

Investigation on Single Nucleotide Polymorphism in Candidate Genes and Their Association with Occurrence of Mycobacterium avium Subspecies Paratuberculosis Infection in Cattle

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Abstract : Paratuberculosis caused by Mycobacterium avium subspecies paratuberculosis (MAP) is a chronic granulomatous enteritis affecting ruminants. It is responsible for significant economic losses in livestock industry worldwide. This organism is also of public health concern due to an unconfirmed link to Crohn's disease. Susceptibility to paratuberculosis has been suggested to have genetic component with low to moderate heritability. Number of SNPs in various candidate genes have been observed to be affecting the susceptibility toward paratuberculosis. The objective of this study was to explore the association of various SNPs in the candidate genes and QTL region with MAP. A total of 117 SNPs from SLC11A1, IFNG, CARD15, TLR2, TLR4, CLEC7A, CD209, SP110, ANKARA2, PGLYRP1 and one QTL were selected for study. A total of 1222 cattle from various organized herds, gauhsalas and farmer herds were screened for MAP infection by Johnin intradermal skin test, AGID, serum ELISA, fecal microscopy, fecal culture and IS900 blood PCR. Based on the results of these tests, a case and control population of 200 and 183 respectively was established for study. A total of 117 SNPs from 10 candidate genes and one QTL were selected and validated/tested in our case and control population by PCR-RFLP technique. Data was analyzed using SAS 9.3 software. Statistical analysis revealed that, 107 out of 117 SNPs were not significantly associated with occurrence of MAP. Only SNP rs55617172 of TLR2, rs8193046 and rs8193060 of TLR4, rs110353594 and rs41654445 of CLEC7A, rs208814257 of CD209, rs41933863 of ANKARA2, two loci {SLC11A1(53C/G)} and {IFNG (185 G/r)} and SNP rs41945014 in QTL region was significantly associated with MAP. Six SNPs from 10 significant SNPs viz., rs110353594 and rs41654445 from CLEC7A, rs8193046 and rs8193060 from TLR4, rs109453173 from SLC11A1 rs208814257 from CD209 were validated in new case and control population. Out of these only one SNP rs8193046 of TLR4 gene was found significantly associated with occurrence of MAP in cattle. ODD ratio indicates that animals with AG genotype were more susceptible to MAP and this finding is in accordance with the earlier report. Hence it reaffirms that AG genotype can serve as a reliable genetic marker for identifying more susceptible cattle in future selection against MAP infection in cattle.

Keywords : SNP, candidate genes, paratuberculosis, cattle

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