



Polymorphism of SCD1 and DGAT1 gene in Isfahan Holstein cows

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ABSTRACT

In this study we estimated the allele and genotype frequencies of SCD1 and DGAT1 gene polymorphism. The analysis was conducted on 408 Holstein cows from five dairy herds in Isfahan province. Genotypes were identified using PCR-RFLP technique. Two genetic variants (A and V) of the SCD1 gene were observed in this experiment. The frequency of A-allele ranged from 0.49 to 0.66, while frequency of V-allele 0.34 to 0.51. Regards with DGAT1 gene, also two genetic variants (A and K) were determined that frequency of A-allele ranged from 0.54 to 0.68 and K-allele 0.32 to 0.46. It was found that these two genes were polymorphic in Isfahan Holstein cows, which suggested that could be associated with composition and production traits.

Key words: Holstein cow, SCD1 gene, DGAT1 gene, polymorphism, milk traits

INTRODUCTION

Gene mapping research has led to the discovery of many polymorphic sites throughout the dairy cattle genome that can serve as genetic markers for selection in breeding schemes. Among many different candidates, diacylglycerol acyltransferase 1 (DGAT1) and stearoyl-CoA desaturase 1 (SCD1) gene, seems to be directly associated with production traits [12 and 15]. In dairy cows, DGAT1 gene is considered to be a very strong positional candidate gene for fat percent of milk. This gene is located on the centromeric end of the bovine chromosome 14 (BTA14), harboring the QTL with a large impact on milk production traits [3, 9 and 21]. DGAT1 encodes an integral microsomal membrane enzyme that catalyses the final step in triglyceride synthesis [14]. Milk fat contains approximately 98 percent triglycerides, so this is a key enzyme for milk triacylglycerol synthesis in the mammary gland [16]. Kaupe *et al.* [2004] studied polymorphism of this gene in *Bos taurus* and *Bos indicus* breeds. They claimed that K allele of DGAT1 gene is a wild type and the A allele substitution probably occurred after the divergence of *Bos taurus* and *Bos indicus* [10]. Recently, many studies showed a significant association between polymorphism of this gene and milk production traits [8, 12 and 20]. The SCD1 locus has been mapped on BTA 26 [2]. This gene encodes a key enzyme introducing a double bond between carbons Δ^9 and Δ^{10} in a large spectrum of medium and long-chain fatty acids. SCD1 plays a role in the endogenous synthesis of the conjugated

linoleic acid (CLA) in ruminants. Also it was suggested that this protein plays an important roles in the regulation of fatty acid oxidation [4 and 6]. This gene is present in several tissues such as: adipose tissue and liver. And its expression is controlled by insulin, liver X receptor (LXR), sterol regulatory element binding protein (SREBP-1c), PPARs and leptin [18]. Additionally, there is a suggestion that the SCD1 protein involved in some aspects of energy homeostasis like: lipogenesis, lipid oxidation, and thermogenesis [4 and 6]. Based on these considerations, the aim of the present study was to estimate the allelic and genotypic frequencies of all two these genes polymorphism in Isfahan Holstein dairy cows.

MATERIAL AND METHODS

In this experiment, blood samples were collected from 408 Holstein dairy cows that randomly selected among 10000 cows from five dairy herds in Isfahan province. DNA was extracted from whole blood samples using standard salting out protocol [17], and these two genes were amplified with the standard polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) technique. The PCR amplification was performed in a 20- μ L reaction volume, which included 25-50 ng genomic DNA, 2 μ L 10x PCR buffer, 10 pmol of each primer of two genes (Table 1), 1.5 mM MgCl₂, 200 μ M dNTP, 1 unit of taq DNA polymerase and sterilized distilled water to make a final volume of 20 μ L. Thermal cycling conditions were as follows: 94°C for 5 min; 30 cycles of 94°C for 30 s, annealing temperature (Table 1) for 30 s, and 72°C for 30 s, followed by a final step of 72°C for 5 min. Seven microliters PCR products was digested with five units of respective (Table 1) restriction enzymes (Fermentas Co.) in 20 μ L of reaction volume at 37°C for 6 hours. The digested products plus 2 μ L loading dye were run on 2% ethidium bromide-stained agarose gel for 3 h, and genotype bands were visualized under UV light.

RESULT AND DISCUSSION

Looking for candidate genetic markers of potential value in Marker Assisted Selection (MAS) in dairy cows is lately very popular. The PCR-RFLP method was useful for DGAT1 and SCD1 genotype marking and could be useful for selection in dairy cattle. In the population studied, the allelic and genotypic frequency of all two genes DGAT1 and SCD1 are given in table 2. Two genetic variant (A and K) of the DGAT1 polymorphism were observed in this experiment. The A and K alleles of this gene were identified based on amplification of a 411 bp fragment, followed by digestion with the restriction enzyme *Cfr1*. Genotype AA was determined by the present of a single 200-bp fragment, while genotype KK was characterized by a single 400-bp fragment. Also KA individuals present two fragments of 203 and 208 bp. The KA and KK genotypes were the most and least frequent in all herds, respectively (Table 2). The following DNA restriction fragments were obtained for SCD1 gene using *Nco1* enzyme. The fragments were 400 (no digestion) for the VV genotype, 200 and 400 bp for the AV and 200 bp for the AA genotype. Study on SCD1 gene shown that frequencies for A and V alleles were 0.58 and 0.42 respectively (Table 2). The AV genotype showed the highest frequency (0.65), whereas the VV had the least frequent genotype (0.09).

