Marie Lipoldová

marie.lipoldova@img.cas.cz

For more information, publications and grants please visit:
www.img.cas.cz/research/marie-lipoldova

In the picture:
1. Adéla Štěpánová | **2.** Barbora Zavoloková | **3.** Daniel Jetenský | **4.** Jana Turňová | **5.** Imtissal Krayem | **6. Marie Lipoldová** | **7.** Lucie Mrázková | **8.** Martina Slapničková

Not in the picture:
Jarmila Vojtíšková | Yahya Sohrabi | Valeriya Volková | Monika Buddeusová | Marie Čepičková | Gabriela Jansová | Aigerim Aidarova

LABORATORY OF

MOLECULAR AND CELLULAR IMMUNOLOGY

genetics of pathogenesis of leishmaniasis, gene mapping, functional diversity, general and species-specific control

The research programme of the laboratory aims to identify the genes and molecular mechanisms involved in the control of immune response and susceptibility to complex infectious diseases. We focus on complex diseases because they are responsible for the largest part of human morbidity and mortality. They are controlled by multiple genes, and hence their pathogenesis cannot be explained by effects of a single gene with omission of others. Leishmaniasis is such a complex disease and it has served as a major paradigm of immune response to an infectious agent. We aim to identify the genes and functions controlling this disease. The disease is caused by protozoan parasites of genus *Leishmania* that multiply in macrophages. Different species of *Leishmania* induce different symptoms, but even the patients infected by the same species develop different clinical manifestations. Many phenomena observed in human leishmaniases can be investigated in the mouse. Our approach uses a combination of genetic dissection with screening of a large set of immunological and clinical parameters of the disease. We were able to dissect the complexity of the host response to *L. major,* which is characterized by many immunological and pathological parameters, by use of a special system – recombinant congenic strains of mice – and we detected and mapped more than 24 novel QTLs (quantitative trait loci) influencing the response to this parasite. We mapped seven QTLs by combination of recombinant mapping and in silico approaches to less than 1 or 2 cM. This will enable us to screen for candidate genes, detect those with altered expression after infection, and use systems analysis to identify the functional networks of genes that would define the critical pathogenetic pathways. Last but not least, we have identified diphenyleneiodonium (DPI) as an effective inhibitor of *Leishmania* parasites both in vitro and in vivo. It kills parasites more effectively than the current drugs such as amphotericin B. Moreover, DPI is also effective in killing *Trypanosoma*. The effective concentrations of the compound were non-toxic to the tested human cell lines.

Selected recent papers:

Slapničková M, Volkova V, Čepičková M, Kobets T, Šíma M, Svobodová M, Demant P, Lipoldová M: Gene-specific sex effects on eosinophil infiltration in leishmaniasis. **Biology of Sex Differences** 7:59, 2016.

Šíma M, Kocandová L, Lipoldová M: Genotyping of short tandem repeats (STRs) markers with 6 bp or higher length difference using PCR and high resolution agarose electrophoresis. **Protocol Exchange. 2015** doi:10.1038/protex.2015.054.

Grekov I, Pombinho A, Šíma M, Kobets T, Bartůněk P, Lipoldová M: Pharmaceutical composition comprising diphenylene iodonium for treating diseases caused by the parasites belonging to the family Trypanosomatidae, Patent no. 305247, Awarded 15. 6. 2015, Úřad průmyslového vlastnictví České republiky. WO2015039638-A1; CZ201300729-A3.


1
2
3
4
5
6
7
8
2
20
21