

Genetic resistance to BSE based on polymorphism of prion protein gene (PRNP) in Iranian cattle populations

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Bovine spongiform encephalopathy (BSE) is a fatal infectious neurodegenerative disease in cattle, characterized by the accumulation of an abnormal, protease resistant prion protein (PrP^{Sc}) in the brain. BSE is similar to scrapie in sheep and goats and Creutzfeldt-Jakob disease in humans. Susceptibility in cattle has been shown to be under the influence of two polymorphic locations, which are a 23 bp indel polymorphism and a 12 bp indel within intron 1 of the prion protein gene (PRNP). DNA was extracted from blood samples of three Iranian cattle populations including Sistani (*Bos indicus*) (n=60), Golpayegani (*Bos indicus*) (n=62) and Iranian Holstein (*Bos taurus*) (n=50). In order to identify the putative polymorphisms of the PRNP gene of those breeds, allele, genotype and haplotype frequencies were determined. Susceptibility analysis was considered as per literature, upon which, it was suggested that the two *Bos indicus* native populations are more resistant to BSE than the Iranian Holstein (*Bos taurus*), due to higher gene frequency for insertion allele of the intron 1 of the PRNP gene polymorphism.

Keywords: bovine spongiform encephalopathy (BSE), genetic susceptibility, Iranian cattle, PRNP gene.

Association of SNPs in the IL2 gene with resistance against gastrointestinal infection in a F2 goat population

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There is considerable evidence that part of the variation in resistance to nematode infection is under genetic control. The gene IL2 encodes an interleukin which plays a role in induction of maturation of T and B cells, being important in the immune response to parasites in several species. A goat population of 229 F2 Saanen x Anglonubian will be studied aiming to find genetic markers for resistance to gastrointestinal infection. To accomplish this, SNPs in the IL2 gene will be prospected and associations with resistance to gastrointestinal infection will be tested. The phenotypes considered will be eggs per gram of feces (EPG) obtained by parasitological examination of feces samples. After data analysis, 44 extreme phenotypes for EPG will be selected and the gDNA of these animals will be isolated from leukocytes. Promising SNPs identified will be further analyzed by different statistical approaches for association with the 44 phenotypes for parasite resistance and will later be validated in the 229 available F2 goat population.

Keywords: eggs per gram, interleukin, nematodes, statistical models.