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# DIFFERENTIAL GENE EXPRESSION IN BONE MARROW CELLS CLASSIFIES DOGS DIFFERENT CLINICAL OUTCOMES NATURALLY INFECTED WITH *LEISHMANIA INFANTUM*

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**INTRODUCTION:** Visceral leishmaniasis (VL) is the most severe form of leishmaniasis, affecting internal organs like the spleen, liver, and bone marrow. It is endemic in 76 countries and present in at least 12 in the Americas, with Brazil accounting for 90% of Latin American cases. Dogs serve as reservoirs, transmitting VL to humans via *Lutzomyia longipalpis* bites. In a cohort study in an endemic area of Camaçari, Bahia, Brazil, dogs were classified as resistant or susceptible based on clinical, immunological and parasitological evaluations. **OBJECTIVE:** Given the critical role of bone marrow in the persistence of parasites in infected animals, this study aims to assess the immunocellular responses of bone marrow cells in naturally infected dogs from the cohort study using RNA sequencing (RNAseq). **METHODOLOGY:** RNAseq was conducted on bone marrow cells from dogs classified as susceptible or resistant. We compared global gene expression by bone marrow cells of infected dogs versus healthy controls to identify differentially expressed genes (DEGs) and biomarkers. Machine learning identified four predictive genes—TINAGL1, FOS, ADCY9, and EGR2—that can distinguish susceptible and resistant from healthy dogs. RT-qPCR was used to validate the RNAseq findings. For this process, RNA was extracted, converted into cDNA, and then analyzed through RT-qPCR using specific primers. In addition, pathway enrichment analyses were conducted and identified in bone marrow cells from susceptible dogs, reduction in the expression of genes involved in DNA double-strand break repair. These alterations will be validated in cells from susceptible dogs. **RESULTS:** *TINAGL1* was more expressed in susceptible dogs, while *FOS* was higher in controls; *ADCY9* and *EGR2* showed no significant differences. Future analyses will include western blotting to confirm gene expression. Genomic DNA will be extracted to assess double strand breaks in susceptible dogs. **CONCLUSION:** *TINAGL1* and *FOS* may play key roles in VL infection.

**KEYWORDS:** Visceral Leishmaniasis, genes, dogs, biomarkers, bone marrow.

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