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Minireview

The role of diglyceride acyltransferase (DGAT) genes polymorphisms on milk production in dairy goats

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Abstract

Milk quantity, fat, and protein contents are important traits in dairy animals, particularly in dairy goats. However, little is known about the genetics and genomics in dairy goats that influence these traits. The diacylglycerol O-acyltransferase (DGAT) genes are considered the most important genes in dairy goats for milk quantity and fat contents. The DGAT genes have two isoforms as DGAT1 and DGAT2, that have similar reactions but no sequence homology in-between. The DGAT1 gene in chromosome 14 is a functional and potential candidate gene for fat content in goats, while DGAT2 is associated with milk yield and fat percentage in goats. The phylogenetic analyses revealed similar topologies and evolutionary partitioning of DGAT family proteins into two major clades: DGAT1 and DGAT2. Moreover, DGAT1 proteins were found to play a significant role in the milk yield in dairy goats. In this review, the role of polymorphisms in DGAT family genes on milk production in dairy goats is discussed.

Keywords: DGAT genes, Polymorphisms, Milk production, Dairy goats

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Introduction

Diacylglycerol O-acyltransferase or diglyceride acyltransferase (DGAT) genes are involved in the formation of triglycerides from diacylglycerol and Acyl-CoA. These genes have two isoforms, such as DGAT1 and DGAT2, with no sequence homology to each other. DGAT1 is essential for triglyceride synthesis and intestinal absorption, while DGAT2 is important for adipose tissue formation. DGAT1 is located in the absorptive enterocyte cells that are reconstituting triglycerides with cholesterol and proteins. However, DGAT2 is present in fat, liver, and skin cells.

The DGAT1 gene was discovered to encode a specific DGAT protein with enzyme activities (Liu et al., 2020). Later, the DGAT2 gene was discovered and found to be producing DGAT-like enzyme activity. This gene is associated with lipid synthesis and storage in eukaryotes and is known as the candidate gene for quantitative traits. A study explained that the DGAT1 gene is a candidate gene for milk traits in dairy animals such as buffaloes, cattle, and goats (Winter et al., 2002; Nayeri et al., 2016). Previous studies demonstrated a potential effect of the DGAT2 on goat milk quantity and fat percentage due to some novel variations in the goat's genome (Martin et al., 2017). The milk production traits are polygenic; thus, we cannot assume that one or two genes only influence milk production. This review focuses on these genetic variations/polymorphisms of DGAT family genes and their effect on dairy goat's milk traits.

Variations of DGAT1 and their effects on milk production

The DGAT1 gene is essential to control triacylglycerol biosynthesis to produce animals' lipid contents. The DGAT1 gene has a particular mutation, K232A, associated with milk yield and fat percentage in dairy animals (Grisart et al., 2004; Näslund et al., 2008). The mutation GCT (Ala) in exon 17 of the DGAT1 gene was found to have a particular role in the milk traits in dairy goats (Yang et al., 2011). Another study showed that the mutation 273T*C found in intron 16 in Saanen, Maltase, Damascus, Halep, and Kilis goats could have an important role in the dairy goats (Ozmen and Kul, 2014). Similarly, the variations T6852 in exon 7 and C408 in intron 14 of DGAT1 were found in Saanen and Guanzhong goats (An et al., 2011). These studies

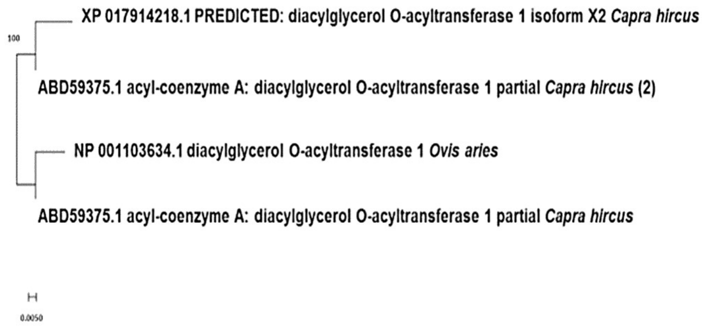

Figure 1: Genomic evolutionary relationships of taxa of diacylglycerol O-acyltransferase (DGAT) genes in goat (*Capra hircus*). The phylogenetic tree was generated using the Neighbor-Joining method. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches

showed that particular variations in the DGAT1 gene could explain variations in traits that could help to select dairy goats.

