Journal of the Hellenic Veterinary Medical Society

Vol 76, No 4 (2025)

Relationship Between DGAT1 Gene Polymorphism and Some Growth Traits in Anatolian Merino and Akkaraman Sheep

AN Tanış, İ Keskin

doi: 10.12681/jhvms.40497

To cite this article:

Tanış, A., & Keskin, İ. (2025). Relationship Between DGAT1 Gene Polymorphism and Some Growth Traits in Anatolian Merino and Akkaraman Sheep. *Journal of the Hellenic Veterinary Medical Society*, *76*(4), 9937–9946. https://doi.org/10.12681/jhvms.40497

J HELLENIC VET MED SOC 2025, 76 (4): 9937-9946
ΠΕΚΕ 2025, 76 (4): 9937-9946

Research article
Ερευνητικό άρθρο

Relationship Between DGAT1 Gene Polymorphism and Some Growth Traits in Anatolian Merino and Akkaraman Sheep

A.N. Tanış,[1]* İ. Keskin[2]

[1]*Selçuk University, Faculty of Agriculture, Konya, Turkey*

[2]*Selçuk University, Faculty of Agriculture, Konya, Turkey*

ABSTRACT: A strong correlation exists between growth traits and particular genes. Determining genotypes linked to advantageous morphometric features allows for selective breeding, promoting the establishment of flocks with preferred attributes. The DGAT1 gene is strongly connected to growth, meat quality, production, and carcass characteristics in sheep, making it a key target in research on growth efficiency and overall productivity. This study aimed to investigate the relationship between DGAT1 gene polymorphism and its variation with growth traits in 40 Anatolian Merino and 33 Akkaraman ewes. Data on traits such as weight (six months weight (LW6), weaning weight (WW), birth weight (BW)), and body measurements were collected. Additionally, average daily weight gain (ADWG) and Kleiber ratios were computed. Using PCR-RFLP analysis with the *Alu*I enzyme, three genotypes were identified, revealing polymorphisms: CC, CT, and TT. The analysis showed no statistically significant differences between genotypes and body measurements. These findings indicate that the DGAT1 gene is unlikely to be a suitable candidate for Marker-Assisted Selection (MAS) in Anatolian Merino and Akkaraman sheep, especially concerning traits associated with growth.

Keyword: Sheep; DGAT1; Anatolian Merino; Akkaraman; PCR-RFLP; MAS; Kleiber ratio

Correspondence author:
A.N. Tanış,
Selçuk University, Faculty of Agriculture, Konya, Turkey
E-mail address: aysenur.tanis@selcuk.edu.tr

Date of submission: **19-2-2025**
Date of acceptance: **2-4-2025**

INTRODUCTION

Growth traits in sheep are economically important traits. Growth occurs through the interaction of many genes, along with factors such as muscle growth, birth weight, body condition, weaning weight, and bone formation (Afifi *et al.* 2019). Various studies have been conducted to explain the relationship between growth and genetic diversity (Abegaz *et al.* 2002; Abousoliman *et al.* 2020; Molabe 2023; Besufkad *et al.* 2024; Tanış and Keskin 2025). Nonetheless, a notable link between the DGAT1 gene and phenotypic parameters could not be established in most studies (Mukanova *et al.* 2024). The DGAT1 gene has been primarily linked to meat quality, meat production, and milk production (Grisart *et al.* 2002; Yen *et al.* 2008; Xu *et al.* 2009; Yang *et al.* 2011; Cerit and Demir 2016; Martin *et al.* 2017).

The enzyme Diacylglycerol o-acyltransferase 1 (DGAT1) facilitates the final step in the synthesis of triglycerides and is classified as a microsomal enzyme (Winter *et al.* 2002). Due to this property it may also be involved in lipoprotein formation, energy metabolism in muscle, fat storage, intestinal fat absorption, and milk production, including mammalian oocytes (Cases *et al.* 1998). The DGAT1 gene is located on chromosome 9 in sheep and contains approximately 1470 nucleotides consisting of 17 exons. This gene encodes a polypeptide of 489 amino acids (Xu *et al.* 2009). Studies have shown that DGAT1 gene is an important candidate gene for carcass quality and quantity (Pannier *et al.* 2010; Souza *et al.* 2010; Armstrong *et al.* 2018; Dai *et al.* 2022).

