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Effects of DGAT1, Leptin and Kappa Casein Gene Variants on Milk Production in Sudanese Cattle

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Abstract

The present study aimed to study the allelic and distribution pattern of candidate genes and to investigate the genetic variation of the selected polymorphisms located within diacylglycerol acyltransferase 1 (DGAT1), leptin (LEP), and kappa casein (CSN3) genes on milk production traits in Sudanese dairy breeds. The samples of milk and blood were collected from 40 Butana and 20 Kenana dairy cows. The polymorphism of DGAT1 promoter variable number tandem repeat (VNTR) was genotyped using LI-COR -DNA analyzer, while the LEP and CSN3 were genotyped using the polymerase chain restriction fragment length polymorphism. The effect of polymorphisms was analysed using SAS software.

For the DGAT1 promoter VNTR, three different alleles (3, 4, and 5) were segregated in Butana cattle, while two alleles (3 and 4) were found in Kenana cattle. Allele 3 was the most frequent with a frequency of 70.46 % and 81.25 % in Butana and Kenana breeds, respectively. The DGAT1 promoter VNTR genotypes significantly affected the fat content. The VNTR allele 3 significantly increased both fat (0.84 ± 0.22 %) and protein (0.19 ± 0.08 %) contents. A similar trend was observed in Kenana cattle, where the 33 homozygous genotypes at the VNTR locus showed higher fat and protein contents than the 34 heterozygous genotypes.

For the Mbo1-RFLP on the LEP locus, the frequencies of allele A were 97.50 % and 97.06 % in Butana and Kenana cows respectively. Both breeds showed a complete absence of homozygous BB carriers. The AB heterozygous means were higher for milk, protein and fat yields when compared with those of AA homozygous cows in Butana and Kenana dairy cattle.

In the CSN3 variant, the allele A was the major with a frequency of 86.25 % and 89.29 % for Butana and Kenana cows respectively. Results from the statistical association analysis between CSN3 genotypes and milk production parameters were not significant.

The results of the present study demonstrate that polymorphisms in the candidate genes, which show a significant association with milk production traits, may provide a high potential for marker-assisted selection (MAS) programs in dairy cattle and could be used for selection at the genomic level.

Keywords: CSN3 gene, dairy cattle, DGAT1, LEP, milk production traits, polymorphism