Variations of DGAT2 and their effects on milk production

Recently, some studies have been done on the DGAT2 gene in animals. Interestingly, few studies have shown that the variations in the DGAT2 gene were linked to economic traits such as milk and meat quality, carcass, and fat percentage in feedlot animals (Li et al., 2009). Additionally, the carcass weight and shear forces have been studied in pigeons using these gene variations (Mao et al., 2018). Al-Shuhaib et al. (2017), found that cattle's body weight and length are associated with specific variations of the DGAT2 gene. An and co-workers found that particular variations in the DGAT gene are strongly associated with milk quantity and fat contents in goats (An et al., 2011).

Genomics of dairy goats

Most genomics scientists believed that single nucleotide polymorphism (SNPs) and genome-wide association studies (GWAS) have a great potential for trait evaluation in dairy animals, particularly dairy goats (Visscher et al., 2012). It is essential to know that the 52K goat SNPs chip has been developed to evaluate dairy goats' production traits. This chip is combined with genotypic and phenotypic data such as milk quantity and udder conformation traits in chromosome 19 and other chromosomes (Mucha et al., 2018), confirming these traits polygenic nature in eukaryotes. In a recent study, the DGAT1 gene on chromosome 14 has been identified as a functional candidate gene that affects fat content by using the GWAS technique. Interestingly, 29 polymorphisms have been found, along with two novel mutations, such as R251L and R396W. These mutations are associated with a decreased fat percentage and an increase in milk yield.

Genomic selection for milk production in dairy goats

Genomic selection is an approach that uses molecular genetic markers to design novel future breeding plans and to develop molecular models based on new markers for genetic evaluation. In animal breeding, genomic selection can improve the genetic gain from complex traits per unit of time and cost. Additionally, it provides genomic breeding values that are precise than estimated breeding values (Ding et al., 2013). For instance, Saanen and Alpine bucks were genotyped using caprine SNP chip with the next-generation sequencing for the first time using genomic best linear unbiased prediction (GBLUP). Additionally, their genomic breeding values were improved from 22% to 37% for both breeds after final evaluations (Carillier et al., 2014). In another study, GWAS and the genomic selection method were used to measure breeding values in dairy goats (Desire et al., 2016). The feeding efficiency and body weight were evaluated to improve goat genetics toward increasing the milk yield. Additionally, the single-step genomic best linear unbiased prediction (ss-GBLUP) methodology has 1.06% more reliability than the classical best linear unbiased prediction (BLUP) for calculation of correlation between estimated breeding values and genomic estimated breeding values. These data were produced with the next-generation sequencing and SNPs chips (Molina et al., 2018).

Evolutionary relationship of DGAT genes in goat and other organisms

The genomic evolutionary history of DGAT genes and proteins were inferred with the Neighbor-Joining method in the first stem. This analysis involved four amino acid sequences with 80 positions in the final dataset in MEGA X with a bootstrap test (1000 replicates). The evolutionary distances were computed using the p-distance method and are in the units of a number of amino acid differences per site (Figure 1). Accordingly, 50 amino acid sequences containing DGAT proteins from different organisms and all protein isoforms identified in goats were aligned to generate relationships using the same genomic evolutionary analysis used in DGAT genes (Figure 2). Assessment of the evolutionary relationship of DGAT proteins was conducted in goat and other organisms, including a comprehensive phylogenetic analysis of animals (*Bubalus bubalis*, *Bos taurus*, *Homo sapiens*,

Figure 2: Evolutionary relationships of taxa of DGAT proteins (DGAT1 and DGAT2) in goats (*Capra hircus*) in relation to other animals

Mus musculus, *Rattus norvegicus*, *Capra hircus*, *Ovis aries*, *Equus caballus*, *Chlorocebus aethiops*, *Danio rerio*, *Xenopus laevis*, and *Xenopus tropicalis*). Results revealed DGAT family proteins clustering into two major clades: DGAT1 and DGAT2 in all animals. The DGAT1 protein sequence in goats, sheep and cattle is conserved (Figure 2), and no difference between the DGAT proteins in goat and sheep (Martin et al., 2017).

Conclusions

It has been concluded that milk contents and yields are controlled by polymorphisms of the polygenic DGAT family in dairy goats. The phylogenetic analyses revealed similar topologies and evolutionary partitioning of DGAT family proteins into two major clades: DGAT1 and DGAT2. Moreover, DGAT1 protein's relationship with other animals (buffalo, cattle, goat, sheep, horse, mouse, rat, and monkey) and humans suggested that the DGAT family genes have similar functions. The advancements in understanding the genomics of DGAT genes will help to improve the management and future breeding systems of dairy goats.

Article Information

Conflict of Interest.The author declares no conflict of interest.

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