RESUMO SIMPLES - MICROBIOLOGIA E IMUNOLOGIA

DIFFERENTIAL EXPRESSION OF IMMUNE-RELATED REDOX METABOLISM GENES IN DIFFERENT DEVELOPMENTAL STAGES OF RHIPICEPHALUS MICROPLUS IN RESPONSE TO THEILERIA EQUI INFECTION

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Equine piroplasmosis is one of the main diseases affecting equids worldwide, with the protozoan Theileria equi being one of its etiological agents. Transmission occurs mainly through infected ticks during blood feeding. In Brazil, Rhipicephalus microplus is the only tick species with experimentally confirmed vector capacity to transmit T. equi. However, there are still several

gaps regarding the mechanisms involved in this pathogen-vector interface. To survive and be transmitted to a susceptible host, the parasite needs to evade the tick's innate immune response. One of the main components of this response is the redox metabolism, which involves a series of enzymes that regulate the synthesis and levels of reactive oxygen species (ROS) in the cellular environment. ROS play a role in infectious processes due to their toxic nature, potentially causing cellular damage to pathogens. However, this toxicity also extends to the host cell, necessitating a coordinated response involving both pro- and antioxidants to ensure cellular survival. Therefore, the aim of this study was to evaluate the differential expression of genes related to redox metabolism in different developmental stages of Rhipicephalus microplus in response to Theileria equi infection. For this, a chronically infected equine with T. equi (positive control) and a non-infected equine (negative control) were infested with T. equi-free R. microplus larvae. After the fixation and blood feeding period, whole larvae and nymphs were collected and stored individually, while the females were dissected, and the midgut and the salivary glands of each specimen were collected and stored separately. RNA extraction and cDNA synthesis were performed for each sample, followed by relative gene expression assays using qPCR. In the midgut of R. microplus, the pro-oxidant genes CuZnSOD, DUOX-1, DUOX-2, and ERO1 were upregulated in the infected group compared to the control, while in the salivary gland, only the DUOX-1 and DUOX-2 genes were positively regulated, suggesting that these enzymes may play a significant role in the oxidative response of R. microplus to T. equi infection in different tissues. Regarding the antioxidant genes analyzed, only the catalase (CAT) gene was upregulated in the infected group in both tissues, suggesting that this enzyme may be crucial in controlling ROS levels in the cellular environment. In the salivary glands, however, it was observed that the gene encoding the enzyme glutathione S-transferase (GST-1) was significantly downregulated in the infected group, suggesting that this enzyme may play a key role in the antioxidant response in this tissue, and its downregulation indicates a mechanism favoring the oxidative response by the tick. In the larva and nymph stages, T. equi infection did not significantly stimulated the differential expression of analysed genes, indicating a immunological immaturity of the early developmental stages of the tick in responding to T. equi infection. The results obtained in this study help to elucidate the oxidative response of R. microplus to T. equi infection and highlights potential key molecules for the development of new tools for the prevention and control of equine piroplasmosis in Brazil.

Palavras-chave: equine piroplasmosis; pathogen-vector interface; tick-borne pathogen; immune system.