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Genetic Polymorphisms of *Cyp19* and *Myostatin* Genes in Turkish Indigenous Sheep Breeds

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ABSTRACT. Growth and meat production traits are very important in sheep breeding. *Cyp19* gene has a major role in reproductive activity and growth due to its function in estrogen synthesis. Another gene affecting growth traits is *Myostatin (MSTN)* gene, which mainly regulates skeletal muscle growth. In this study allele frequencies of genetic polymorphism in *Cyp19* and *Myostatin* genes were identified by PCR-RFLP method in five indigenous Turkish sheep breeds, Chiose, Imroz, Kivircik, Zom and Morkaraman. Digestion of *Cyp19* gene with *HaeIII* only revealed uncut AA genotype and digestion of *MSTN* with *DraI* also revealed only uncut AA genotype. Both loci analyzed in this study were found to be monomorphic in five Turkish indigenous sheep breeds. These highly conserved parts of the two genes can be useful for molecular evolutionary studies in sheep. Further studies regarding association analysis of *Cyp19* and *MSTN* in sheep should be conducted.

Key words: *Cyp19*, myostatin, sheep, SNP, PCR-RFLP

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INTRODUCTION

Sheep is one of the most important livestock animals bred in Turkey. Turkey has 31 million sheep and 10% of total meat production in the country consists of sheep meat (www.tuik.gov.tr). There are several indigenous sheep breeds in Turkey, which are bred for different production traits like meat, milk and wool (Yalcin, 1986).

Growth and meat production traits are significant economic traits in sheep. In the past years many single nucleotide polymorphisms (SNPs) and in/del polymorphisms in livestock have been identified by genome-wide association studies in order to facilitate the potential utilization of genes involved in growth and meat production traits. But the number of quantitative trait loci (QTL) identified in sheep still remains limited (Zhang et al., 2013).

Oestrogen is an important endocrine, paracrine and autocrine acting hormone, which has a major role in the regulation of reproduction system. It is also involved in fat deposition and growth (Heine et al., 2000; Jones et al., 2000, Simpson et al., 2000). The aromatase cytochrome P450 enzyme encoded by the *Cyp19* gene, is responsible for estrogen biosynthesis by conversion or aromatization of androgens into estrogens (Simpson et al., 1994).

In sheep, the *Cyp19* gene that encodes the aromatase enzyme is located in chromosome 7 (Payen et al., 1995). It is transcribed by four different promoter regions that have organ-specific activities. The P2 promoter region is mostly active in granulosa cells, P1.5 and P1.1 in the placenta and P1.4 is active in the brain (Vanselow et al., 1999; Vanselow et al., 2001).

Myostatin (growth and differentiation factor - GDF8) is the major regulator of myogenesis in mammals. It is a member of the transforming growth factor- β superfamily and acts as a negative regulator of muscle growth. It directly affects muscular hypertrophy and carcass conformation (Nakev et al., 2013; Zhang et al., 2013). It has been reported, that mutations in *MSTN* gene located on OAR2, which encodes myostatin, are associated with increased skeletal muscle mass in sheep (Kijas et al. 2007). The *MSTN* gene has 3 exons and 2 introns (Bellinge et al., 2005) and encodes a glycoprotein which is widely expressed in skeletal muscle. The differentiations

in this protein may be responsible for changing the composition of muscle fibers and causing a variation of muscle weight (Chen, 2008). Increased levels of muscle myostatin protein may also have a role in mediating effects of estrogen on growth in skeletal muscle (Jung et al., 2007).

The aim of the present study is to determine allele frequencies of genetic polymorphisms for *Cyp19* and *MSTN* genes in indigenous Turkish sheep breeds, namely Chios, İmroz, Kivircik, Zom and Morkaraman.

MATERIALS AND METHODS

Animals and DNA isolation

In this study unrelated animals from Chiose (n=35), İmroz (n=35), Kivircik (n=38), Zom (n=35) and Morkaraman (n=33) sheep breeds were investigated. Blood samples were collected into 2 ml sterilized tubes with EDTA from *V. jugularis*. Genomic DNA was isolated by standard salt-out method (Miller et al., 1998).

The study had an approval from the Ethical Committee of Istanbul University, Faculty of Veterinary Medicine with number 30/04/2008- 39.

PCR-RFLP analysis

PCR was performed in a reaction volume of 25 μ l using 1 U Taq DNA polymerase (Fermantas Life Sciences, Canada), 2-2.5 μ l 10X PCR buffer, 1.5mM MgCl₂, 50-100 ng genomic DNA, 100 μ M dNTP (Takara, Biotechnology Co, Ltd, Japan) and 10 pmol of each primer. Amplification was carried out with an initial denaturation at 94 °C for 5 min; 35 cycles of 94 °C for 1min, primer specific annealing temperature for 1 min, 72 °C for 1 min; and a final extension at 72 °C for 10 min. Primer sequences used to amplify intron 9 of *Cyp19* gene and 5'UTR of *MSTN* gene, their annealing temperatures (T_m) and product sizes were given in Table 1.

