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Recognition of the 4th International Conference on Malaria and Related Haemosporidian Parasites of Wildlife, held Nov. 1–5, 2018 in Beijing China



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ABSTRACT

Over the past 10 years, much research has been done and remarkable discoveries have been made in various fields of research regarding wildlife malaria parasites (*Plasmodium*, Plasmodiidae) and related haemosporidians, the agents of infections, which affect all major groups of terrestrial vertebrates. Recent molecular studies show that these blood parasites cause more harm to wildlife than formerly believed, calling for new fundamental and applied research on this subject. The 4th International Conference on Malaria and Related Haemosporidian Parasites of Wildlife highlighted the recent accomplishments of many research groups throughout the world at the Beijing Normal University, with additional hosts being the Beijing Zoo and the China Ornithological Society. Please see: <http://malariacommunity2018.com/>. We are grateful to the organizers of the meeting and Drs. Gediminas Valkiūnas, Staffan Bensch, and Lu Dong for their contributions to this review.

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Over the past 10 years, much research has been done and remarkable discoveries have been made in various fields of research regarding wildlife malaria parasites (*Plasmodium*, Plasmodiidae) and related haemosporidians, the agents of infections, which affect all major groups of terrestrial vertebrates. Recent molecular studies show that these blood parasites cause more harm to wildlife than formerly believed, calling for new fundamental and applied research on this subject. The 4th International Conference on Malaria and Related Haemosporidian Parasites of Wildlife highlighted the recent accomplishments of many research groups throughout the world at the Beijing Normal University, with additional hosts being the Beijing Zoo and the China Ornithological Society. Please see: <http://malariaconference2018.com/>.

The format of the meeting allowed for 49 oral presentations plus three keynote and 9 plenary addresses on various topics of wildlife haemosporidian research. The participants arrived in Beijing from more than 20 nations, and were treated to the tremendous hospitality of the Chinese organizers. Dr. Lu Dong of Beijing Normal University and Dr. Ting Jia of the Beijing Zoo were the co-chairs and directors of the meeting. The organizers provided full support for 10 PhD students who arrived from the Americas, Europe, Asia and Africa. The sessions were broadly delineated into topics of pertinence to the field. Some of the main areas included biogeography, ecology, experimental approaches to studying haemosporidians, multiple and co-infections of parasites, work with vectors, environmental effects on parasite prevalence and transmission, and advances in molecular methods. The majority of presentations studied avian malaria and its relatives.

Some talks highlighted the new breakthroughs using transcriptomics and genomics to study wildlife haemosporidians. Studying genomics of avian malaria has been hampered due to the nucleated erythrocytes of bird blood, so it is exceedingly difficult to obtain high quality genomes due to the overabundance of host DNA. Sequencing the RNA appears to be more successful, and several presentations were made documenting advances in gene discovery and new markers for detecting biodiversity.

Experimental work, pioneered by the researchers of P. B. Šivickis Laboratory of Parasitology at Nature Research Centre, Lithuania, has shed light on pathologies caused by the exo-erythrocytic stages of avian haemosporidians. With *Haemoproteus*, for example, the tissue stages can cause morbidity and death before the parasites enter the blood stages. Such infections are difficult to diagnose, but seem to be common in wildlife. The first data about successful application of chromogenic in situ hybridization (ISH) in diagnostics of exo-erythrocytic meronts of *Haemoproteus* and *Leucocytozoon* parasites were presented at the conference, and they look promising for better understanding exo-erythrocytic development of these infections. Future work will focus on why different parasite species cause different pathologies, and how this varies with bird species. In addition, it remains unclear how haemosporidian parasites affect populations of wild birds, and how many die from undetected infections.

At this point, there are over 3200 unique cytochrome *b* haplotypes (lineages) described in the MalAvi database (<http://mbio-serv2.mbioekol.lu.se/Malavi/>). This important resource, curated by researchers of the Dept. of Biology at Lund University, provides the community with carefully checked information about molecular characterization of pathogens and their geographic and host spread. Because there are many more lineages than microscopically described morphospecies, it suggests that there may be many cryptic species of parasites. From the meeting, although there is no consensus on what constitutes a species, it is becoming increasingly clear that distinct cytochrome *b* lineages may represent independently evolving entities. Nonetheless, implementing both microscopy and DNA sequencing remain essential in species descriptions, particularly due to insufficient sensitivity of currently used PCR-based protocols in reading co-infections of haemosporidian belonging to different and, particularly the same genera.

Considerable progress has also been made in the study of the vectors of avian haemosporidians. Mosquitoes transmit *Plasmodium* spp., blackflies spread *Leucocytozoon* spp., and *Haemoproteus* parasites are transmitted by hippoboscids flies in the case of the subgenus

Haemoproteus, and biting midges in the case of the subgenus *Parahaemoproteus*. It has been recently recognized that high parasitemia of *Haemoproteus* species can cause severe mortality of biting midges and other blood-sucking insects. In general it is also accepted that mosquitoes can feed on many hosts, but there is also compelling evidence that these insects also feed preferentially on certain avian hosts. Whether this is an ecological or physiological association remains unanswered.

Many new findings have advanced the field, but several questions remain open. For example, not much is known and there is still not much progress about how the avian immune system combats infections. It is clear that a parasite species can have differing effects on different avian species, and even individuals. It will be important to further investigate what immunological factors affect the success of parasitic infections. In addition, why are some parasites generalists and others

specialists? Is this governed by the host immune system or the parasite, or both?

In sum, the 4th International Conference on Malaria and Related Haemosporidian Parasites of Wildlife brought together an international group of enthusiastic researchers to promote more collaborations and foster new ideas. Research into avian malaria parasites of wildlife is growing every year, and scientists are welcomed to contribute their names and contact information at the website <https://www.facebook.com/malariarcn/> to learn of upcoming events and meetings.

Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.ijppaw.2018.12.003>.