

Abstract

Leishmania are vector-borne dixenous protozoan parasites of vertebrates causing diseases collectively called leishmaniases, which threaten more than 1 billion people mainly in tropical and subtropical regions. These parasites are divided into four subgenera: *Leishmania*, *Viannia*, *Sauroleishmania*, and *Mundinia*. The last named are geographically widely dispersed and their distribution covers all continents except Antarctica. Although their medical and veterinary importance is increasing, there is currently almost no information on natural reservoir hosts, vector species, and experimental research options due to the very limited range of model animals. This thesis summarizes our efforts to unravel possible vectors and laboratory models for this subgenus. In the first three studies, we focused on potential models; therefore, we experimentally infected guinea pigs (*Cavia porcellus*), BALB/c mice, Chinese hamsters (*Cricetulus griseus*), and steppe lemmings (*Lagurus lagurus*) with five species of *Mundinia* and we also tested reservoir potential of African grass rat (*Arvicanthis niloticus*) and Natal multimammate mouse (*Mastomys natalensis*) to *Leishmania chancei*. The second part focused on potential vectors of the parasites. We experimentally infected biting midges *Culicoides sonorensis* and sand flies sharing geographical distribution with respective *Mundinia* species to test their susceptibility and vector competence by transmission experiments. We proved that *C. porcellus* are a good model for *L. enriettii*, but their utilisation for other species is limited since only animals infected with *L. enriettii*, *L. orientalis* and *L. martiniquensis* developed temporary pathological changes on the ears. BALB/c mice and *A. niloticus* are not good models for *Mundinia* as they have been proven resistant to the infection. In contrast, *M. natalensis* cannot be excluded from possible involvement in circulation of *L. chancei* in nature because parasites sporadically disseminated to different tissues and survived up to 5 months, albeit in relatively small numbers. *Cricetulus griseus* and *L. lagurus* were proved susceptible to *Mundinia*. While *C. griseus* were asymptomatic but infectious to sand flies and DNA of parasites was detected in animals by the end of experiment 20 weeks post infection, *L. lagurus* exhibited signs of cutaneous and visceral leishmaniases and were also infectious to sand flies during the whole experiment. The second part of our study proved that *C. sonorensis* support the development of *Mundinia* and three human-infecting species, *L. martiniquensis*, *L. orientalis*, and *L. chancei*, can be transmitted to the naïve host by bites of these insects. On the other hand, sand flies sharing geographical distribution with tested *Mundinia* did not transmit parasites to mammals and only *L. martiniquensis* and *L. orientalis* developed late stage infections in *P. argentipes*. These data support the hypothesis of the involvement of biting midges in circulation of *Mundinia*. If these findings will be supported by field studies, it may ultimately lead to redefinition of the entire *Leishmania* genus, where sand flies are dogmatically considered the sole vectors or the removal of *Mundinia* to a separate genus.