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# Editorial: Molecular advances of host-parasite associations in wildlife

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## Editorial on the Research Topic

### Molecular advances of host-parasite associations in wildlife

Parasites live on or inside their hosts and gain resources at the expense of the latter. Due to their abundance and phylogenetic diversity, parasites have been the focus of increasingly abundant co-evolutionary studies. Understanding the associations between parasites and their hosts is important to both basic studies on disease evolution and whole ecosystem health. However, the establishment of host-parasite associations in wildlife and their selection pressures are far from well understood, partly limited by available molecular methods, which are rarely revised and updated to higher standards and novel questions. The recent development of molecular methods has enabled the detections with higher resolutions of the patterns and mechanisms behind host-parasite associations (Videvall, 2019; Huang, 2021). In this Research Topic, we collect six articles based on their development and use of molecular methods for the study of host-parasite associations.

Acknowledging that for vector-borne parasites, vectors are equally important intermediate hosts, Fischer and Chakarov ask where is the critical population bottleneck in the life cycle of parasites, and how large their population sizes are. Using qPCR of blood parasites in vector organs, they identify salivary glands to harbour very low numbers of parasite individuals, suggesting substantial consequences for host-parasite co-evolutionary dynamics due to such bottlenecks.

Directly transmitted parasites present simpler life cycles, which may be influenced by fewer factors and thus be more tractable. Ren et al. estimated the coevolutionary history between avian head lice and their hosts, aiming at establishing the role of host switching and cospeciation in shaping host-parasite associations. Through analysis of multiple genes with different cophylogenetic methods, they show that host switches have been as likely as or more common compared to co-speciation events. This is surprising given that head lice need to overcome the challenge of spreading from one host group to another. The importance of host-switching in shaping host-parasite associations has been addressed by case studies and model studies (Ellis et al., 2015; Nylin et al., 2018), which enhanced our understanding in this complex and cryptic process.

Host switches may be accompanied by genomic changes in the parasite. Here we collected two articles performing different levels of genomic analyses of parasites. Korneenko et al. analysed the diversity of alphacoronaviruses (Alpha-CoV) in bats (natural reservoirs of

many viruses) from European Russia, and compared this with other regions. Whole genome sequencing results suggest that the same viruses have been circulating in a particular area for several years, and may be transmitted with host migration. Meanwhile they found two cases of mixed infection (*Pedacovirus* and *Myotacovirus* in one *Myotis daubentonii*, and *Pedacovirus* and *Nyctacovirus* in one *Pipistrellus kuhlii*), predisposing for recombination and an insertion not known from other regions or hosts, which might be related to transmission. [Brandler and Chakarov](#) point out that most organisms, including parasites, contain multiple genomes, which fulfil different functions and may have meaningful differences in abundance between cells. For example, haemosporidian parasites contain a nuclear genome, as well as variable numbers of mitochondrial and apicoplast nucleoids per cell. The presented first qPCR-based quantification of relative abundances of these nucleoids across host species and parasite lineages suggests an interaction of coevolutionary processes and physiological pathways relying on organelle genes.

As most parasites are likely to switch to novel hosts that are related to current hosts, (phylogenetically close or sharing the same niches), illustrating the current infection pattern of a parasite can help with illustrating the past and future of its association with different hosts. [Zhan et al.](#) and [Strehmann et al.](#) have respectively investigated the infection patterns of avian haemosporidians in wild communities in China and Germany. [Zhan et al.](#) assessed whether infection probability is correlated with ecological and life-history traits of host species in two different landscapes, and found that smaller bird species and omnivores are less likely to be infected than others. They did not detect any negative effect of infection in sampled individuals, probably because heavily infected birds are rarely captured. [Strehmann et al.](#) estimated that half of the small forest birds in Germany are infected with blood parasites. While great differences in lineage diversity and prevalence between avian families are evident, parasite prevalence of a family does not appear to correlate with diversity.

Articles in this Research Topic contribute to elucidating different facets of coevolution, including the past and current infection patterns in ecological communities, bottlenecks in established and novel associations, and genomic variations, which

may relate to host-switching and ecological niche occupation. With these efforts, we are getting closer to, but still call for more molecular-based studies to complete our understanding of host-parasite associations and their dynamics.

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XH: Writing – original draft, Writing – review & editing. NC: Writing – original draft, Writing – review & editing. JD: Writing – review & editing.

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## References

- Ellis, V. A., Collins, M. D., Medeiros, M. C., Sari, E. H., Coffey, E. D., Dickerson, R. C., et al. (2015). Local host specialization, host-switching, and dispersal shape the regional distributions of avian haemosporidian parasites. *Proc. Natl. Acad. Sci.* 112, 11294–11299. doi: 10.1073/pnas.1515309112
- Huang, X. (2021). Assessment of associations between malaria parasites and avian hosts—A combination of classic system and modern molecular approach. *Biology* 10, 636. doi: 10.3390/biology10070636
- Nylin, S., Agosta, S., Bensch, S., Boeger, W. A., Braga, M. P., Brooks, D. R., et al. (2018). Embracing colonizations: A new paradigm for species association dynamics. *Trends Eco. Evol.* 33, 4–14. doi: 10.1016/j.tree.2017.10.005
- Videvall, E. (2019). Genomic advances in avian malaria research. *Trends Parasitol.* 35, 254–266. doi: 10.1016/j.pt.2018.12.005