Altered metabolism in tropical diseases: the case of visceral leishmaniasis

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¹Institute of Tropical Medicine of Rio Grande do Norte, ²Department of Biochemistry, ³Department of Infectious Diseases, Federal University of Rio Grande do Norte, Natal, RN, Brazil; Institute of Science and Technology of Leishmania infantum infection can evolve with a spectrum of outcomes including self-resolution of infection to disease development, visceral leishmaniasis (VL). We hypothesized that altered metabolism may be involved in the pathogenesis of L. infantum infection. To uncover host and parasite factors, which would affect pathogenesis, global gene expressions of peripheral blood mononuclear (PBMC) cells from humans with symptomatic and asymptomatic L. infantum infections, and splenocytes and PBMC from dogs with disease were compared. Microarray analyses of human RNA revealed that 1700 genes were differentially expressed in human VL. Among the characterized metabolic pathways, immunological response signaling (MAPKs cascades, ERK1 and ERK2, cytokines production), cell cycle and lipid metabolism were the most represented ones. This allow to trace the transcription profile that might be associated to symptomatic individuals. It should be noted that these results are in accordance to functional studies. A higher number of differentially expressed transcripts (about 3000) were observed in PBMC and spleen samples from dogs with VL when compared to healthy dogs or with low parasite loads. As observed to human VL, pathways related to immune response were also well represented, confirming that there are some common pathways related to VL establishment and outcomes in Leishmania infection in both dogs and humans.