In this study, the relationship between DGAT1 genotypes and selected weight traits (birth weight, weaning weight, and 6-month weight), body measurements, live weight gains for these three periods, and Kleiber ratios were investigated in Anatolian Merino and Akkaraman sheep. Furthermore, the study sought to investigate the potential of the DGAT1 gene as a candidate for Marker-Assisted Selection (MAS) in these breeds.

MATERIALS AND METHODS

Study Population and Data Collection

The study involved 40 Anatolian Merino and 33 Akkaraman lambs born at Selçuk University's Prof. Dr. Orhan Düzgüneş Research Farm. The gender of the lambs was recorded immediately after birth, and their birth weights were determined by weighing them on a scale with 10-gram precision. The weaning process for the lambs was carried out at 75 days. And their weaning weights (WW), 6-month-old weights (LW6), and body measurements—including rump height (RH), withers height (WH), chest circumference (CC), chest width (CW), and chest depth (CD), body length (BL)—were recorded following Ertuğrul (1996)'s guidelines. The animal experiment was conducted according to the guidelines of the local ethics committee of Selçuk University that were arranged according to the "European Union 2010/63/EU is the European Union (EU) legislation" All processes in this experiment agree with the ethical rules of animal welfare.

Genomic DNA Extraction and PCR-RFLP Methodology

Blood samples were obtained from the jugular veins of the animals into EDTA tubes and stored at -20°C until DNA extraction. The DNA isolation process was based on a salt precipitation method, as described by Miller *et al.* (1988), and adapted for the laboratory conditions. For amplifying the DGAT1 gene region, the PCR method of Xu *et al.* (2009) was adapted. The PCR products were verified by electrophoresis on a 2% agarose gel, with a 100 bp marker. PCR's thermal profile and components, as listed in Table 1, were followed, and the primers provided below were used to amplify the gene region.

Forward primer: 5'-GCATGTTCCGCCCTCTCTCTGG-3'

Reverse primer: 5'-GGAGTCCAACACACCCCTGA-3'

The primers used for the DGAT1 gene amplify 309 base pairs of exons 16th-17th of the sheep DGAT1 gene region. As a result of a silent mutation in the 17th exon of the DGAT1 gene, the GCT codon encoding the amino acid Alanine was found to be changed to the GCC codon. Since the *Alu*I enzyme was used to identify polymorphisms, recognizing the sequence 5'….AG/CT…3', this mutation can be detected with the *Alu*I enzyme (Nanekarani *et al.* 2016). The partial sequence of this region (accession no.EU178818.1), the primers (italicized sections) and *Alu*I restrict sites (bolded segments) are given below (Figure 1).

Following the PCR process, variations in the DGAT1 gene region were identified using the *Alu*I restriction enzyme. The digestion reaction was carried out in a total volume of 16 µl, consisting of 0.4 µl restriction enzyme, 1 µl 10X buffer, 4.6 µl ddH2O,

*GCATGTTCCGCC*TCTGGGCCTTCACCGGCATGATGGCACAGGTGAGCAGCCCTGGACCC
CCACCTGCGAGCCCACCCCGTGGGCGCAGAGGCTCACTCCCGTCCCATGTCCCCAGATC
CCGCTGGCCTGGATAGTCGGCCGCTTCTTCCGTGGCAACTATGGCAACGCGGCTGTGTG
GCTGTCACTCATCATTGGGCAGCCAGTGGCCGTCCTGATGTACGTCCACGACTACTACG
TGCTCCCGCGAGGCCCCAACAGCCGGCACCTG**AGCT**CCTCCAGGCTGGTTCCC*TCAGGG*

Figure 1. The partial sequence of DGAT1 gene region between 16th exon and 17th exon. *Alu*I restriction sites (bolded segments), the primers (italicized sections), and the variation-forming restriction region (AGCT).

