

DNA Polymorphism Studies of β -Lactoglobulin Gene in Native Saudi Goat Breeds

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Abstract : β -Lactoglobulin (β -LG) is the dominant non-casein whey protein found in bovine milk and of most ruminants. The amino acid sequence of β -LG along with its 3-dimensional structure illustrates linkage with the lipocalin superfamily. Preliminary studies in goats indicated that milk yield can be influenced by polymorphism in genes coding for whey proteins. The aim of this study is to identify and evaluate the incidence of functional polymorphisms in the exonic and intronic portions of β -LG gene in native Saudi goat breeds (Ardi, Habsi, and Harri). Blood samples were collected from 300 animals (100 for each breed) and genomic DNA was extracted using QIAamp DNA extraction Kit. A fragment of the β -LG gene from exon 7 to 3' flanking region was amplified with pairs of specific primers. Subsequent digestion with Sac II restriction endonuclease revealed two alleles (A and B) and three different banding patterns or genotypes i.e. AA, AB and BB. The statistical analysis showed that β -LG AA genotype had higher milk yield than β -LG AB and β -LG BB genotypes. Nucleotide sequencing of the selected β -LG fragments was done and submitted to GenBank NCBI (Accession No. KJ544248, KJ588275, KJ588276, KJ783455, KJ783456 and KJ874959). Two already established SNPs in exon 7 (+4601 and +4603) and one fresh SNP in the 3' UTR region were detected in the β -LG fragments with designated AA genotype. The polymorphisms in exon 7 did not produce any amino acid change. Phylogenetic analysis on the basis of nucleotide sequences of native Saudi goats indicated evolutionary similarity with the GenBank reference sequences of goat, *Bubalus bubalis* and *Bos taurus*.

Keywords : β -Lactoglobulin, Saudi goats, PCR-RFLP, functional polymorphism, nucleotide sequencing, phylogenetic analysis

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