Summary:

The study focused on investigating *Babesia bigemina* infection, commonly known as Texas fever, as a significant causative agent of bovine babesiosis worldwide. The primary objectives included molecular detection and phylogenetic analysis of *B. bigemina*, as well as the evaluation of oxidative stress, procalcitonin and arginase activity in infected animals. A cohort of 360 male cattle from northwest Iran was examined, with 20 individuals identified as *B. bigemnia* positive. Phylogenetic analysis revealed that the obtained sequences clustered within *B. bigemina* and distinct from *B. bovis* and *Theileria annulata*. The infected animals were categorized into two groups based on parasitemia severity (>20% and <20%), with 10 healthy cattle serving as controls. The study found a parasitemia-dependent reduction in red blood cell (RBC) and white blood cell (WBC) counts, hemoglobin, and hematocrit levels, indicating severe anemia following *B. bigemina* infection. Additionally, the levels of superoxide dismutase (SOD) and malondialdehyde (MDA) increased significantly, while catalase (CAT) and total antioxidant capacity (TAC) decreased significantly ($p < 0.05$) in a parasitemia-dependent manner. The relationship between pollution intensity, lipid peroxidation levels, and antioxidant enzyme activities was significantly correlated ($p < 0.05$). Positive correlations were observed between parasitemia and MDA levels ($r=0.86$, $p < 0.0005$; $r=0.75$, $p < 0.0005$) and an inverse relationship between parasitemia intensity and packed cell volume (PCV) levels ($r=-0.98$, $p < 0.0005$; $r=-0.88$, $p < 0.0005$) in infected animals. Furthermore, a negative correlation was found between parasitemia intensity and the activities of SOD, glutathione peroxidase (GSH-Px), CAT, and TAC in infected animals. Significantly lower levels of arginase and higher levels of procalcitonin were observed in infected animals compared to controls, with noticeable changes corresponding to different levels of parasitemia. These findings suggest that *B. bigemina* infection induces anemia, tissue damage, and inflammation, leading to alterations in metabolic enzymes and inflammatory markers like procalcitonin and arginase. Arginase and procalcitonin emerged as sensitive parameters reflecting active inflammatory processes during *B. bigemina* infection at various parasitemia levels. These results highlight the potential utility of arginase and procalcitonin as indicators of inflammatory responses associated with *B. bigemina* infection. In conclusion, *B. bigemina* infection impacts cell metabolism, inflammatory markers, and enzyme activities, emphasizing the importance of monitoring these parameters to understand the pathogenesis and severity of bovine babesiosis caused by *B. bigemina*.

Keyword: Oxidative stress, Lipid peroxidation levels Arginase, Procalcitonin, *Babesia bigemina*.