Table 1. Components and Thermal Profile for DGAT1 PCR

Components	Thermal Profile	
3 µl DNA (5 ng)	95 °C 4 min	
2 µl 5x PCR Master Mix	95 °C 30 sec	
0.5 µl F primer (10 µM)	58 °C 30 sec	35 cycles
0.5 µl R primer (10 µM)	72 °C 30 sec	
4 µl ddH_2O	72 °C 10 min	

and10 µl PCR product. The digested products were separated on a 2.5% agarose gel and visualized with a 50 bp marker. Genotypes were assigned based on the band lengths observed.

Statistical Analysis

Using the POPGENE (Yeh *et al.* 1997) software for the DGAT1 gene, allele and genotype frequencies were determined. Statistical analysis was conducted using the General Linear Model in SPSS 29.0 software. Below is the statistical model employed in the study.

$Y_{ijk}=\mu+A_i+B_j+C_k+e_{ijk}$

Y_{ijk}: i^{th} breed, j^{th} value of genotype

µ: population mean

A_i: effect of the breed factor

B_j: effect of the genotype factor

C_k: effect of the sex factor

e_{ij}: experimental error

The Kleiber ratio (KR) is considered an indicator of an animal's growth efficiency and feed conversion capability (Abegaz *et al.* 2002; Mohammadi *et al.* 2011). The Kleiber ratios for the periods were computed following the method outlined by Kleiber (1947).

$$KR1 = \frac{ADWG1}{WW^{0.75}} \qquad KR2 = \frac{ADWG2}{LW6^{0.75}} \qquad KR3 = \frac{ADWG3}{LW6^{0.75}}$$

LW: Live weight
ADWG1: pre-weaning
ADWG2: birth to six months
ADWG3: weaning to six months

RESULTS

PCR was used to amplify the DGAT1 gene region in Anatolian Merino and Akkaraman ewes, and genotyping was performed through RFLP-PCR analysis. After digesting the DGAT1 gene with the *Alu*I enzyme, the resulting genotypes and the anticipated sizes of the base pairs are displayed below.

CC: 309 bp

CT: 309, 272, 37 bp

CC: 272, 37 bp

The image of the PCR product for the DGAT1 gene region is shown in Figure 2.

Agarose gel image of the digestion result with the *Alu*I restriction enzyme in Figure 3.

Following genotyping, the identified genotypes were analyzed, and the frequencies of alleles and genotypes were determined. Table 2 presents the determined frequencies of alleles and genotypes, along with Chi-Square (χ^2) values.

The frequencies of alleles and genotypes were determined, and the genotypes were identified through genotyping. The frequencies of genotypes and alleles, along with the chi-square (χ^2) values, are provided

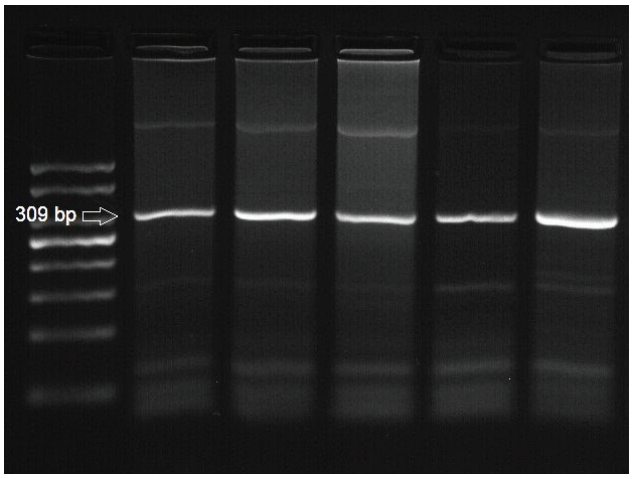

Figure 2. PCR products' agarose gel image for DGAT1 gene region. 1st line shown 50bp marker.

