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Allelic Frequencies of a *Sac*II RFLP at Exon 7 of the β -lactoglobulin Gene in Turkish Hair Goat Breed

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Abstract: Polymorphism in the exon 7 to the 3' flanking region of β -lactoglobulin (β -lg) gene in Turkish hair goat populations were investigated. The study was carried out including 233 hair goats using PCR-RFLP. Digestion of amplification product with *Sac*II restriction enzyme revealed two alleles namely S_1 and S_2 (which was produced by a single nucleotide substitution) and three genotypes (S_1S_1 , S_1S_2 and S_2S_2) in the studied population. The genotypic frequencies of S_1S_1 and S_1S_2 were almost equal. S_2S_2 genotype was found to be lower than other genotypes (S_1S_1 and S_1S_2) in the studied population. The allele frequencies of S_1 and S_2 at β -lg locus were 0.67 and 0.33 in hair goat population, respectively. Deviation from Hardy-Weinberg equilibrium was not detected.

Key words: β -lactoglobulin, goat, polymorphism, PCR-RFLP

INTRODUCTION

The first report of genetic polymorphism of bovine β -lactoglobulin (β -lg) was reported by Aschaffenburg and Drewry (1955). Since, then genetic polymorphism of milk proteins has been of considerable interest in animal breeding and in the dairy industry and possible relationships between milk protein polymorphism and production traits, milk composition and quality have been widely studied by Pagnacco and Caroli (1987), Ng-Kwai-Hang *et al.* (1990) and Baranyi *et al.* (1993). β -lg is a major whey protein in the milk of ruminants. It is also found in the milk of most mammals with exception of man, rodents and lagomorphs (Perez and Calvo, 1995). Until now, several variants of bovine and ovine β -lg have been described both at protein level and DNA level (Gaye *et al.*, 1986; Erhardt, 1989; Elmaci *et al.*, 2006). The two genetic variants (A and B) of β -lg were reported in goat milk (Moioli *et al.*, 1998) at protein level. However, no variants resulting in amino acid substitution have been identified at DNA level in goat but Pena *et al.* (2000) and Yahyaoui *et al.* (2000) have described polymorphism in exon 7 and in the β -lg proximal promoter region of Spanish and French goats. β -lg gene polymorphism at the DNA level has been analyzed by PCR-RFLP (Pena *et al.*, 2000) and they also reported two novel genetic variants of the β -lg gene in goat breeds. β -lg polymorphism was reported in different goat populations at protein level in Turkey (Ozdil and Asal, 2002; Turkyilmaz, 2003; Gurcan, 2005) and two alleles, β -lg^A and β -lg^B, at β -lg locus in the studied goat populations were reported. However, no information has been reported in Turkish goats regarding β -lg polymorphism at the DNA level. Therefore, the aim of present research was to study the genetic polymorphism of the β -lg gene (exon 7) at DNA level in Turkish hair goat using PCR-RFLP method.

MATERIALS AND METHODS

Animal Resources and DNA Isolation

Hair goats are raised in all parts of Turkey, particularly in mountainous and bushy areas of Mediterranean. Hair goat is also called ordinary goat or black goat. It is major goat breed of Turkey.

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Blood samples were collected randomly from a total of 233 hair goats belonging to four different flocks around Bursa region in their natural habitats. An effort was made to collect samples from unrelated individuals based on information provided by farmers. Genomic DNA was isolated using Genomic DNA isolation kit following the manufacturer's protocol. The quality of DNA was checked on 0.8% agarose gels and concentrations were measured by UV-spectrophotometer.

Amplification of β -Ig Gene and Restriction Enzyme Digestion

PCR amplifications of the β -Ig gene were performed in a 25 μ L reaction volume containing 50-100 ng genomic DNA, 2X PCR Master Mix and 0.5 μ M each of the primers, Forward 5'-CGGGAGCCTTGGCCCTCTGG-3' and reverse 5'-CCTTTGTCGAGTTTGGGTGT -3', (Pena *et al.*, 2000). The amplification reactions were performed in an Techgene Thermal Cycler (Techne, Cambridge, UK) programmed for an initial denaturation at 95°C for 5 min, followed by 35 cycles each with denaturing at 95°C for 30 sec, annealing at 65°C for 1 min, extension at 72°C for 90 sec and a final extension at 72°C for 5 min. The products were visualized by staining with ethidium bromide after electrophoresis of 10 μ L reaction mixture on a 2 % agarose gel.

PCR products (12 μ L) were digested with 10 U of the *Sac*II (Fermentas) restriction enzyme in a 20 μ L total reaction volume overnight at 37°C. The restriction fragments were directly analyzed by electrophoresis in 3% agarose gels in 1X TAE buffer stained with ethidium bromide and visualized under UV light.

Statistical Analysis

Direct counting was used to estimate genotypic and allelic frequencies of β -Ig genetic variants. The chi-square test (χ^2) was used to check whether the populations were in Hardy-Weinberg equilibrium. All calculations and the χ^2 analysis were carried out using PopGene32 software (Yeh *et al.*, 2000).

RESULTS AND DISCUSSIONS

β -Ig polymorphism was reported in different goat populations at protein level in Turkey. Ozdil and Asal (2002), Turkyilmaz (2003) and Gurcan (2005) described two allele, β -Ig^A and β -Ig^B, at β -Ig locus in different goat breed populations in Turkey. In Turkish hair goat population, β -Ig^B allele were found to be predominant at protein level (Ozdil and Asal, 2002; Gurcan, 2005). However, no information has been reported in Turkish goats regarding β -Ig polymorphism at the DNA level.

