites in humans and other animals. These tools offer more sensitive detection of pathogens, can differentiate morphologically identical species, allow the tracking of infection sources and pathogen disseminations at the subtype level, and can detect the emergence of drug resistance. They are commonly used in the diagnosis and characterization of enteric protists such as *Cryptosporidium, Giardia*, and microsporidia. Genotyping tools are frequently used in the identification of host-adapted *Cryptosporidium* species, *Giardia duodenalis* assemblages, and *Enterocytozoon bieneusi* genotypes, allowing the assessment of infection sources in both humans hosts and the environment. In contrast, subtyping tools are more often used in case linkages, advanced tracking of infections sources, and assessment of disease burdens attributable to anthroponotic and zoonotic transmission. More recently, multilocus sequence typing tools are available for diagnosing enteric protists based on whole genome sequence data. They offer higher differentiation capacity, thus are increasingly used in population genetic characterization of transmission dynamics in disease endemic areas, and delineation of mechanisms for the emergence of virulent subtypes. The recent development in next generation sequencing techniques has now made comparative genomic analysis of protists possible. Although they are not yet widely used in characterization of enteric protists, their use in *Toxoplasma gondiii* research has significantly improved our understanding of evolution and dispersal of virulent isolates at the global scale, and genetic determinants for virulence and other phenotypes associated with parasite transmission. Efforts are underway to adopt advanced molecular detection in disease surveillance and outbreak investigation, especially metagenomics in pathogen detection and comparative genomics in pathogen typing. Challenges are to develop user-friendly bioinformatic mechanisms for analyzing the vast volumes of sequence data, and to develop guidance on interpretation of pathogen variants in the context of surveillance and epidemiologic data.

Fabian H. Leendertz: „Viruses and wild great apes“

Robert Koch Institute, Germany

A variety of viruses have been described in wild great ape populations, and more will surely be discovered within the coming years. The pathological effects of SIV, Ebola virus and pneumoviruses are known; however, the biological importance of these and other viruses on the natural ecology of primate hosts is much more equivocal. It is critical that we perform systematic, long-term evaluations, accounting for host (e.g., microbiomes) and ecological factors, to identify the potential negative (and possibly beneficial) effects of viruses in wild great ape populations. This will be challenging given the restrictions of non-invasive diagnostic methods.

Andres Gomez: „A Meta-"OMICS" systems approach to microbial community studies in non-human primates”

Illinois University, USA

The application of high-throughput molecular techniques has allowed scientists to pinpoint multiple markers of host health and disease simultaneously, in diverse biological systems. One such system is the mammalian microbiome: the collection of bacteria, fungi, viruses and micro-eukarya that line the body surfaces of mammals. I describe how system-scale microbiome studies provide valuable information and contribute to our knowledge of wild primate fitness and health, with emphasis on communities of intestinal bacteria. I focus primarily on three microbial community descriptors: 1) taxonomic/phylogenetic composition; 2) functional potential/gene pool (metagenomics); and 3) metabolite pool (metabolomics). The need to integrate molecular markers of fitness into descriptors of primate behavior and ecology are discussed.

Ananias Escalante: "Phylogenetic systematic analyses of nonhuman primate malarias"

Arizona State University, USA

Ascertaining the evolutionary history of human malarias has motivated phylogenetic and molecular clock studies involving *Plasmodium* species from non-human primates. Of particular importance has been the access to recent parasite samples from great apes and lemurs. Overall, there is compelling evidence that primate malaria has a broader host range than previously thought. Indeed, extant species of *Plasmodium* in primates are the result of complex evolutionary processes where host switches have likely been common. Host range seems to be essential in explaining part of the observed patterns of primate malaria species. The challenge of providing a time estimate for such events is discussed by revising different molecular clock approaches applied to malaria species. The importance of exploring multiple scenarios is highlighted. Finally, the role played by processes such as adaptive radiation facilitated by the diversity and host geographic distribution is discussed.

Julius Lukeš: “Trypanosome infections in primates”

Institute of Parasitology, Biology Centre, Czech Academy of Sciences, Czech Republic