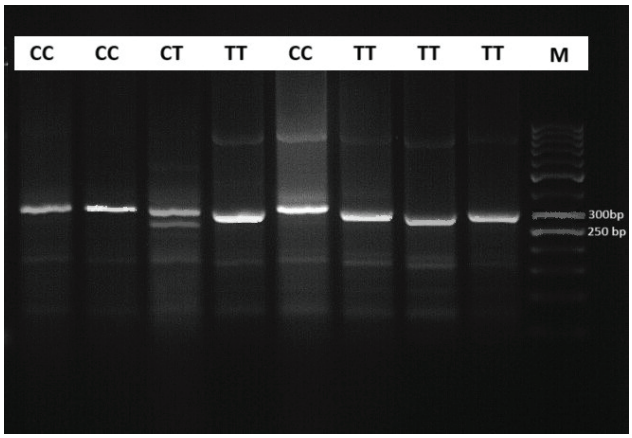

Figure 3. Image of agarose gel showing the DGAT1 gene region after digestion with the *Alu*I enzyme. Line 9 shown 50bp marker. Line 1, 2, and 5 was determined to be CC genotype, line 3 was CT, and line 4, 6, 7, and 8 were TT genotype.

Table 2. Summary of Genetic Variation and Frequencies for the DGAT1 Gene Region

Gene	Breeds	Genotypes (n)			Genotype Frequencies			Allel Frequencies		Chi-Square	H_o	H_e
		CC	CT	TT	CC	CT	TT	C	T			
DGAT1	AM	15	9	8	0.460	0.281	0.250	0.609	0.391	5.8*	0.281	0.484
	A	9	7	8	0.375	0.292	0.333	0.521	0.479	4.5*	0.292	0.510

AM: Anatolian Merino, A: Akkaraman, H_e: expected heterozygosity, H_o: observed heterozygosity

in Table 2. When Table 2 analyzed, it was observed that C allele frequency was the highest in Anatolian Merino and Akkaraman ewes following digestion with the *Alu*I enzyme in the DGAT1 gene region. Chi-Square ($\chi 2$) test results showed that DGAT1 gene was not found to be in Hardy-Weinberg equilibrium ($p<0.05$). The genotype frequencies of CC, CT, and TT were determined as 0.375, 0.292, and 0.333 for Akkaraman sheep, and 0.460, 0.281, and 0.250 for Anatolian Merino sheep, respectively. The Chi-Square values were calculated as 4.5 and 5.8 for each breed, respectively.

The elevated heterozygosity levels, combined with the frequencies of alleles and genotypes, suggest a notable level of polymorphism or variation among individuals. This enhances the probability that the analyzed gene regions could serve as potential candidates for the traits being studied. Higher diversity tends to occur when allele frequencies are more evenly distributed (Doğan and Doğan 2019). These results suggest that genetic variation in the DGAT1 gene region is more pronounced in the Akkaraman sheep breed.

Table 3 displays the genotypes derived from *Alu*I enzyme digestion of the DGAT1 gene region, along with the statistical analysis outcomes for weights and body measurements, categorized by breed and sex.

The mean values for birth weight, weaning weight, and body measurements were calculated for lambs with CC, CT, and TT genotypes in Anatolian Merino and Akkaraman breeds (Table 3). No statistically significant differences were identified in the examined traits among sheeps of various types of genotypes and breeds. The polymorphism in the DGAT1 gene region was found to have no statistically significant effect on weights or on any body measurements recorded at 75 days or six months of age.

Upon reviewing Table 3, the average live weight at the six months of age was found to be 34.90 kg for female sheep and 37.25 kg for male sheep. Male ewes have a heavier weight at six months than females. Sheep with the CT genotype had the heaviest average six months weight. The average body length was measured as 56.65 cm in sheep with the CC

Table 3. Breed, Sex, and Genotype-Based Statistical Analysis for Selected Weights and Body Measurements

