

Determination of *CAST/MspI* gene polymorphism in selected sheep breeds reared in Türkiye*

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ABSTRACT

Sheep breeding plays a crucial role in meeting the increasing demand for high-quality meat, milk, and wool. Traditional selection methods based on phenotypic traits have led to genetic improvement; however, progress remains slow for traits with low to moderate heritability. Marker-assisted selection (MAS) has emerged as a promising complementary approach, enabling faster genetic gains. Among candidate genes studied for MAS, the calpastatin (*CAST*) gene is notable for its association with meat yield and quality. This study aimed to identify *CAST/MspI* gene polymorphisms in four sheep breeds reared in Türkiye (Central Anatolian Merino-CAM, Pirlak-PRL, Romanov-RMV, and Suffolk-SFK) and assess their potential use in MAS. A total of 176 individuals were genotyped using the PCR-RFLP method. All breeds in this study were found to be polymorphic for the *CAST* gene. The frequency of the M allele ranged from 0.67 in CAM to 0.76 in SFK. Genotype frequencies for MM ranged from 0.40 (CAM) to 0.71 (SFK), for MN from 0.10 (RMV and SFK) to 0.54 (CAM), and for NN from 0.06 (CAM) to 0.20 (RMV). Significant deviations from Hardy-Weinberg equilibrium were observed in CAM, RMV, and SFK populations, but not in PRL. Observed heterozygosity ranged from 0.10 to 0.54 and expected heterozygosity from 0.37 to 0.44. The presence of all three genotypes and substantial genetic variation suggests that the *CAST* gene may be a valuable marker in MAS for these breeds. However, further association studies are required to confirm the relationship between *CAST* genotypes and economically significant traits related to meat production.

1. Introduction

Traditional selection methods, which have been employed for many years to increase yields in animal production, are often slow, laborious, labor-intensive, and costly. Most economically important traits in livestock are quantitative in nature, characterized by low heritability and influenced by a multitude of genes as well as environmental factors. Genetic progress tends to be slower for phenotypic traits such as meat or milk yield, which typically have low heritability and can only be measured in the later stages of an animal's life. However, the early identification of candidate genes associated with various performance traits, and their subsequent application in marker-assisted selection (MAS) programs, can significantly accelerate genetic improvement (Karlı et al. 2017; Demir et al. 2022). Identifying candidate genes suitable for MAS is a complex process that requires establishing associations between genotypic and phenotypic data (Javanmard et al. 2010; Kania et al. 2019). Calpastatin (*CAST*) gene is one of the most studied genes reported to be associated with meat yield and quality in different livestock species (Javanmard et al. 2010; Ropka-Molik et al. 2014; Kania et al. 2019).

In sheep, approximately one-quarter of the total body weight consists of skeletal muscle. Skeletal muscle growth in animals is primarily determined by three factors: the number and size of muscle cells, the rate of muscle protein synthesis, and the rate of

protein degradation (Ibrahim et al. 2015). Various physiological and genetic factors influencing muscle growth act upon one or more of these fundamental mechanisms. However, in domestic animals, variations in the rate of muscle growth are more commonly attributed to differences in protein degradation rather than changes in protein synthesis (Goll et al. 1998).

Muscle protein degradation, or proteolysis, is mediated by several well-characterized proteolytic enzyme systems, among which the calpain-calpastatin system (CCS) is particularly prominent. This system comprises calpains, a family of calcium-dependent cysteine proteases, with at least fifteen isoforms identified and their endogenous inhibitor, calpastatin. The role of the CCS has been well established in both normal and postnatal skeletal muscle development, as well as in muscle wasting conditions. In general, increased skeletal muscle growth is associated with reduced rates of protein degradation and decreased calpain activity, primarily resulting from elevated calpastatin activity (Goll et al. 1998). Importantly, the calpain-to-calpastatin ratio is considered to be a key determinant of muscle accretion in animals (Kania et al. 2019; Valencia et al. 2022). In contrast, during the post-mortem conversion of muscle to meat, reduced calpastatin activity permits enhanced proteolysis, which significantly contributes to meat tenderization (Kawasaki and

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Kawashima 1996; Goll et al. 1998; Ciobanu et al. 2004; Jawasreh et al. 2019).

