

GLOBAL GENE EXPRESSION PROFILING OF TICK-INFESTED SKIN IN CONTRASTING PHENOTYPES OF INFESTATIONS IN BOVINES.

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Background: Bovines present contrasting, heritable levels of resistance to the cattle tick, *Rhipicephalus microplus*. In order to elucidate the mechanisms that result in these outcomes, we examined global gene expression profiles and inflammation of cutaneous reactions to tick bites in indicine and taurine cattle, respectively resistant and susceptible to ticks.

Methods: Biopsies of skin were made from resistant and susceptible bovines that were naïve or infested with larvae and nymphs. Gene expression for individual samples was determined with Affymetrix chips. Data was normalized using RMA. RankProd and LIMMA packages were employed to obtain differentially expressed genes (DEGs). Functional analysis was done using Metacore. Differential counts of leukocytes infiltrating skin were made by means of Giemsa staining. Lymphocytes were phenotyped with specific antibodies.

Results and Conclusions: The transcriptional profile revealed that cutaneous inflammation is greater in resistant hosts because they express more message than susceptible bovines for chemokines for basophils, eosinophils and T and B lymphocytes; this result is reflected by significantly higher numbers of these cells recruited in the corresponding local inflammation. Other DEGs are involved in extracellular matrix and tissue repair and suggest that resistant hosts have a more resilient skin to tick bites and respond more vigorously to wounding. The top scored maps produced by Metacore analysis indicate that production of odoriferous substances differs between phenotypes. Finally, tick saliva may be classified as a xenobiotic and, accordingly, top networks were formed with DEGs that participate in responses to organic substances and xenobiotics.

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