

Editorial Note on Risk of Bovine Tuberculosis in Cattle

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Editorial

Many studies suggest significant genetic variation in the resistance of cattle and humans to infection with *Mycobacterium bovis*, the causative agent of zoonotic tuberculosis. The natural resistance associated macrophage protein 1 (NRAMP1), encoded by the SLC11A1 gene, plays a key role in the immunological control of a broad spectrum of infectious agents. The aim of the present study was to investigate the influence of single nucleotide polymorphisms (SNPs) of the SLC11A1 gene on bovine tuberculosis (bTB) susceptibility. We genotyped the SLC11A1 gene in 60 bTB-infected Holstein cows and 90 healthy control animals. The influence in the exon 4 and intron 4 regions of SLC11A1 genetic variations on bTB susceptibility was subsequently investigated by association analysis. Our finding demonstrated that the g.107117166A>G and g.107117369C>T polymorphisms of the SLC11A1 gene associated with bTB in Holstein cattle. The susceptibility of cattle with the g.107117166A>G genotype compared with the GG genotype was 3.40 (95% CI: 1.10-10.51; p=0.048) fold higher. The g. 107117166A>G SNP located in the exon 4 of the SLC11A1 gene and the functional consequence was missense.

M. bovis can be transmitted to humans via infectious bacilli through respiratory contact with infected cattle or consumption of unpasteurized dairy products. The host immune response to *M. bovis* infection is complex; following initial exposure, the bacilli are phagocytosed by host macrophages via transporters such as natural resistance-associated macrophage protein 1 (NRAMP1), encoded by the solute carrier family 11 member 1 (SLC11A1) gene. This transporter – which functions as part of the innate immune response – plays a key role in inhibiting proliferation of *Mycobacterium tuberculosis* (*M. tuberculosis*), through its involvement in acidification of phagosomes. The relationships between various polymorphisms in the human SLC11A1 gene and mycobacterial diseases have been explored, including INT4 (single nucleotide G>C change in intron 4, 469+14G/C, rs3731865), D543N (conservative single base G>A substitution at codon 543, resulting in a change to asparagine from aspartic acid), and 3'UTR TGTG (a deletion in the 3' untranslated region, 1729+55del) [6-10]. Additionally, a Taiwanese aboriginal casecontrol study revealed that individuals possessing one of the three polymorphism of the SLC11A1 gene have higher susceptibility to tuberculosis, with those who are heterozygous for the INT4 polymorphism being at greatest risk.

Keywords: Animal disease; Bovine

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