Toll Like Receptor 1 (+1380 G/A) SNP is Associated with Paratuberculosis Susceptibility in Holstein and Indigenous Crossbred Cattle in Turkey

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Abstract: Paratuberculosis (Johne's disease) is an economically significant condition caused by Mycobacterium avium subsp. paratuberculosis (MAP). Paratuberculosis remains one of the most important diseases of cattle breeding. In cattle, the disease is debilitating and is characterized by weight loss and chronic diarrhea in the later stages of infection. Paratuberculosis infection susceptibility is suspected to be controlled by host genetics so selecting individuals according seroprevalence could help to obtain bovine populations that are increasingly resistant to MAP infection. The aim of the present work was to investigate association between Toll-like receptor 1 (TLR1 +1380 G/A and +1446 C/A), Toll-like receptor 4 (TLR4 +10 C/T), Toll-like receptor 9 (TLR9 +1310 G/A) and Solute Carrier Family 11 Member 1 (SLC11A1 +1066 C/G) SNPs and MAP infection status (case/control) in 813 cattle comprising East Anatolian Red crossbred (n=281), Anatolian Black crossbred (n=108) and Holstein breed (n=376). In order to detect MAP Idexx Paratuberculosis Screening ELISA kit was used. Data were analyzed using logistic regression model (breed and sex were tested as fix factors) and odds ratios (OR) with 95% CI were calculated. TLR1 (+1380 G/A) mutation showed an association with bovine MAP ($P < 0.05$). For TLR1 (+1380 G/A) locus, the odd ratios for AG and AA genotypes versus GG genotypes were 2.31 (1.24–4.30; 95 % CI) and <0.001 (< 0.001 to > 999.999; 95 % CI) which indicated that proportion of AG genotype was significantly higher in paratuberculosis affected animals as compared to control. Our results suggest selecting animals against TLR1 +1380 AG genotype may decrease risk of paratuberculosis in cattle belongs to Bos taurus species.

Keywords: Johne's disease; Bovine; Genetics; Disease risk; Anatolian indigenous cattle

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