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Common virulence factors in Leishmania infection

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Leishmania parasites cause a broad spectrum of clinical manifestations. This study is focused on virulence factors in *Leishmania* that are shared between two different *Leishmania* species. Common virulence factors are important for design of universal drug against leishmaniases. In this work, we compared the expression profiles of the virulent and attenuated strains of *L. major* and different developmental stages of *L. mexicana* using next-generation sequencing. A virulent line LV561/AV with attenuated infectivity for mice and sand fly vectors was obtained by long-term cultivation of the *L. major* virulent strain LV561 (LRC-L137; MHOM/IL/1967/Jericho-II). Whole transcriptome analysis revealed that 230 transcripts are upregulated in LV561/V (virulent) strain. Procyclic promastigote, metacyclic promastigote and amastigote stages were obtained by differentiation of *L. mexicana* in axenic culture. RNA-seq analysis revealed that 8 genes are up-regulated in infective for human metacyclic promastigotes; 276 genes are up-regulated in a blood-dwelling amastigotes. Among common virulence factors in *Leishmania*, e.g., genes that are up-regulated both in virulent strain of *L. major* and metacyclic promastigotes or amastigotes of *L. mexicana*, we found genes encoding for major surface protease gp63, casein kinase I, pteridine transporters and several hypothetical proteins.

Biography

Aygul Ishemgulova is a PhD student at the Life Science Research Centre, University of Ostrava, Czech Republic. She graduated from Department of Plant Physiology and Biochemistry of Faculty of Biology and Soil Sciences of Kazan State University, Russia in 2011. Her current work is focused on analysis of *Leishmania* pathogenicity.

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