Leishmania spp. have a great clinical significance, being a causative agent of leishmaniasis. *Leishmania* is transmitted to its vertebrate hosts by phlebotomine sand flies. In vertebrates, the parasites infect professional phagocytes (neutrophils, monocytes and macrophages) and a variety of other cells. Clinical symptoms of leishmaniasis range from lesions, local or disseminated, to mucosal and visceral pathology. Twelve million people are infected with *Leishmania* and 350 million people are under risk of infection in 88 countries. Yet, no vaccine has been developed and the treatment needs significant improvement. In this regard, animal models of leishmaniasis play a key role in understanding the mechanisms of the disease and in finding ways to treat and prevent it.

This thesis summarizes the results of my Ph.D. project devoted to refinement of procedures relevant to *Leishmania* studies and to the use of the optimized protocols for gene mapping and search for antileishmanial drugs. Large-scale cultivation of infective *Leishmania* parasites is important in a wide range of experimental setups. We adapted a biphasic SNB-9 medium for the large-scale cultivation of *Leishmania* and compared it with a common liquid medium. We also modified and optimised detection and quantification of *Leishmania* with PCR-ELISA by using two labeled primers.

The optimized protocols enabled us to map new loci participating in the control of resistance to leishmaniasis, including control of parasite spreading. They also allowed us to characterize calcimycin as a new leishmanicidal compound and to propose nitric oxide synthase of *Leishmania*, implicated in calcimycin-induced parasite death, as a new target for antileishmanial therapy.