Subspecies of the *Trypanosoma brucei* clade are the causative agents of various forms of African sleeping sickness. These subspecies differ in the molecular mechanisms each evolved to escape lysis by host serum. For example, sera baboons, mangabeys and macaques kill *T. brucei brucei*, *T. b. rhodesiense* and *T. b. gambiense* very efficiently via the apolipoprotein L1 (ApoL1) protein, while human serum lyses only *T. b. brucei*. Although chimpanzees live in endemic regions and are known to be susceptible to the infection, they lack the ApoL1 gene and hence do not lyse any of these trypanosomes. We amplified trypanosome intergenic region 1 (ITS1) from about 10% of tissue samples of dead chimpanzees collected in several African countries. Moreover, we succeeded in amplifying trypanosome DNA from fecal samples of wild chimpanzees from the Tai National Park, allowing for the identification of these parasites in highly protected or endangered species. With just one sequence falling into the *T. theileri*/*T. cervi* clade, all remaining ITS1 sequences belong to the *T. brucei* clade. Additionally, we trapped 1033 tsetse flies belonging to either *Glossina pallicera newteadi* or *Glossina tabaniformis*, from which DNA was isolated and subjected to library-based screening for host blood. While most fed on buffaloes, humans, antelope and pigs, we provide evidence that tsetse flies of both sexes occasionally take bloodmeals from chimpanzees, providing evidence that trypanosomes can be transmitted to apes via these vectors. All attempts to amplify single-copy trypanosome genes failed. Based on the ITS sequences (that do not allow us to distinguish among the *T. brucei* subspecies), we speculate that chimpanzees are infected with these flagellates, and likely control the infection by an ApoL1-independent mechanism.

Christopher Whittier: "Managing primate health in the wild: philosophy and practice"

Tufts Cummings School of Veterinary Medicine, USA

Applied veterinary medicine can be a valuable tool in wildlife conservation and management efforts, especially for endangered species including great apes. There are increasing examples across the globe where wildlife health professionals have played integral roles in helping to sustain and conserve wildlife at both the individual and population levels. For different reasons and under different scenarios, applied *in-situ* veterinary care and interventions with wildlife are sometimes welcomed or rejected. There are complex reasons for this relationship, some based on subjective feelings and dogmatic approaches, some based on objective science and risk assessments. All issues pertain to recent successful efforts to increase veterinary involvement, research and applied veterinary medicine to free-ranging, human-habituated western lowland gorillas (*Gorilla gorilla*) in the Central African Republic (CAR). A partnership between multiple conservation institutions, individuals, and other local and global stakeholders has led to significant strides in applied veterinary medicine for this critically endangered species. Successful campaigns to deliver preventative medicine in the form of vaccinations, to treat a serious infectious disease outbreak, and to save an individual gorilla from a life threatening ensnarement have all been accomplished in the past two years. These activities and interventions, their integration into the comprehensive gorilla conservation and health management efforts in CAR, and some comparison to efforts with mountain gorillas (*Gorilla beringei*) are discussed.

Thomas Gillespie: "Ecological and anthropogenic drivers of zoonotic disease transmission in primates"

[1]*Ecology and Evolution and Department of Environmental Sciences, Emory University, Atlanta, USA*
[2]*Department of Environmental Health, Rollins School of Public Health, Emory University, Atlanta, USA*

Pathogen emergence is disproportionately associated with the tropics and is often linked to anthropogenic change. Unique human and primate behaviors associated with this interface can also contribute to zoonotic transmission and pathogen emergence. To understand better these transmission dynamics, we use a mixed-methods, systems approach throughout tropical Africa and Latin America. In doing so, we attempt to integrate epidemiology, molecular ecology, behavioral ecology, vector ecology, social and clinical survey, and spatially-explicit modeling. Using examples from our research in Madagascar, Mexico, Tanzania, and Uganda, I demonstrate how key human behaviors, primate behaviors, ecological conditions, and landscape features increase the risk of interspecific disease transmission among people, primates, and domesticated species.

David Modrý: „What the names are for: taxonomy in medical parasitology”

Department of Pathology and Parasitology, UVPS Brno, CR

Systematics is a science of biological classification and nomenclature serves as the language by which we communicate about the biodiversity and its key unit: the species. Undoubtedly, the human civilization is linked to the biodiversity and its exploitation. Interestingly, the taxonomy has been called "the world's oldest profession“, competing for this title with prostitution. It would always have been important to distinguish by names those animals and plants that are poisonous from the edible-ones and to share this information with the others. If we speak about scientific names, we refer to binominal nomenclature, as was introduced by Carl von Linné in series of his works in second half of 18 century. In fact, it is one of the most successful and universal systems of communication in Science as it is used for more than 250 years! Nomenclature is formal system of naming species; the names themselves do not embody the information, but rather relate to the concepts of sharing the information. The age of Linnaean taxonomy does not mean that it is dead discipline. Without general consensus what each name means we communicate our results by language which is only partly understood. In the era of databases and meta-analytical approaches, the need for correct language used by taxonomists and other users of scientific names in medical parasitology is even more prominent. The major aim of the talk is to discuss the basics and obstacles of parasite taxonomy and to show the examples how (in)correct using of scientific names interfere with sharing and analysing the knowledge on the diversity and ecology of primate parasites.