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Species diversity of Microsporidia in selected hematophagous arthropods and the impact of the occurrence of microsporidians on the host microbiome

ABSTRACT

Microsporidians are a group of intracellular obligate parasites that infect a wide range of hosts. About 15% of them infect mosquitoes (Culicidae), which are themselves hosts of many pathogens of vertebrates. In fact, the hematophagous arthropods, such as mosquitoes and ticks (Ixodidae) are the most important disease vectors. Therefore, microsporidians infecting these arthropods are a very good model to study ecological interactions between both pathogens and the other components of the host microbiome. The aim of my dissertation was to attempt to answer the questions: (1) what is the actual microsporidian species diversity in these hosts; (2) whether the microsporidians co-occurring in the same host individual interact with each other; and (3) whether the microsporidian infection affects the host's microbiome. To detect microsporidians, I developed a high-throughput method, which I used to determine their species-diversity in the tested models. My results demonstrate that mosquitoes are common hosts of numerous microsporidian species, and most of that species are polyxenic parasites. I also noted a relatively high level of the co-occurrences of different microsporidians in mosquitoes, which resulted in interactions between the co-infecting species. Additionally, I found that microsporidian infection leads to changes in the composition of the host microbiome and activities of the microbiome metabolic pathways; especially it concerns the synthesis of antibiotics and nucleotides. Among host-seeking ticks, I identified only

one microsporidian species that occurred with negligible prevalence, which indicates that ticks probably have developed a defense mechanism against these pathogens. Results of my dissertation provide new opportunities in such research areas as ecology of parasites and medical diagnostics.

Key words: Culicidae, metagenome functional content, *Ixodes ricinus*, co-infections,

DNA metabarcoding