The exon 7 to the 3' flanking region of β -Ig gene of Turkish hair goat were investigated. A fragment of 426 bp from exon 7 to the 3' flanking region was successfully amplified by PCR and digested with *Sac*II restriction enzymes to detect the presence of S₁ or S₂ variants. Digestion with *Sac*II restriction enzyme reveals the polymorphic sites, which were produced by a single nucleotide substitution in position of +4601. Allele discrimination was based on size differentiation of digested fragments. Restriction digestion of 426 bp PCR products with *Sac*II enzymes revealed three genotypes (Fig. 1) of S₁S₁ (349 and 77 bp), S₁S₂ (426, 349 and 77 bp) and S₂S₂ (426 bp). Screening for allele frequency at β -Ig locus at DNA level in goat population revealed the presence of two alleles, namely S₁ and S₂.

Table 1 shows the allelic and genotypic frequencies in investigated goat population. The genotypic frequencies of S₁S₁ and S₁S₂ were almost equal. S₂S₂ genotype was found to be lower than other genotypes (S₁S₁ and S₁S₂) in the studied population. The frequency of S₂ allele at β -Ig locus was found to be lower than that of S₁ allele. It means that, the frequency of S₁ allele was clearly predominant. The chi-square test results are shown in Table 1 and revealed that population was in Hardy-Weinberg equilibrium.

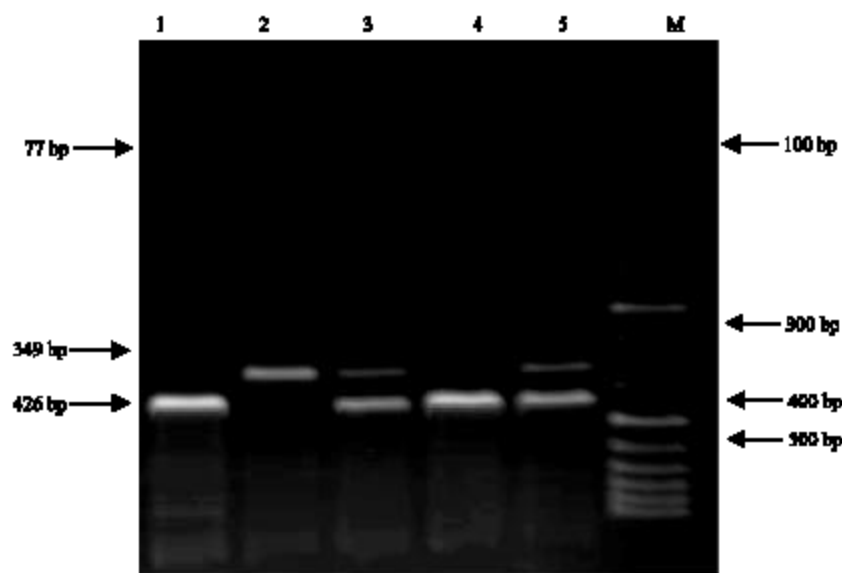


Fig. 1: Electrophoresis of exon 7 of goat β -lg gene amplified by PCR of animal with S_1S_1 , S_1S_2 and S_2S_2 variants and digested with *Sac*II. The 426 bp band was restricted into two bands 349 and 77 bp in the S_1 polymorphism (Lane 1 and 4: S_1S_1 ; Lane 2: S_1S_2 ; Lane 3 and 5: S_2S_2 ; M: marker)

Table 1: Gene and genotypic frequencies of β -lg locus in the studied Turkish hair goat population

N	Gene frequency		Genotypic frequency			Chi-square test
	S_1	S_2	S_1S_1	S_1S_2	S_2S_2	
233	0.67	0.33	0.45	0.44	0.11	0.155 ^{ns}

^{ns}: Non significant

Polymorphism studies conducted in some Indian breeds (Kumar *et al.*, 2006) showed higher frequencies of S_2 allele than the present study. Kumar *et al.* (2000) showed that the frequency of S_2S_2 genotype was more frequent than other genotypes (percentage of S_2S_2 genotype varied from 41.7% to 100%) and S_2 allele frequency was found to be the higher than S_1 allele frequency. The frequencies of S_1 and S_2 allele in this study found to be similar to French and Spanish goat breeds studied previously by Pena *et al.* (2000). Consistent with the result of this study, an S_1 allele frequency in French and Spanish goat breeds was higher than S_2 allele frequency. On the other hand, some polymorphic sites were reported different region of goat β -lg gene. Graziano *et al.* (2003) and Ballester *et al.* (2005) described different polymorphism in proximal promoter region and in exons 1, 2, 3 and 6 of the goat β -lg gene in different goat breeds.

CONCLUSION

In the present study, we demonstrated that there was a genetic polymorphism in samples collected from Turkish hair goat breed. Milk protein polymorphism has been considered a potential tool for selection of goat breeds. The results of this study showed that Turkish hair goat breed have a genetic variability in the β -lg locus, which may lead to extensive study of genetic polymorphism of milk proteins in Turkish hair goat breed. This record may be useful for marker-assisted selection between different genotypes and the technological properties of milk. But, it is necessary to screen further goat breeds for determining the polymorphism at proximal promoter region of β -lg gene.

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