Morphometric Parameters and Weight Data

Breed		RH	WH	CW	CG	CD	BL	BW	WW	RH6	WH6	CW6	CG6	CD6	BL6	LW6
AM	$\bar{X}$	53.41[a]	53.97[a]	15.97[a]	64.26[a]	21.94[a]	48.59[a]	4.26[a]	19.47[a]	62.82[a]	62.96[a]	20.04[a]	83.89[a]	26.86[a]	58.04[a]	36.76[a]
	S_X	3.878	4.160	2.249	6.170	1.999	4.258	0.763	4.486	3.232	3.144	3.226	6.040	2.068	3.776	8.040
A	$\bar{X}$	53.88[a]	54.12[a]	15.04[a]	61.56[a]	21.56[a]	46.08[a]	4.19[a]	17.94[a]	63.00[a]	61.86[a]	19.41[a]	85.27[a]	27.23[a]	58.14[a]	35.04[a]
	S_X	4.076	4.285	2.491	6.100	2.200	7.500	0.525	4.555	5.100	4.411	1.919	6.090	2.487	4.507	6.690
Sex																
Female	$\bar{X}$	53.00[b]	53.69[b]	15.45[b]	63.00[b]	21.66[b]	48.55[b]	4.17[b]	18.41[b]	62.22[b]	61.91[b]	19.39[b]	84.09[b]	26.74[b]	57.17[b]	35.06[b]
	S_X	3.982	3.974	2.277	5.970	2.109	4.770	0.547	4.303	3.825	3.679	1.751	5.910	2.359	4.207	6.840
Male	$\bar{X}$	54.40[b]	54.17[b]	15.70[b]	63.23[b]	21.90[b]	46.53[b]	4.29[b]	19.25[b]	63,48[b]	62.96[b]	20.07[b]	84.85[b]	27.26[b]	58.85[b]	36.81[b]
	S_X	3.847	4.418	2.507	6.570	2.074	6.800	0.774	4.798	4.327	3.818	3.339	6.240	2.159	3.860	7.980
Genotype																
CC	$\bar{X}$	53.67[c]	54.00[c]	15.92[c]	63.46[c]	21.75[c]	46.92[c]	4.31[c]	19.18[c]	62.33[c]	62.33[c]	19.29[c]	83.29[c]	26.95[c]	56.91[c]	34.80[c]
	S_X	3.738	4.294	2.083	6.570	1.800	7.580	0.564	4.780	4.590	3.773	2.053	6.990	2.355	4.323	7.650
CT	$\bar{X}$	53.50[c]	53.81[c]	15.81[c]	62.69[c]	21.88[c]	48.06[c]	4.14[c]	18.54[c]	62.71[c]	62.29[c]	20.64[c]	85.29[c]	26.57[c]	58.29[c]	37.21[c]
	S_X	3.882	3.781	2.971	6.600	2.217	4.390	0.649	4.530	3.361	3.870	4.220	5.440	2.209	4.100	8.500
TT	$\bar{X}$	53.95[c]	53.95[c]	14.95[c]	63.05[c]	21.74[c]	47.84[c]	4.21[c]	18.62[c]	63.87[c]	62.87[c]	19.60[c]	85.47[c]	27.53[c]	59.53[c]	36.56[c]
	S_X	4.430	4.550	2.172	5.770	2.377	4.800	0.817	4.460	4.140	3.852	1.502	5.140	2.167	3.357	6.300

*[a]:For the breed trait, no statistically significant difference was observed between the means indicated by the same letters in the same column

[b]: For the sex trait, no statistically significant difference was observed between the means indicated by the same letters in the same column

[c]: For the genotype trait, no statistically significant difference was observed between the means indicated by the same letters in the same column

AM: Anatolian Merino, A: Akkaraman, S_X: standard deviation, $\bar{X}$: mean, RH: Rump Height, WH: Width Height, CW: Chest Width, CG: Chest Girth, CD: Chest Depth, BL: Body Length, BW: Birth Weight, WW: Weaning Weight, RH6: 6th months Rump Height, WH6: 6th months Width Height, CW6: 6th months Chest Width, CG6: 6th months Chest Girth, CD6: 6th months Chest Depth, BL6: 6th months Body Length, LW6: 6th months Live Weight

genotype, 58.41 cm in those with the CT genotype, and 59.46 cm in those with the TT genotype.

No statistically significant differences were detected for the ADWG and KR traits among ewes of different breeds, sexes, and genotypes in Table 4. Anatolian Merino sheep displayed higher ADWG compared to Akkaraman sheep, with male ewes generally achieving higher ADWG than females. Male sheep consistently exhibited greater daily live weight gains than female sheep across all periods. The daily live weight gains of Anatolian Merino sheep were consistently higher than those observed in Akkaraman sheep. Nevertheless, no particular genotype was associated with either the highest or lowest live weight gain. For ADWG1, the CC genotype showed the highest live weight gain, whereas for ADWG2 and ADWG3, the CT genotype exhibited the greatest gains (Table 4).

