



ANNOTATION OF TICK RESISTANCE ASSOCIATED SNPS IN CATTLE.

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In tropical countries, losses caused by bovine tick *Rhipicephalus (Boophilus) microplus* infestation have a tremendous economic impact on cattle production systems. Advances in genomics and the availability of the bovine genome sequence, occurred in the last three years, are helpful in order to identify useful genes controlling cattle tick resistance. Genome-wide association studies (GWAS) are being applied to identify genomic regions associated with tick burdens. In this experiment, 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. A partial genome scan study were carried out from chromosome 1 to chromosome 10 and significant SNPs were found on many chromosomes, especially on BTAs 2, 4, 6, and 7. In total, 75 SNPs were detected to be significantly associated genome-wide with the breeding value for tick counts. The majority of the significant SNPs is located within the reported QTL regions and some are within or close to the reported candidate genes. In particular, two SNPs, BTB-01041631 and BTB-01597787, are located on chromosome 7, close to the TNFAIP8 gene. Our findings herein not only provide confirmatory evidences for previously findings, but also explore a suite of novel SNPs associated with tick resistance in dairy cattle.

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