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## Differential gene expression profiles in skin of resistant and susceptible cattle to tick infestation

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The cattle tick, *Rhipicephalus (Boophilus) microplus*, is a major threat to the improvement of bovine cattle production in tropical and subtropical countries worldwide. Generally, zebuine breeds are more resistant to infestation with ticks than taurine breeds. Several factors might be involved in the breeds' variation regarding resistance to tick, including skin characteristics and immune activation. The aim of this work was to access the gene expression profile in the cattle's skin and compare the distinct mechanisms activated between resistant and susceptible animals. From a Gyr x Holstein F2 population with wide variation in resistance to tick, six highly resistant and six highly susceptible animals were selected. The animals were infested with almost 20,000 tick larvae and skin biopsies were performed at the site of tick attachment at three times: before, 24 and 48 hours after the infestation. The RNA extracted from the biopsies was submitted to microarray using the bovine gene chip. The quality control, preprocessing and statistical analyses were performed in the computational statistics language R using the *Bioconductor* project. For the evaluation of quality of chips the packages *affQCreport* and *simpleaffy* were used. After each of three different of summarization methods (MAS5, RMA and GCRMA) the differential expression analyses were tested using the *limma* package. Only differentially expressed probes detected in two out of the three summarization methods ( $p < 0.01$ ) were considered to be significant. Making comparisons between the times in the same group and between the groups of resistance in the same time, one hundred and three genes were differentially expressed. The main biological processes which these genes take part are: antigen processing and presentation, immune response regulation, coagulation and complement cascades and calcium binding factors. It's notable a greater expression of coagulation and complement genes in the resistant animals. These can block the feeding of the tick at the site of attachment. Another gene, CLDN1, was more expressed in the resistant group before the infestation when compared with the susceptible group at the same time. The protein encoded by this gene participates as a component of the tight junctions, which form a virtually impermeable barrier to fluid, interfering in the feeding of ticks. Financial Support: CNPq and Fapemig

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