

An Across-Breed Genome Wide Association Analysis of Susceptibility to Paratuberculosis in Dairy Cattle

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Paratuberculosis is a chronic disease of ruminants caused by *Mycobacterium avium* subspecies paratuberculosis (MAP). It causes a significant loss in the animal production industry worldwide. Additionally, there are concerns regarding its potential relevance to humans Crohn's disease. Identification of susceptibility genetics could be a useful adjunct for programs that focus on management, testing and culling of diseased animals. A case-control, genome-wide association study (GWAS) of susceptibility to MAP infection was conducted using Holstein and Jersey cattle in a combined analysis in order to identify the most common markers and chromosomal regions associated with MAP infection across the two breeds. The GRAMMAR-GC method implemented in the GenABEL R package and a Bayes C analysis implemented in the GenSel software were used as different approaches in GWAS analysis focused on single SNP and chromosomal segments, respectively. After conducting quality control criteria; 22,399 markers and 2,161 individuals were included in the analysis. One SNP located on BTA27 (8.6 Mb) was identified as moderately significantly associated ($p < 5 \times 10^{-5}$). Nine 1 Mb windows located on BTA 2, 3 (3 windows), 6, 8, 25, 27 and 29 each explained $\geq 1\%$ of the total proportion of genetic variance in the Bayes C analysis. Two moderately significantly associated SNPs were also identified on BTA23 (32 Mb) and BTA19 (61 Mb) based on the combined p-values from separate analyses of the two breeds (ie. ignoring potential phase differences between breeds). New common genomic regions and candidate genes have been identified that might be involved in susceptibility to MAP infection.