For RFLP analysis 10 μ l of the PCR products were digested with 10 units of *Hae*III and *Dra*I restriction enzymes at 37°C overnight in order to genotype *Cyp19* and *MSTN* polymorphisms, respectively. The digested DNA fragments were separated by electrophoresis in 2% agarose gel including ethidium bromide and visualized under UV light.

Table 1. Primer sequences, annealing temperatures and PCR products' sizes

Gene symbol	Primer sequence	T _m (°C)	Product size (bp)
Cyp19	F: 5' - CCA AAG CCT AAT GAA TTT ACT C - 3'	56	266
	R: 5' - CTC TCG TGT GCC CTC CAT GAA G - 3'		
MSTN	F: 5' - TGC CGT TAC TCA AAA GCA AA - 3'	54	497
	R: 5' - AAC AGC AGT CAG CAG AGT CG - 3'		

Statistical analysis

Direct counting was used to estimate genotype and allele frequencies of the genetic variants for all loci. Genetic relationships regarding *Cyp19* gene among populations analyzed in this study and seven sheep breeds from Europe (Zsolnai et al., 2002) were visualized in a dendrogram constructed by unweighted paired group cluster analysis (UPGMA), from a modified NEIGHBOR procedure implemented in PHYLIP version 3.5 software also using PopGene32 (Yeh et al., 2000). The UPGMA dendrogram of population was constructed based on Nei's genetic distance (Nei, 1972). No further analysis was carried out, since the two loci analyzed in five sheep breeds were found to be monomorphic.

RESULTS

The SNP in intron 9 of *Cyp19* gene could be assayed by RFLP analysis with *Hae*III restriction enzyme. Digestion of the 266 bp PCR product reveals allele G (266 bp undigested fragment) and allele C (190 and 76 bp fragments). All of the breeds analyzed in this study were found to be monomorphic for this locus (Table 2). Only GG genotype was observed (Figure 1).

The digestion of 5'UTR of *MSTN* gene by *Dra*I restriction enzyme results in two alleles, A (497 bp undigested fragment) and B (427 and 70 bp fragments). In this study only AA genotype was observed (Figure 1). The indigenous Turkish sheep breeds were found to be monomorphic for this locus (Table 2).

The phylogenetic tree based on G/C SNP in ovine *Cyp19* gene presented two clusters among the sheep breeds analysed in this study and different European

breeds (Figure 2). All the Turkish sheep breeds were clustered in the same branch with the Racka breed from Hungary.

DISCUSSION

Due to its function in reproductive activity and growth, many studies have been conducted on ovine *Cyp19* gene in different sheep breeds (Vanselow et al., 1999; Lobo et al., 2009; Tanamati et al., 2013).

The G/C transversion in intron 9 of ovine *Cyp19* gene was firstly identified in Spanish breeds Carranzana, Latxa Black Face and Latxa White Face, the Merino and British Milk Sheep breeds and indigenous Hungarian breeds, Cikta, Racka and

Figure 1. PCR-RFLP fragments of two SNPs. M: 100 bp marker, Lane 1, 2 and 3: Cyp19/*Hae*III GG genotype (266 bp), Lane 4, 5 and 6: MSTN/*Dra*I AA genotype (497 bp)