The *CAST* gene, which plays a critical role in post-mortem meat tenderization and skeletal muscle development, is located on chromosome 5 in sheep and comprises 29 exons spanning a total of 89576 base pairs (NCBI 2021). Polymorphisms in the *CAST* gene have been reported to be associated with several economically important traits, including birth weight, growth performance, growth rate, muscle development, and carcass yield. In addition to these production traits, variations in *CAST* have also been linked to meat quality characteristics such as pH, meat color, cooking loss, and tenderness (Palmer et al. 1997; Chung and Devis 2012; Knight et al. 2012; Ramadevi et al. 2020). In this context, the aim of the present study was to identify *CAST/MspI* gene polymorphisms in four sheep breeds in Türkiye (CAM, PRL, RMV, and SFK) and to evaluate their possibilities for use in MAS studies.

2. Materials and Methods

Ethical approval and permission for this study was obtained from Eskisehir Osmangazi University Animal Experiments Local Ethics Committee (Date: 09/10/2020; Decision No: 809).

To carry out *CAST* gene polymorphism in sheep breeds, blood samples were taken from the jugular vein of animals into sterile vacuum tubes containing EDTA. Information about the blood samples used in the study (breed, number of samples and where collected) is shown in Table 1. Genomic DNA from whole blood was extracted using a commercial DNA isolation kit (BLIRT DNA isolation kit, EM13-250) according to the manufacturer's instructions. DNA quality and quantity were determined using gel electrophoresis (1%) and ND 1000 NanoDrop spectrophotometer (A260/A280 nm).

Table 1. Sampling regions and sample sizes

| District | Breed (Abbreviation) | Sample size (n) |
|--------------|--------------------------------|-----------------|
| Çifteler | Central Anatolian Merino (CAM) | 32 |
| | Pırlak (PRL) | 8 |
| | Romanov (RMV) | 10 |
| | Suffolk (SFK) | 21 |
| Sivrihisar | Central Anatolian Merino (CAM) | 64 |
| Mahmudiye | Central Anatolian Merino (CAM) | 41 |
| Total | | 176 |

Polymorphisms in the *CAST* gene were determined in the studied sheep breeds using the PCR-RFLP method. After the DNA isolation step, the primers reported by Palmer et al. 1998 were utilized for the amplification of the *CAST* gene by PCR. To amplify the 622 bp region of the cast gene, 25 µl of reaction mixture was prepared by adding 100 ng DNA, 10 X PCR buffer, 0.6 mM of each dNTP, 1.5 mM MgCl₂, 1 pM of each primer and 1 U of Taq polymerase. The PCR amplification was performed using 35 cycles of 95°C for 1min, 62°C for 1min and 72°C for 2 min, followed by 72°C for 10 min. The 622 bp products were digested with *MspI* restriction enzyme. The bands were visualized using ultraviolet transillumination and the size of the amplified fragments was compared to a Solis Biodyne 100 bp DNA ladder (Cat 07-11-00050).

Based on the results of electrophoresis, the presence of the relevant genotypes was identified. The Popgene software package was used to calculate allele and genotype frequencies, observed (Ho) and expected heterozygosity (He), and Hardy-Weinberg equilibrium for the *CAST* gene (Yeh et al. 1997). The chi-squared test (χ^2) was also used to test whether or not the populations were in Hardy-Weinberg equilibrium.

3. Results and Discussion

PCR amplification successfully produced 622 bp *CAST* gene fragments, and a 100 bp ladder was used for comparison of the amplification length. The PCR products were then digested with the restriction enzyme *MspI* and separated on 2% agarose gel electrophoresis. As a result of PCR-RFLP, the presence of polymorphism in *CAST* gene presented two alleles M and N. Enzyme *MspI* produced two fragments of 336 bp and 286 bp for allele M, whereas the PCR product remained uncut for allele N. The PCR-RFLP profile of M allele homozygous animals (MM) showed two bands of 336 and 286 bp. All three genotypes were observed, and the *CAST* gene locus was found to be polymorphic in all populations studied. The heterozygous genotype (MN) showed three bands of 622, 336 and 286 bp and homozygous for the N allele (NN) showed only one band of 622 bp, as shown in Figure 1.

