

## **Effects of heat stress on the transcriptomic profile of blood cells in lactating dairy goats**

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Short title: Blood transcriptomics of heat-stressed goats

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## Summary

High temperature is a major stress that negatively affects welfare, health, and production of dairy animals. Heat-stressed animals are more prone to diseases, suggesting that their immunity is hindered. Although productive and physiologic responses of dairy animals to heat stress are well known, there is still limited information on the response at the transcriptome level. Our objective was to evaluate the changes in blood transcriptomics of dairy goats under heat stress. Eight adult Murciano-Granadina dairy goats in mid-lactation were exposed to 2 climatic treatments for 35 d. Treatments and temperature-humidity index (THI) were: 1) thermal neutral (TN: 15-20°C, 40-45%, THI = 59-65), and 2) heat stress (HS: 12 h at 37°C-40%, THI = 86; 12 h at 30°C-40%, THI = 77). Blood samples were collected at d 35 and RNA was extracted for microarray analyses (Affymetrix GeneChip Bovine Genome Array). The signal intensity of globin genes was low and did not affect the detection of gene expression. The analysis revealed that 55 genes were up-regulated, whereas 88 were down-regulated by HS. Bioinformatics analysis using the Dynamic Impact Approach revealed that 31 biological pathways were impacted by HS. Pathways associated with leukocyte transendothelial migration, cell adhesion, hematopoietic cell lineage, calcium signaling, and PPAR signaling were negatively impacted by HS, whereas nucleotide metabolism was activated. Overall, these changes are suggestive of alterations in the functionality of immune cells during heat stress, making the immune system of heat-stressed goats less capable of fending-off diseases.