Methods for *Leishmania* parasite detection and quantification as a tool for study of the pathogen-vector-host interactions

Leishmaniasis in human is caused by total 21 species of the intracellular protozoan parasite *Leishmania*, which are transmitted by about 30 species of phlebotomine sand flies. Besides human, *Leishmania* can infect a number of vertebrate hosts. The major host cell is the macrophage, in which parasites multiply, eventually rupturing the cell and spreading to uninfected cells. Infected monocytes and macrophages circulating in the peripheral blood are thought to be carriers of the parasite to distal sites. Depending on the infected sites of the body, there are three forms of leishmaniasis: cutaneous, mucocutaneous and visceral. Leishmaniasis is a disease for which we still lack effective, affordable and easy to use drugs. In addition, surveillance and control are also neglected.

This thesis summarizes the results of several projects using different approaches for parasite load measurement in the mouse model of leishmaniasis, including two methods that were developed and optimized in our laboratory. Detection and quantification of pathogens belongs to the major topics of the research of various infectious diseases. This parameter is necessary for confirmation of the diagnosis, characterization of the host defense, complex pathological changes in the infected organisms, and for the evaluation of the effectiveness of therapy. We use quantification of *Leishmania* parasites to study influence of the genotype on susceptibility to the disease and to estimate the effectiveness of immunization with sand fly saliva.

Application of various parasite measurement assays revealed gene- and sex-dependent differences in susceptibility to *Leishmania.* Two genetic loci that control parasite dissemination in the internal organs were first detected by our laboratory in genome-wide screening using a mouse model of leishmaniasis. The obtained knowledge brings more complex understanding of the pathogen-vector-host interactions.