

Transcriptional Level of Antioxidant Enzyme genes in *Rhipicephalus microplus* Tissues

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INTRODUCTION: Antioxidant enzymes act to maintain cell homeostasis, controlling the oxidative stress trough decreasing the toxicity of reactive oxygen species and xenobiotics. In ticks, these enzymes are involved in heme detoxification during blood feeding and in resistance of acaricides, howeverthe role of various antioxidant enzymes in their physiology is still unknown. OBJECTIVE: the aim of this work is characterize the transcriptional level of the antioxidant enzymes glutathione Stransferase, glutathione peroxidase, thioredoxon reductase and peroxiredoxin in Rhipicephalus microplus salivary glands, midgut and ovary. MATERIALS AND **METHODS:** Tissues from partially and fully engorged *R. microplus* females were dissected to total RNA extraction and cDNA synthesis. The transcriptional level of antioxidant enzyme genes are being evaluated by real-time guantitative PCR (gPCR) including actin as normalizer gene. The relative expression ratio of enzyme genes was calculated with in Relative Expression Software Tool (Pfaffl 2001) **RESULTS AND DISCUSSION:** The transcriptional level of glutathione-s-transferase gene was higher in midgut of fully engorged female and in ovary from partially engorged female. For glutathione peroxidase, the transcriptional gene level was higher in salivary glands from fully engorged female. Thioredoxin reductase transcripts were more abundant in ovaries from both female stages. Whereas peroxiredoxin genes has a relative expression similar in all analyzed tissues. The transcriptional levels of each enzyme is controlled by redox signaling that activate transcription factors, and it depends on the level and on the microenvironment where reactive species occurs. CONCLUSIONS: In ticks, the constant modification of metabolism during feeding and embryogenesis contributes for the different levels of antioxidant enzyme genes observed in the tissues. The role of each enzyme through the development of the tick in different tissues and the cause of major transcription for each enzyme are in progress to better comprehension of their physiological role.

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