DISCUSSIONS

In research conducted on various sheep breeds, the reported genotype frequencies for the DGAT1 gene region were 0.42 for CC, 0.47 for CT, and 0.23 for TT, respectively (Malewa *et al.* 2014; Bayraktar and Shoshin 2022). Mukanova *et al.* (2024) in purebred Edilbay x Edilbay sheep, the frequencies of the CC, CT, and TT genotypes were found to be 0.70, 0.27, and 0.03, respectively. In Edilbay × Gissar crossbred sheep, the genotype frequencies were determined as 0.58 for CC, 0.42 for CT, and 0.00 for TT. The genotype frequencies for TT, TC, and CC were determined to be 0.309, 0.258, and 0.433, respectively. The allele frequencies were calculated as 0.438 for the T allele and 0.562 for the C allele (Nanekarani *et al.* 2016). Overall, the CC genotype is found to be the most frequent, while the TT genotype is the least frequent. In the same manner, the current study also revealed that the CC genotype had the highest frequency and the TT genotype had the lowest, aligning with the findings of earlier studies.

Örkiz *et al.* (1984), reported birth weight 4.4 kg of Kangal-type Akkaraman lambs, Öztürk (1995) and Akçapınar and Özbeyaz (2001) recorded birth weights 4.7 kg – 4.8 kg for Akkaraman lambs, Alarslan and Aygün (2019) reported 4.49 kg for curly lambs in their studies. Saleh *et al.* (2020), reported that the average birth weight for Awasi x Suffolk, Rahmani x Barki, Ossimi, Rahmani, and Barki sheep breeds was reported to range between 3.50 kg and 4.40 kg, with weaning weights ranging from 17.00 kg to 23.23 kg. For Akkaraman sheep, the average birth weight was reported as 4.19 kg, while the average weaning weight was 24.13 kg Behrem (2021). The average birth and weaning weight of Akkaraman lambs were determined to be 4.15 kg and 17.82 kg, respectively in our study. For Anatolian Merino lambs, the average weaning weight was 19.49 kg, while the average birth weight was recorded as 4.26 kg. It is seen that this value for birth weight is slightly lower than the weights reported in the liter-

Table 4. Breed, Sex, and Genotype-Based Statistical Analysis for ADWGs and KRs ($\bar{X} \pm S_{\bar{X}}$)

ADWGs and KRs						
Breed	**ADWG1**	**ADWG2**	**ADWG3**	**KR1**	**KR2**	**KR3**
AM	202.77[a]±58.110	169.65[a]±84.300	180.36[a]±45.500	21.54[a]±2.949	19.71[a]±6.000	10.20[a]±4.503
A	183.40[a]±62.700	166.00[a]±68.300	171.26[a]±37.260	20.51[a]±3.655	11.80[a]±0.976	11.26[a]±3.840
Sex						
Female	189.80[b]±55.200	157.60[b]±69.800	171.16[b]±38.490	20.99[b]±2.949	17.06[b]±6.310	10.65[b]±3.978
Male	199.20[b]±65.500	166.00[b]±83.700	180.78[b]±44.850	21.12[b]±3.470	15.52[b]±5.740	10.68[b]±4.485
Genotype						
CC	198.20[c]±62.700	145.80[c]±88.300	168.98[c]±42.440	21.18[c]±3.305	15.41[c]±5.710	9.63[c]±5.260
CT	192.00[c]±56.600	173.90[c]±76.900	183.40[c]±48.100	21.16[c]±2.670	17.55[c]±7.490	11.23[c]±3.369
TT	192.10[c]±63.300	174.10[c]±58.500	180.09[c]±35.750	20.96[c]±3.611	16.14[c]±4.950	11.60[c]±3.047

* [a]: For the breed trait, no statistically significant difference was observed between the means indicated by the same letters in the same column
[b]: For the sex trait, no statistically significant difference was observed between the means indicated by the same letters in the same column
[c]: For the genotype trait, no statistically significant difference was observed between the means indicated by the same letters in the same column

