

Abstract

Phlebotomine sand flies are proven vectors of many pathogens including parasites of genus *Leishmania*. *Leishmania* develop in sand fly midgut which is colonized also by many others microorganisms, creating rich community known as gut microbiota. The presence and composition of gut microbiota affect sand fly mortality, but also development of transmitted pathogens. In contrast to mosquitoes, sand fly gut microbiota is not well studied. This thesis focuses on bacteria of the genera *Asaia* and *Wolbachia* and their potential impact on *Leishmania* in sand fly midgut.

Thesis reports the first finding of *Asaia* sp. and *Wolbachia* sp. in sand flies from Balkan peninsula – hotspot for visceral leishmaniasis and phleboviruses. In 273 individuals from subgenera *Larrousius* were *Asaia* sp. and *Wolbachia* sp. detected with infection prevalence 2,5 % and 8,4 %, respectively. In addition, laboratory-reared sand flies were tested for presence of these bacteria: from twelve studied colonies, only *Phlebotomus perniciosus* was infected by *Wolbachia* sp. Then, we focussed on elimination of *Wolbachia* sp. from this laboratory colony with the aim to use *Wolbachia*-negative sand flies in future experiments with *Leishmania*.

The final part of the thesis was dedicated to bacteria of the genus *Asaia* (specifically *A. krungthepensis*), their experimental infection of *Phlebotomus duboscqi* and superinfection with *Leishmania major*. *Asaia* were capable to colonize sand fly midgut and affect *Leishmania* localization during superinfection. This finding might be important for *Leishmania* transmission and epidemiology of leishmaniasis.

Key words: *Lutzomyia*, *Phlebotomus*, *Asaia*, *Wolbachia*, *Leishmania*