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## A PARTIAL GENOME SCAN STUDY TO IDENTIFY LOCI FOR TICK RESISTANCE IN CATTLE.

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SNP, GWAS, ticks, dairy cattle.

In tropical and subtropical regions, the cattle tick *Rhipicephalus (Boophilus) microplus* is responsible for large losses in livestock productivity, which are estimated to be around 18 billion dollars per year. Genome-wide association studies (GWAS) are approaches being applied to study the tick-host interaction to understand the biological processes involved with host immune responses to tick infestation, and to identify genomic regions associated with tick burdens. DNA has been acquired for 476 animals from Holstein, Gyr and Gyr x Holstein F1 and F2 populations, and a total of about 54,000 SNPs genotyped with the Illumina BovineSNP50 Bead Chip (Illumina Inc., San Diego, CA) were investigated to determine usefulness of the associated SNPs for the breeding value of tick resistance. For this study, a partial genome scan study was developed from chromosome 1 to chromosome 10. Any SNP with low call rate (<99%), departure from Hardy-Weinberg equilibrium (exact test  $p < 0.01$ ), and minor allele frequency below 5 percent, were excluded from the final analysis (34,218 markers retained). Bonferroni corrected level of 0.01 were used. SNPAssoc software, an R package, was used in order to detect association. For this trait, significant SNPs were found on many chromosomes, especially on BTAs 2, 4, 6, and 7. The presence of significant SNPs in these chromosomes suggests further SNP discovery in this region to detect causal mutations would be warranted.

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