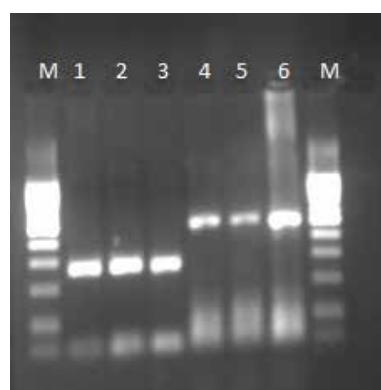
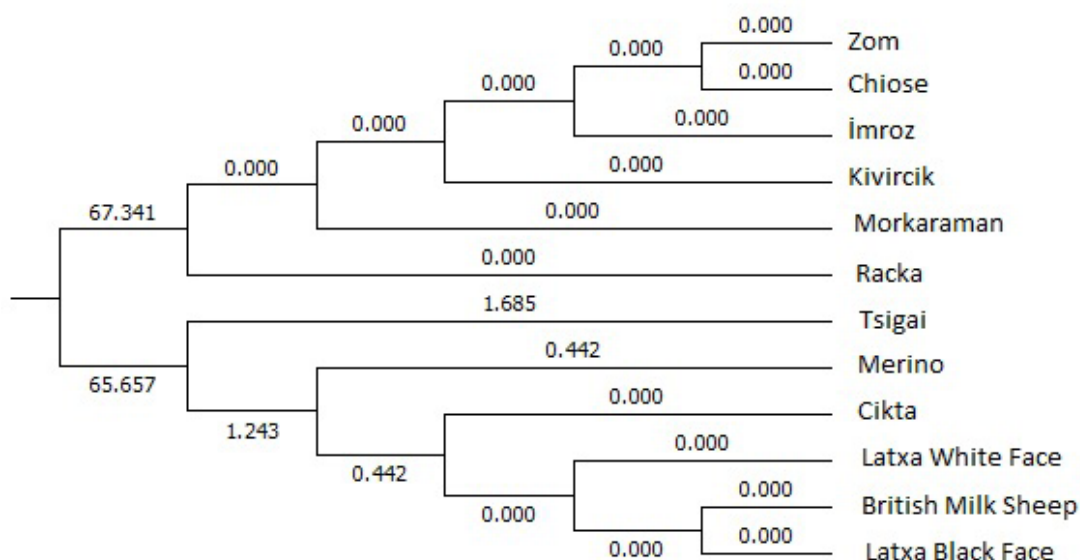


Figure 2. Genetic distance between Turkish and European sheep breeds according to *Cyp19*/HaeIII polymorphism. Dendrogram based on Nei's genetic distance.



Tsigai. Allele C were observed more frequently in all the breeds with frequencies ranged between 0.650 and 0.988 (Zsolnai et al., 2002). In the present study the five indigenous Turkish sheep breeds, Chiose, İmroz, Kivircik, Zom and Morkaraman were found to be GG homozygous. Based on the analysis of this genetic locus the breeds from Turkey seem to be genetically apart from the breeds originated from Europe. The phylogenetic tree (Figure 2) obtained from the *Cyp19* G/C polymorphism analysis of the five Turkish sheep breeds analyzed in the present study and seven European breeds mentioned above, presented two clusters. The Turkish breeds clustered with Racka breed from Hungary and the rest European breeds were grouped in the second cluster.

Absence of allele C in indigenous Turkish breeds may be due to a mutation exists in sheep from warmer regions. The geographic origin of the animals is an important factor regarding the sheep reproductive activity, as it determines the photoperiods (Sa and Sa, 2006), which affects melatonin synthesis. Melatonin

is an indoleamine derived from the serotonin secreted during darkness that acts as a natural inhibitor of the aromatases (Hafez and Hafez, 2003). The climatic and seasonal conditions of Turkey differ from the ones in Europe. Especially, three breeds in this study Kivircik, Zom and Morkaraman are raised mainly in central and south-eastern parts of Turkey, where the climate is semi-arid (Bilgili et al., 2013). We may suggest a relationship between *Cyp19* G/C polymorphism and the geographical origin of sheep breeds.

Another gene, which is largely investigated in different sheep breeds is *MSTN*, which is associated with meat-related traits, especially muscle growth (Nakev et al., 2013).

A deletion of a small DNA fragment (TTTTA) in the 5'UTR of myostatin gene was identified in several goat breeds (Xianglong et al., 2008; Singh et al., 2014). Xianglong et al. (2008) suggested a relationship of this deletion with body weight and size in goats and that the heterozygote populations present

better growth traits than homozygotes. In a study on Indian goat breeds researchers observed that the allele A which presents TTTA deletion, is almost fixed with a frequency of 0.98 (Singh et al., 2014). The results of the study on Egyptian sheep breeds showed that this deletion is not unique for goats. The researchers could only observe AB genotype. Allele A had frequencies ranged between 0.07 and 0.23 in three Indian sheep breeds (Shafey et al., 2014). In the present study, five indigenous Turkish sheep breeds were found to be monomorphic for this deletion. All individuals analyzed had AA genotype. No association analysis of this deletion has been performed in sheep breeds until now. Regarding to its effects in goats, we may suggest that the Turkish breeds analyzed in the present study may have a disadvantage in terms of growth traits.

In addition, Khani et al. (2014) reported a significant association of TTTTA deletion in 5'UTR of *MSTN* gene with twinning in goats. Although Chiose sheep breed has a higher twinning rate compared to the other indigenous breeds in this study, our

results did not present any difference among the five sheep breeds. Association analysis of this in/del polymorphism in sheep may provide results different than these found in goats.

CONCLUSION

Both loci analysed in this study were found to be monomorphic in five Turkish indigenous sheep breeds. *Cyp19* and *MSTN* genes have highly conserved parts, which can be helpful for molecular evolutionary studies in sheep. Further analysis which will analyze the association between these polymorphisms and production traits in sheep should be conducted.

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