The gene frequencies of the *CAST* locus were estimated using both the Popgene V.1.31 (Yeh et al. 1997) software package and counting the number of genes. The chi-squared test (χ^2) was used to test whether or not the populations were in Hardy-Weinberg

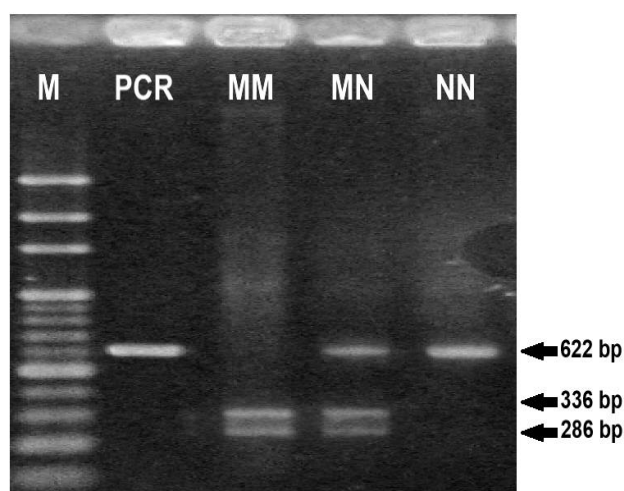


Figure 1. Agarose gel image of *CAST* genotypes detected using the PCR-RFLP.

equilibrium. The frequencies of genotypes and alleles of the CAST locus are shown in Table 2.

The estimated genetic diversity parameters for the CAST gene in the studied sheep breeds are presented in Table 3.

In all breeds, except the Central Anatolian Merino, the homozygous MM genotype had the highest frequency, and M was the most common allele. The allele frequencies reported from previous studies on different sheep breeds are summarized in Table 4.

The calculated allele frequencies (M and N) in the Pırlak, Romanov and Suffolk sheep breeds were consistent with studies by [Shahroudi et al. \(2006\)](#) in Karakul breed, [Szkudlarek-Kowalczyk \(2011\)](#) in Polish merino, [Gharahveysi et al. \(2012\)](#) in Zel breed, [Tohidi \(2013\)](#) in Sanjabi sheep, [Sunilkumar et al. \(2014\)](#) in Bandur sheep, [Avanus et al. \(2015\)](#) in Karakul sheep, [Bozhilova-Sakova et al. \(2020\)](#) in Northeast Bulgarian Merino breed and [Bayraktar and Shoshin \(2022\)](#) in Awassi sheep. The

Table 2. Genotype and allele frequencies of CAST gene

| Breed | N | Genotype Frequencies | | | Allele Frequencies | |
|--------------------------|-----|----------------------|-----------|----------|--------------------|------|
| | | MM | MN | NN | M | N |
| Central Anatolian Merino | 137 | 0.40 (55) | 0.54 (74) | 0.06 (8) | 0.67 | 0.33 |
| Pırlak | 8 | 0.63 (5) | 0.25 (2) | 0.12 (1) | 0.75 | 0.25 |
| Romanov | 10 | 0.70 (7) | 0.10 (1) | 0.20 (2) | 0.75 | 0.25 |
| Suffolk | 21 | 0.71 (15) | 0.10 (2) | 0.19 (4) | 0.76 | 0.24 |

Table 3. Genetic diversity parameters in the studied breeds

| Breed | n | Ho | He | Ne | χ^2 |
|--------------------------|-----|------|------|------|----------|
| Central Anatolian Merino | 137 | 0.54 | 0.44 | 1.78 | 6.86 |
| Pırlak | 8 | 0.25 | 0.40 | 1.60 | 0.88 |
| Romanov | 10 | 0.10 | 0.39 | 1.60 | 5.37 |
| Suffolk | 21 | 0.09 | 0.37 | 1.56 | 12.64 |

n: sample size, Ho: Observed heterozygosity, He: Expected heterozygosity, Ne: Number of effective alleles. $\chi^2_{1,0.05}$: 3.841 Hardy-Weinberg equilibrium ($P < 0.05$).

