PE0246: Differential Gene Expression in the Cattle Tick *Rhipicephalus microplus* Fed on Resistant and Susceptible Cattle

Rhipicephalus microplus is an ectoparasite that has substantial economic impact on the cattle breeding industry, through direct effects of feeding and by transmission of significant cattle diseases. The use of acaricides is the conventional form of control of the parasite, but efforts have been employed in the search for alternative forms of control. In this context, genomic tools can contribute to the understanding of molecular mechanisms to the discovery of targets that can be used in new control strategies, such as vaccine development. Insights into the components involved in ticks blood feeding, blood digestion and reproduction are essential to understanding tick-host interactions and development and to identify novel targets that can serve for the basis to tick control strategies.

Using RNA-Seq technology, we obtained the transcriptional profiling of salivary glands, ovary and gut from *R. microplus* fed on resistant (Nelore), susceptible (Holstein) and crossbreed cattle, with the aim to understand the host breed effects on tick gene expression during the tick-host interaction. A total of 484,754,177 Illumina paired-ended sequences (2x100bp) were *de novo* assembled using Trinity. Differentially expressed genes (DEG) between the transcriptomes of ticks fed on resistant, susceptible and crossbreed cattle were identified by EdgeR and revealed 137, 252 and 134 DEG (FDR-adjusted p-value <0.05) in salivary glands, ovary and gut, respectively.

Functional analysis using Blast2GO showed an enrichment in upregulated genes that code for proteins with transferase activity in crossbreed cattle compared to Holstein cattle at tick salivary glands. Genes that code for proteins with transferase and peptidase activity also were upregulated in crossbreed cattle fed tick gut, compared with Holstein fed ticks. Most ovarian DEG were upregulated in crossbreed cattle, including genes that code for proteins with transferase, hydrolase and with binding functions. Further analysis are planned to focus on the role of these genes to unveil the molecular bases of the tick interaction with resistant and susceptible cattle.

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