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Genetic Variability of β -Lactoglobulin Gene in Sudanese Goat Breeds

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Abstract

Sudanese indigenous goat breeds have an important contribution to food security, livelihood, and rural economy. The improvement of the productivity of goat local breeds contributes to rural development. Therefore, the identification of the genetic variations is important for genetic improvement of economical production traits. The aim of this study was to detect the variation of the goat β -lactoglobulin (LGB) gene in four Sudanese goat breeds (Nubian, Desert, Nilotic and Taggar goats). Genomic DNA samples from 20 animals were screened for the variability in the coding and upstream region of the LGB gene. This was done by comparative sequencing to the goat reference genome at NCBI.

The sequence analysis of 5,316 bp detected 30 SNPs in comparison to the reference sequence, with an average of 5.6 SNPs per 1,000 sequenced base pairs. We found eight SNPs in the upstream gene region, two synonymous SNPs, three in the 3'-UTR, and 17 in introns. Three out of eight SNPs at the upstream gene region were novel. One of the novel SNP and additionally SNP in the promoter region reside in putative transcription factor binding sites for M6097, Elk3, Elf5, and GABPA. These SNPs could affect the gene regulation, influencing the transcriptional rate, and hence may potentially influence the milk protein content. The novel synonymous SNP in exon 2 was found only in Nubian and Desert goats. Among the 17 SNPs in introns, nine were novel. The above mentioned findings show high genetic variability among Sudanese goats in the LGB gene which could potentially affect protein yield in goat milk production. Further research is required to identify the phenotypic effects of the novel SNPs found in this study.

Keywords: Beta lactoglobulin, genetic variants, single nucleotide polymorphism, Sudanese goat breeds