Table 4. The allele frequencies in different sheep breeds

| Breed | Allele Frequencies | | Reference |
|----------------------------|--------------------|------|--|
| | M | N | |
| Karagül | 0.79 | 0.21 | Shahroudi et al. (2006) |
| Tsigai x Lacaune | 0.90 | 0.10 | Gabor et al. (2009) |
| Tsigai | 0.91 | 0.09 | |
| Polonya Merinos | 0.76 | 0.24 | Szkudlarek-Kowalczyk et al. (2011) |
| Berrichon du Cher | 0.92 | 0.08 | |
| Ile de France | 0.95 | 0.05 | |
| Atabi | 0.64 | 0.36 | Nanekarani et al. (2011) |
| Zel | 0.75 | 0.25 | Gharahveysi et al. (2012) |
| Balkhi | 0.88 | 0.12 | Khan et al. (2012) |
| Kajli | 0.86 | 0.14 | |
| Lohi | 0.87 | 0.13 | Suleman et al. (2012) |
| Kajli | 0.81 | 0.19 | |
| Thalli | 0.90 | 0.10 | |
| Sanjabi | 0.72 | 0.28 | Tohidi (2013) |
| Ghezel | 0.69 | 0.31 | |
| Afshari | 0.63 | 0.37 | |
| Makui | 0.88 | 0.12 | |
| Bandur | 0.72 | 0.28 | Sunilkumar et al. (2014) |
| Lori | 0.63 | 0.37 | Asadi et al. (2014) |
| Güney Karaman | 0.67 | 0.33 | Balçioğlu et al. (2014) |
| Akkaraman | 0.69 | 0.31 | |
| Awassi | 0.59 | 0.41 | |
| Kangal | 0.92 | 0.08 | |
| Karayaka | 0.89 | 0.11 | |
| Morkaraman | 0.87 | 0.13 | |
| Gökçeada | 0.99 | 0.01 | Yılmaz et al. (2014a) |
| Kıvrıcık | 0.85 | 0.15 | |
| Karacabey Merino | 0.80 | 0.20 | |
| Kıvrıcık | 0.84 | 0.16 | Yılmaz et al. (2014b) |
| Karagül | 0.73 | 0.27 | Avanus et al. (2015) |
| Shumen | 0.92 | 0.08 | Georgieva et al. (2015) |
| Northeast Bulgarian Merino | 0.73 | 0.27 | Bozhilova-Sakova et al. (2020) |
| Awassi | 0.78 | 0.22 | Bayraktar and Shoshin (2022) |

allele frequencies calculated in Central Anatolian Merino sheep breed were similar to the results of Nanekarani et al. (2011) in Atabi sheep, Tohidi (2013) in Ghezel and Afshari sheep, Asadi et al. (2014) in Lori sheep and Balcioglu et al. (2014) in Güney Karaman, Akkaraman and Awassi sheep breeds.

However, this study is not in agreement with the following studies:- Gabor et al. (2009) in Tsigai x Lacaune and Tsigai sheep, Szkudlarek-Kowalczyk et al. (2011) in Berrichon du Cher and Ile de France sheep, Khan et al. (2012) in Balkhi and Kajli sheep, Suleman et al. (2012) in Lohi, Kajli and Thalli sheep, Tohidi (2013) in Makui sheep, Balcioglu et al. (2014) in Kangal, Karayaka and Morkaraman sheep, Yilmaz et al. (2014a, 2014b) in Gökçeada, Kıvrıcık, Karacabey merino sheep and Georgieva et al. (2015) in Shumen sheep. The frequency of the M allele in these studies is considerably higher than in the results of this study.

There was no statistical significance between the observed and expected frequency differences for the *CAST* gene in the Pırlak population. In terms of the *CAST* polymorphism, the Pırlak population was found to be in Hardy-Weinberg genetic equilibrium (Table 3, $P < 0.05$). However, the higher χ^2 values calculated for the Central Anatolian Merino, Suffolk, and Romanov populations indicated that the χ^2 values for these three breeds were significant (Table 3, $P < 0.05$). The chi-square test showed that these sheep populations were not in Hardy-Weinberg equilibrium for the *CAST* locus. This unexpected result could be due either to a sampling error or to the fact that a few rams were used for breeding.

