

Abstract

The first part of this thesis is focused on testing the ability of selected European sand fly species to support the development of *Leishmania major*, *L. donovani* and *L. martiniquensis*. A total of 15 experimental infections were performed and 1601 female sand flies were analysed. The results show that *Phlebotomus perniciosus* and *P. tobbi* support development of *L. major* and *L. donovani* (mature infections with colonization of the stomodeal valve and metacyclic promastigotes developed), while *L. martiniquensis* did not survive defecation. The vector competence of *Sergentomyia minuta* to *Leishmania* could not be tested because the females of this species refused to take blood meal on feeders, although several types of membranes, blood and experimental conditions were tested.

Further, biting midges were studied in two areas of Czech equine autochthonous cases of *L. martiniquensis*. A total of 3341 bloodfed and parous females from Slatiňany and 119 from Ústí n. L. were analysed. The most abundant were biting midges from the *Culicoides obsoletus* complex. None of the 97 pools were positive for *Leishmania* DNA, but in 15 pools from Slatiňany was detected DNA of *Herpetomonas ztiplika* and one pool from Ústí n. L. contained DNA of *Trypanosoma* sp. from *T. theileri* group. The isolation of *L. martiniquensis* was unsuccessful, and the insects fed on the horse were negative for *Leishmania* DNA. Apparently, viable parasites did not survive in near the lesion after treatment.

Key words: *Phlebotomus*, *Leishmania*, *Mundinia*, *Culicoides*, range expansion, global warming, migration