

Abstract

Trypanosomes of the subgenus *Herpetosoma* are considered highly host-specific and nonpathogenic to their hosts. They are commonly found in rodents (and some insectivores), and fleas are believed to be their vectors. Around 50 trypanosome species have gradually been assigned to this subgenus, mainly based on the morphology of blood forms and their host specificity. However, due to the application of molecular methods, this number is beginning to increase. This thesis aims to investigate the prevalence and evolution of trypanosomes of the subgenus *Herpetosoma* in different mammalian hosts and their fleas in the Czech Republic. In total, samples from 17 mammalian species (mainly rodents) were tested for the presence of trypanosomes; only three species were found: with 1% prevalence *Trypanosoma* in the bank vole (*Clethrionomys glareolus*) similar to *T. microti* (typical for the field vole, *Microtus agrestis*), with 4% prevalence *T. grosi* in field mice (*Apodemus* spp.), and with 40% prevalence *Trypanosoma* sp. B08-471 in the European edible dormice (*Glis glis*). This trypanosome species was also detected in the flea *Ceratophyllus (Monopsyllus) sciurorum*, which is a typical ectoparasite of edible dormice. In fleas, the development of trypanosomes and also commonly occurring monoxenous trypanosomatids of the genus *Blechnomonas* was recorded and monitored (of three detected species, *B. maslovi* being the dominant). Finally, the host specificity of *Trypanosoma* sp. B08-471 and *T. lewisi* was investigated using experimental infections of rodents.

Keywords: *Trypanosoma*, *Herpetosoma*, rodents, lagomorphs, insectivores, fleas, development, *Blechnomonas*, prevalence, host specificity