

## Molecular analysis of candidate genes for mastitis in murreh buffaloes (*Bubalus bubalis*)

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Mastitis is one of the most common, complex and costly diseases of dairy animals and is influenced by a number of genes, pathogens and the environment. The molecular analysis and genetic variability of the immune mechanisms underlying mastitis resistance, including genes as lactoferrin, interleukins, toll-like receptors, caspase activating recruitment domain 15 and Fore-brain embryonic zinc finger like the study has been carried out on DNA samples obtained from 150 Murreh animals. Amplicons were obtained using specific sets of primers for all the exons of these five genes. DNA sequences of complete coding regions of each gene were subjected to Clustal W alignment, variations observed and sequences submitted to NCBI gene bank. DNA polymorphism using PCR-SSCP/RFLP with Hae III, Hinf I, Hind III, PvuII, AluI, Bsp1286 I, BsiHKAI, BsaHI, SacI, Dra I, Msp I and Taq I restriction enzymes has been explored for Lf, IL-8, TLR-4, CARD-15 and FEZL gene, which revealed a varying degree of variability exhibiting monomorphic as well as polymorphic patterns. Chi-square analysis indicated significant association of genetic variation with incidence of mastitis in the animals under study. Since buffalo is less explored specie from molecular genetics point of view, this is the first attempt in this direction, which could be an aid in selection of animals for mastitis resistance. BLAST analysis was performed to sequence homology among species and Phylogenetic tree constructed to know the phylogenetic groups.

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