

## **F40 POSTER** seleccionado como presentacion oral

### **IDENTIFICATION OF NEW GENES IN CATTLE OF DIFFERENT GENETIC GROUPS ACTIVATED IN RESPONSE TO TICK *Rhipicephalus (Boophilus) microplus***

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One of the main constraints in Brazilian cattle production and many tropical countries are caused by parasitism of *Rhipicephalus microplus* tick. In order to understand the host – parasite relationship, this study evaluated CHI3L2, CXCL5, IGHG1, ISG15 and PGLYRP1 gene expression in three genetic groups of cattle infested with *R. microplus* tick. For this, skin samples from 45 Nellore and crossbreed females, Senepol x Nellore and Angus x Nellore were collected before the 1<sup>st</sup> infestation and 24 hours after the 4<sup>th</sup> infestation with 20,000 *R. microplus* larvae. Following, total RNA was extracted, cDNA was synthesized and quantitative PCR was performed. Genes chosen for this analysis were previously detected in a microarray experiment. The gene constitutive used was RPS-9 and SYBR Green, as dye. Statistical analysis was performed using REST 2009 software (*Relative Expression Software Tool*), specific to quantitative PCR analysis. There were significant differences ( $P < 0.05$ ) for the five genes studied. These genes were activated within 24 hours after tick infestation and, generally, are involved in many metabolic pathways (e.g. chemokine signaling, peptidoglycan recognition and immune response), and this is the first identification in response to tick. Based on these results, it is possible to conclude that these genes must be related to the mechanisms of protecting the cattle against tick infestation, probably helping the detachment in the early larval infestation, a critical period for the maintenance of tick larvae in cattle and other mammals.

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