Polymorphisms in the *CAST* gene in sheep influence various growth traits and carcass traits. Most of the studies reported a positive effect of the MN genotype on the weight of the animals measured at different ages. In the same way, in different breeds, the MN genotype was reported to have a 15.4% higher birth weight than the NN genotype (Ramadevi et al. 2020; Valencia et al. 2022) and for weaning weight, MN was 1.04 kg higher than MM (Gorlov et al. 2016). It has also been reported that daily weight gain from birth to weaning is greater in MM than in MN and NN (Nassiry et al. 2006; Yilmaz et al. 2014b, Gorlov et al. 2016 and Jawasreh et al. 2017). However, Afanasyeva et al. (2019) reported that higher growth of MM is limited up to weaning in the West Siberian mutton sheep breeds. In most studies, the M allele was superior for all growth-related traits, with few exceptions, for example, in the Prydniprovskaya meat sheep and Altai Mountain breed, animal weight was in favour of the N allele rather than the M allele (Pomitun et al. 2019; Selionova et al. 2020). In addition, Jawasreh and Ismail (2019) reported that MN lambs of the Awassi breed may be healthier due to a higher neutrophils and neutrophil to lymphocyte (N/L) ratio, high triiodothyronine (T3) and cortisol in their blood hematology and serum studies.

In addition to growth traits, *CAST* variants influence carcass and meat quality in sheep. The pre-slaughter live weight of MN genotyped sheep from Volgograd was 3.7 kg more than that of MM genotyped sheep (Kolosov et al. 2021). Palmer et al. (1999) found that the ac genotype had a 15-18% higher age-corrected carcass weight and MN had a higher chilled carcass weight. Furthermore, the aa genotype had the highest percentage of muscle and lowest percentage of fat in the hindquarters, while the ac genotype had the highest intramuscular fat in the ram loin of the two synthetic breeds (Kania et al. 2019). Ibrahim et al. (2015) also reported that the lean and fat percentages of sheep meat were also influenced by the *CAST* gene. MM and MN genotypes tended to have the highest longissimus muscle width, and MN

had heavier longissimus muscle than MM (Jawasreh et al. 2017; 2019). MM and MN had higher backfat thickness and skin plus backfat thickness values of the loin eye muscle in Kıvrıcık sheep than in NN genotypes (Yilmaz et al. 2014b). In a study by Selionova et al. (2020), N was found to be superior (NN genotype) in carcass mass, carcass performance and meat percentage in the Altai Mountain breed.

Kumar et al. (2018) found that the Warner-Bratzler shear force score of the NN genotype was significantly ($P < 0.001$) lower than that of the MM genotype in Bandur ram lambs, and the NN genotype indicated higher meat tenderness. In the Dorset Down breed, ac genotypes had higher shear force (SF) in fillets from ewes (Palmer et al. 1997). Meat samples from ab showed a higher initial mean pH in the Dorset Down breed and aa reported a higher final pH (after ten days) in the Santa Inês breed (Palmer et al. 1997; Esteves et al. 2020). Jawasreh et al. (2017) reported that MN had lighter meat and MN showed lower cooking loss than MM in Awassi sheep.

In contrast, various studies found no association between the *CAST* gene and different traits (Sutikno et al. 2011; Dehnavi et al. 2012; Nikmard et al. 2012; Peirvisi et al. 2020; Bayram et al. 2019). The available research has shown a significant correlation between *CAST* SNPs and various traits in sheep. It is important to note that the same allele may have different effects in different breeds and therefore breed specific studies are required before using the *CAST* gene as a marker in selection.

4. Conclusions

The *CAST/MspI* polymorphism was investigated in the Central Anatolian Merino, Pırlak, Romanov and Suffolk sheep breeds by PCR-RFLP method. In this gene region, variations were observed at different frequencies across all three genotypes (MM, MN, and NN) of the CAM sheep breed. Additionally, a high level of genetic diversity was found within the CAM population. Based on these findings, it is proposed that the relevant gene region could be utilized in Marker-Assisted Selection (MAS) studies aimed at enhancing meat yield and quality in the CAM breed. However, prior to initiating MAS studies, it would be prudent to conduct correlation analyses between the identified genotypes and the phenotypic data associated with meat yield and quality.

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