

Abstract

Leishmaniasis is a human and animal disease caused by digenetic parasites of the genus *Leishmania*, which is now divided into 4 subgenera – *L. (Leishmania)*, *L. (Viannia)*, *L. (Sauroleishmania)* and *L. (Mundinia)*. Subgenus *Mundinia* was established in 2016 and consists of 5 species - *L. enriettii* and *L. macropodum* are parasites of wild mammals and *L. martiniquensis*, *L. orientalis* and unnamed *L. sp.* from Ghana are infectious to humans. *Mundinia* are geographically widely dispersed, their distribution covers all continents, except of Antarctica. Despite phlebotomine sand flies (Diptera: Psychodidae) also biting midges (Diptera: Ceratopogonidae) are supposed to be involved in transmission of these species, which is a unique feature for this subgenus. But there is little to no current information on natural reservoir hosts and vector species for any *Mundinia* species.

In this thesis we tested possible vectors and potential model organisms (Guinea-pigs) and reservoir hosts of *Mundinia* species by experimental infections. We used 3 sand fly species sharing geographical distribution with respective *Mundinia* species and available in our laboratory for experimental infections. Sand flies from Australia had never been colonised so we used the permissive vector *Lu. migonei* for testing development of *L. macropodum*. *Leishmania enriettii* and *L. macropodum* did not survive defecation of *Lu. migonei* and the same trend was observed in *P. duboscqi* infected with *L. sp.* from Ghana. On the other hand, *L. martiniquensis* from Martinique Island and *L. orientalis* developed late stage infections in 7 % and 21.5 % of *P. argentipes* females 8 days post blood meal, respectively. Presence of metacyclic forms in gut smears from females infected with *L. orientalis* was detected. Based on these results, we suggest involvement of *P. argentipes* in transmission of *L. orientalis*. Its important role in transmission of *L. martiniquensis* is less probable, taking in account that experimental infections with Asian isolate of *L. martiniquensis* did not bring positive results.

Model organisms, which are crucial for basic research, are not available for *L. (Mundinia)* species with the only exception of Guinea pig for *L. enriettii*. We tested Guinea pigs as model organism for other *Mundinia* species using experimental infections. Our results do not support suitability of Guinea pigs for this purpose since no external signs of infection were observed in tested animals (with the exception of temporary dry lesions on ears inoculated with *L. orientalis*), leishmania parasites did not survive and disseminate in bodies of Guinea pigs and these animals were not infectious for sand flies.

Leishmania sp. from Ghana is the causative agent of human cutaneous leishmaniasis so identification of its reservoir host is very important. We tested host competence of two sub-Saharan rodents, *Arvicanthis niloticus* and *Mastomys natalensis*, which are very abundant in endemic localities

and live in close vicinity to human settings. Our results do not support their involvement in the life cycle of this leishmania since animals were not infectious to sand flies and we detected only very small numbers of parasites in only one *Mastomys natalensis* by the end of the experiment. On the other hand, they could probably serve as a good reservoir hosts for *L. major*.