AM: Anatolian Merino, A: Akkaraman, $S_{\bar{X}}$: standard deviation, $\bar{X}$: mean, ADWG1: Pre-weaning Average Daily Weight Gain, ADWG2: Birth to Six Months Average Daily Weight Gain, ADWG3: Weaning to Six Months Average Daily Weight Gain

ature. These variations are thought to be affected by environmental factors such as climate, geographical features, nutrition, and herd management practices. Yavuz (2015), reported the average body measurements of 6-month-old Akkaraman ewes as CD (31.48±0.3), WH (80.55±1.24), RH (71.75±0.8), CW (19.3±0.45), CC (86.48±0.57), and BL (70.01±0.51), which exceeded the averages obtained in the present study. Mukanova *et al.* (2024) determined in purebred and crossbred sheep, the birth weights for the CC and CT genotypes as 5.876 and 5.782 kg; 5.844 and 5.821 kg, respectively. The 30-day weights were recorded as 8.381 and 8.269 kg; 8.300 and 8.439 kg, the 60-day weights as 33.668 and 33.718 kg; 32.444 and 33.786 kg, and the 120-day weights as 39.000 and 41.487 kg; 39.111 and 40.929 kg, respectively. This variation is believed to result from environmental factors, particularly nutrition.

Armstrong *et al.* (2018), conducted on Texel sheep, the DGAT1 gene region was investigated for traits such as body weight, weaning weight, weight in ultrasound measurements, fat thickness, rib area, hot carcass weight, and shoulder cut weight. In all these traits, animals with the TT genotype showed a decrease in values, whereas those with the CC genotype exhibited an increase. Similarly in the present study, the highest weights were also observed in sheep with the CC genotype. Cheng *et al.* (2023), demonstrated that sheep carrying the TT genotype in the OSMR gene and the AA genotype in the GHR gene had significantly higher body weights than those with other genotypes ($P < 0.05$). Likewise, Wijayanti *et al.* (2022), reported that, in male LXBH sheep, the II genotype was significantly associated with body length ($p = 0.039$), chest circumference ($p = 0.016$), chest width ($p = 0.019$), and body length index ($p = 0.008$). Individuals with this genotype exhibited greater size compared to those with other genotypes. Furthermore, in male Tong sheep, the DD genotype was the most common for hip height and tail depth, while the ID genotype showed the highest values for head length. In male Tan sheep, the ID genotype was significantly associated with chest circumference ($p = 0.044$) and cannon circumference ($p = 0.020$), with sheep carrying this genotype displaying higher values than those with other genotypes. It was determined that sheep with this genotype had higher values compared to those with other genotypes. Osman *et al.* (2021) in their study on the MSTN gene, found that the c.18 G>T SNP was significantly associated with birth weight, whereas the c.241 T>C SNP showed a significant association with average daily weight gain ($P<0.05$). Aljubouri *et al.* (2021), investigated the association between genetic polymorphisms in the GnRH1 gene and growth traits in Awassi and Karakul sheep. They reported that the AA and AB genotypes exhibited distinct growth patterns, with individuals carrying the AA genotype demonstrating superior growth traits, particularly at sexual maturity. Rashidi *et al.* (2008), in their research on Kermani sheep, determined the Kleiber ratio for lambs during the birth-to-weaning period as 0.020 for males and 0.018 for females ($P<0.01$). Similarly, a study on Sangsari lambs reported statistically significant Kleiber ratios for the birth-to-weaning period, with values of 17.64 for males and 17.13 for females ($P<0.01$) (Mohammadi *et al.* 2011). In a study investigated on Dorper sheep, and calculated Kleiber ratios of 17.21 and 4.96 for males and 17.31 and 4.49 for females during the birth-to-weaning and weaning-to-six-month periods, respectively. However, no significant differences in Kleiber ratios between genders were observed in this breed (Besufkad *et al.* 2024). Similar to the findings of the study conducted on Dorper sheep, no statistically significant association was observed between DGAT1 gene polymorphism and average live weight gain or Kleiber ratio in Anatolian Merino and Akkaraman sheep in this study.

The observed differences in the association between genetic polymorphisms and growth traits across studies may be attributed to multiple factors, including breed-specific genetic backgrounds, environmental influences, management conditions, and sample sizes. The impact of DGAT1 and other candidate genes on growth traits might vary depending on genetic interactions, epigenetic factors, or population-specific selection pressures. Further investigations with larger and more diverse populations are required to clarify these discrepancies and determine the broader applicability of these genetic markers in breeding programs.

