

Molecular Characterization of Functional Domain (LRR) of TLR9 Genes in Malnad Gidda Cattle and Their Comparison to Cross Breed Cattle

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Abstract : Malnad Gidda is the indigenous recognized cattle breed of Shivamogga District of Karnataka state, India is known for its disease resistance to many of the infectious diseases. There are 25 LRR (Leucine Rich Repeats) identified in bovine (*Bos indicus*) TLR9. The amino acid sequence of LRR is deduced to nucleotide sequence in BLASTx bioinformatic online tools. LRR2 to LRR10 are involved in pathogen recognition and binding in human TLR9 which showed a higher degree of nucleotide variations with respect to disease resistance to various pathogens. Hence, primers were designed to amplify the flanking sequences of LRR2 to LRR10, to discover the nucleotide variations if any, in Malnad Gidda breed of Cattle which is associated with disease resistance. The DNA isolated from peripheral blood mononuclear cells of ten Malnad Gidda cattle. A desired and specific amplification product of 0.8 kb was obtained at an annealing temperature of 56.6°C. All the PCR products were sequenced on both sides by gene-specific primers. The sequences were compared with TLR9 sequence of cross breed cattle obtained from NCBI data bank. The sequence analysis between Malnad Gidda and crossbreed cattle revealed no nucleotide variations in the region LRR2 to LRR9 which shows the conserved in pathogen binding domain (LRR) of TLR9.

Keywords : leucine rich repeats, Malnad Gidda, cross breed, TLR9

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