The relationship of DGAT1 polymorphisms and milk fatty acids production of cows bred in Iraq (Local, cross and Holstein-Friesen)

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Abstract

This study was conducted on a sample of 41 cows (6 local, 21 crosses, and 14 Holstein Friesen) raised in Iraq aged 3-4 years. The study included blood and milk samples. The sequencing technique was used to determine mutations in the DGAT1 gene to determine the effect of genotypes on the quality of fatty acids in cow's milk for all breeds. The GC-MS device was used to measure the levels of milk fatty acids. The study showed the presence of a replacement mutation, as the change was in bases 148 and 149 in the entire coding region of the DGAT1 gene. Where the two bases AA in (Allele 1) changed to GC in (Allele 2) and then to GA in (Allele 3). This mutation led to the change from lysine (K) in allele 1 to alanine and glutamine in Alleles 2 and 3, respectively. The local breed outperformed the percentage of saturated fatty acids over the cross and Holstein-Friesian. While monounsaturated and polyunsaturated, crosses and Holstein-Friesian significantly outperformed the local breed. The first allele significantly exceeded (p<0.01) the other alleles of all breeds in the percentage of saturated fatty acids. In comparison to the first allele, the second allele of cross cows displayed higher levels of monounsaturated and polyunsaturated fatty acids. Regarding unsaturated fatty acids, the third allele of the Friesian breed outperformed the other alleles. Therefore, individual patterns of the DGAT1 gene can be relied upon as markers in the selection process for milk quality purposes.

Introduction

The primary goal of studies on quantitative trait loci is to identify genetic markers related to milk production (1). The gene has been identified in cows, as the gene DGAT1 (diacylglycerol O-acyltransferase 1) consists of 14,117 PB, comprises 17 exons and 16 introns, and is located on chromosome 14 in cattle (2,3). The DGAT1 gene has been proposed as a functional candidate gene for milk production traits (4-7). Milk fat composition significantly impacts dairy products, as more unsaturated milk fat is preferred in terms of human nutrition and health (8-10). However, this may make the milk fat more susceptible to oxidation, giving the milk an off-flavor (11-13). A study conducted on Sahiwal cows showed that the quantitative trait locus (QTL) significantly impacts milk production and composition, as

the DGAT1 gene is responsible for fatty acid composition in milk (14,15). DGAT1 is a protein that catalyzes the final step in the formation of triglycerides by encoding the enzyme Acyl-CoA -diacylglycerol acyltransferase, which plays a critical role in converting diglycerol to triglycerol (16-18). Additionally, the DGAT1 gene synthesizes triglycerides deposited in the small intestine, liver, adipose tissue, and mammary gland (19). Agrawel *et al.* (20) indicated that the main cause of many genetic variations in milk production and its components, and for many breeds worldwide, is the resulting mutation in the eighth code of the DGAT1 gene. Furthermore, Banos *et al.* (21) stated that DGAT1 is responsible for 29% of milk fat proportion variations and cattle production. The production of milk and its components depends on the nutrients available in the blood, which are highly correlated with each other. In this regard, traits with