Table 1. Selected PCR-RFLP conditions for the analyzed polymorphisms

| gene | Primers (5'-3') | Annealing temp (°C) | PCR product size (bp) | Restriction endonuclease |
|-------|---|---------------------|-----------------------|--------------------------|
| SCD1 | F- CCC ATT CGC TCT TGT TCT GT R- CGT GGT CTT GCT GTC GAC | 59 | 400 | NcoI |
| DGAT1 | F-GCACCATCCTCTTCCTCAAG R- GGAAGCGCTTTCGGATG | 60 | 411 | CfrI |

Table 2. Genotypic and allelic Frequency of SCD1 and DGAT1 gene in Holstein dairy cows

| Gene | SCD1 | | | | | | DGAT1 | | | | | |
|-------------------|------|--------------|--------------|--------------|------|---------|--------------|--------------|--------------|------|---------|---|
| | Herd | N | Genotypes | | | Alleles | | Genotypes | | | Alleles | |
| | | | AA | AV | VV | A | V | AA | KA | KK | A | K |
| 1 | 83 | 0.28 (23) | 0.42 (35) | 0.30 (25) | 0.49 | 0.51 | 0.40 (34) | 0.50 (41) | 0.10 (8) | 0.66 | 0.34 | |
| 2 | 65 | 0.15 (10) | 0.80 (52) | 0.05 (3) | 0.56 | 0.44 | 0.37 (24) | 0.55 (36) | 0.08 (5) | 0.64 | 0.36 | |
| 3 | 85 | 0.24 (21) | 0.73 (62) | 0.03 (2) | 0.61 | 0.39 | 0.47 (40) | 0.41 (35) | 0.12 (10) | 0.68 | 0.32 | |
| 4 | 79 | 0.35 (28) | 0.62 (49) | 0.03 (2) | 0.66 | 0.34 | 0.35 (28) | 0.61 (48) | 0.04 (3) | 0.65 | 0.35 | |
| 5 | 96 | 0.25 (24) | 0.35 (67) | 0.06 (5) | 0.60 | 0.40 | 0.21 (20) | 0.68 (65) | 0.11 (11) | 0.54 | 0.46 | |
| Total/ Average | 408 | 0.26 | 0.65 | 0.09 | 0.58 | 0.42 | 0.36 | 0.55 | 0.09 | 0.63 | 0.37 | |

There have been many studies of the allelic frequency of DGAT1 gene and influence of this gene polymorphism on milk production traits, especially on milk fat yield in different cattle breeds including: Jersey, Fleckvieh, Normande, and Angeln breed [7, 22, 23 and 24]. For example, the investigations functional polymorphism of the DGAT1 gene on milk composition have been reported in dairy cattle by Grisart *et al.* [2002] and Ripoli *et al.* [2006]. They showed significant effect of DGAT1 genotypes on determination of milk composition [8 and 20]. An association between the DGAT1 gene polymorphism and production traits in Holstein-Friesian and Jersey cattle has been investigated by Komisark *et al.* [2004], who claimed that homozygous KK animals produced milk with higher fat content and yielded more fat than other genotypes [13]. Recently, investigation of the same polymorphism in Iranian Holstein cattle reported by Kharrati Koopaei *et al.* [2012], they provided contrary results as the genotype KA animals showed the more milk fat than other groups [12]. Several studies have reported QTL located on BTA26 affecting milk, fat, and protein yields in Holstein dairy cows [1, 5 and 19]. It has been showed that some genes involved in lipid metabolism such as: SCD, LPF (gastric lipase), or GPAM (glycerol-3-phosphate acyltransferase mitochondrial), located on this chromosome. Some studies were performed about SCD1 gene polymorphism and its correlation with production traits in cattle. In Italian Holsteins, an association between SCD gene polymorphism and milk production traits (milk, fat, and protein yields, fat and protein contents) has been reported on a sample of 701 lactations of 313 cows. Macciotta *et al.* [2008] showed an effect of the SCD genotype on milk and protein yields. Who claimed that animals with VV genotypes producing more milk (about 2 kg/d) and protein (ar 0.07 kg/d) compared with AA cows [15].

These results suggest a possible use of these candidate markers in gene-assisted selection programs for improvement of milk production traits in dairy cattle, although large-scale studies in different breeds are required.

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