

The aim of this thesis was to map the presence of avian hippoboscids in Czechia, clarify which lineages of avian trypanosomes are transmitted by them, and to test vector specificity of the trypanosomes that were isolated from louse flies earlier. In the years 2017 – 2018 we found 7 species of louse flies, namely *Ornithomya avicularia* (91), *O. biloba* (267), *O. fringillina* (45), *Ornithoica turdi* (6), *Stenopteryx hirundinis* (1) and *Ornithophila metallica* (1). The specificity of *O. biloba* and *S. hirundinis* toward Hirudinidae was confirmed. The other louse fly species were found on both migrant and resident birds. The phylogenetic analysis of gene for cytochrome c oxidase I which contained a newly characterised species *O. metallica* revealed that it is related to *O. turdi*.

Avian trypanosomes were present in the following species: *O. biloba* (prevalence 20 %), *O. avicularia* (8 %), a *O. fringillina* (4 %). All trypanosome sequences from hippoboscids belonged to the avian trypanosome group corvi–culicavium. Phylogenetic analysis of trypanosome sequences confirmed the presence of five lineages of avian trypanosomes. Four trypanosome sequences from birds formed two new basal clades. Most of the trypanosome sequences from hippoboscids formed a sister group to the previously described lineages.

The vector specificity of different avian trypanosome lineages was tested using laboratory mosquitoes. A trypanosoma infection did not develop in mosquitoes which fed on lineage I (group corvi-culicavium), it is therefore possible that it is specific for hippoboscids. When fed on avian trypanosomes of the lineage II, the mosquitoes developed strong infections with high prevalence. It was possible to infect a canary with guts of the infected mosquitoes. The Hippoboscids therefore might be opportunistic vectors of these trypanosomes.