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PROTEOMIC IDENTIFICATION OF MOLECULES INVOLVED ON THE ESTABLISHMENT AND CONTROL OF CUTANEOUS LEISHMANIASIS

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CBA/J mice are resistant to *Leishmania major* and susceptible to *Leishmania amazonensis*. The early events of host-pathogen interaction are decisive for the disease outcome. Macrophage plays an important role in the early events of *Leishmania* infection. CBA/J macrophages control *L. major* infection and are permissive to *L. amazonensis*. The large-scale studies of host-pathogen interaction are important for the comprehension of the molecular mechanisms controlling the onset of infectious diseases. We have performed proteomic experiments using bone marrow derived macrophages (BMMΦ) in order to evaluate the macrophage response to *Leishmania* infection. We evaluated the differential expressed proteins at 6 and 24h of *L. major* or *L. amazonensis* infection. Protein extracts from 6 independent experiments were obtained to identify peptides by LC-MS/MS in a MudPIT approach. The results show that 382 proteins were differently expressed in *L. amazonensis*- or *L. major*-infected cells. These proteins are involved in cell death, post-translational modification, lipid metabolism, molecular transport, amino acid metabolism, small molecule biochemistry, cell signaling, cellular assembly and organization, cellular movement, cell cycle, organismal injuries and abnormalities and cell-mediated immune response. Using Ingenuity Pathway Analyses, we showed that a network related to lipid metabolism has most of the proteins higher expressed in *L. amazonensis*-related to *L. major*-infected cells, while a network related to cell-signaling and cellular assembly has most of the proteins with higher expression levels in *L. major*- related to *L. amazonensis*-infected cells. In response to *L. amazonensis* macrophage did not strictly fall into activation profiles, as previously described by others using microarray studies. On the other hand *L. major* modulate cell-signaling network supporting a kind of response compatible with cell activation. These results corroborate the previous observed differences in macrophage response to *L. amazonensis* and *L. major*. Current western-blot analyses are been performed to corroborate the differences detected by proteomic studies.

Keywords: Proteomics, murine bone marrow derived macrophages, Leishmania amazonensis, Leishmania major