IN SILICO AND TRANSCRIPTIONAL ANALYSIS OF GENES THAT ENCODE ENZYMES RELATED TO EICOSANOID METABOLISM OF *LEISHMANIA SPP*

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Parasites of the *Leishmania* genus can synthesize eicosanoids, once they possess enzymes related to their metabolism. In turn, eicosanoids are bioactive lipids capable of controlling inflammatory response in vertebrate hosts. Recently, it was demonstrated that the profile of eicosanoids produced by *Leishmania* varies according to the parasite species and the clinical condition of the leishmaniasis associated with the disease. Herein, we analyzed the differences in the genes involved in eicosanoid metabolism, as well as the alterations in the proteins encoded by these, such as prostaglandin F synthase (PGFS) and cytochrome p450 oxidase 1 (CYP1). For this, we analyzed *in silico* the genes associated with the metabolism of eicosanoids in *Leishmania spp* by means of bioinformatics tools, such as: alignment, phylogenetic analysis of the two identified genes, modeling of proteins encoded by them, and structural alignment of proteins aimed at identifying polymorphisms in regions of interest. We also carried out the development of pairs of primers to subsequently carry out a comparative evaluation of genetic expression by means of the RT-qPCR technique in the different species of *Leishmania*. A reduction was observed in the levels of genetic expression of *cyp1* in *L. braziliensis* compared to *L. infantum* and *L. amazonensis*. Regarding the expression of *pgfs*, no significant differences in gene expression were observed between the *Leishmania* species studied. Furthermore, we identified that the same mutations in the genes and proteins are conserved in *Leishmania species* related with similar clinical forms of leishmaniasis. Then, the data indicate differences of *cyp1* expression between *Leishmania* species, which can be related to virulence during host-pathogen interactions to be investigated in the next studies.

Supported by: UFOB.

Keywords: *cyp1*, *pgfs*, *Leishmania*.