CONCLUSIONS

The investigation of the relationship between the DGAT1 gene and growth traits in Türkiye's native sheep breeds remains scarce. In a study involving 40 Anatolian Merino and 33 Akkaraman sheep, a relationship between DGAT1 gene and certain growth features was observed.

To detect polymorphisms in the DGAT1 gene with *Alu*I enzyme digestion the PCR-RFLP method

was used. Three genotypes were identified for this gene region. The C allele's frequency was found higher in both Anatolian Merino and Akkaraman sheep. The Chi-Square (χ^2) test outcomes indicated that the DGAT1 gene deviated from Hardy-Weinberg equilibrium ($P<0.05$) (Table 2).

Although the DGAT1 gene polymorphism did not show a significant association with growth traits in this study, the identified genetic variation could still contribute to understanding the genetic mechanisms underlying growth and productivity in sheep. Integrating these findings into selective breeding programs may enhance breeding strategies by combining molecular markers with traditional selection methods.

The findings of this study suggest that while DGAT1 gene polymorphism may not be a reliable marker for Marker-Assisted Selection (MAS) in Anatolian Merino and Akkaraman sheep concerning growth traits, further research with larger sample sizes may provide more definitive results. However, the identified genotypic variations can still be valuable in understanding the genetic basis of growth and productivity in sheep breeds. Integrating these findings into selective breeding programs could help improve growth performance and optimize breeding strategies in the long term.

Funding
This work was supported by Selcuk University, The Scientific Research Project Coordinating Office (No. 22101001).

CRediT authorship contribution statement
İ.K. planned the tests; A.N.T. carried out the tests and analyzed the information; A.N.T., wrote the initial sketch of the article; İ.K. reviewed and edited the article.

Declaration of competing interest
All authors declare that there are no competing interests.

Acknowledgements
This study was performed by Ayşe Nur TANIŞ in partial fulfillment of the MSc thesis in Biometry and Genetics, Animal Science Department, Selçuk University.

REFERENCES

Abegaz, S, Negussie, E, Duguma, G, Rege, J (2002) Genetic parameter estimates for growth traits in Horro sheep. *Journal of Animal breeding and Genetics* **119**, 35-45.

Abousoliman, I, Reyer, H, Oster, M, Muráni, E, Mourad, M, Abdel-Salam Rashed, M, Mohamed, I, Wimmers, K (2020) Analysis of candidate genes for growth and milk performance traits in the Egyptian Barki sheep. *Animals* **10**, 197.

Afifi, M, Alkaladi, A, Kadasa, NM, Saddick, S, Baeshen, M, Al-Farga, A, Aqlan, FM, Almulaiky, YQ, Alkhaled, M, Alayafi, AA (2019) Sequencing and Polymorphism detection in growth hormone gene in Najdi Sheep and their association with milk production. *Indian Journal of Animal Research* **53**, 423-428.

Akçapınar, H, Özbeyaz, C (2001) The possibilities of developing dam and sire lines using Akkaraman, Sakız (Chios) and Kıvırcık sheep breeds for lamb production II. Some body measurements in lambs and some production traits in yearling females. *Livestock Studies* **41**, 25-33.

Alarslan, E, Aygün, T (2019) Effects of Some Environmental Factors on Morphological Characteristics of Yalova Kıvırcık Sheep. *Cappadocia, Türkiye* 200.

Aljubouri, TR, Hassan, AF, Al-Shuhaib, MBS, Mahyari, SA (2021) Association of GnRH1 gene with growth traits in two breeds of sheep. *Agricultural Research* **10**, 285-293.

Armstrong, E, Ciappesoni, G, Iriarte, W, Da Silva, C, Macedo, F, Navajas, E, Brito, G, San Julián, R, Gimeno, D, Postiglioni, A (2018) Novel genetic polymorphisms associated with carcass traits in grazing Texel sheep. *Meat science* **145**, 202-208.

Bayraktar, M, Shoshin, O (2022) Estimation of the associations between GH and DGAT1 genes and growth traits by using decision tree in Awassi sheep. *Animal Biotechnology* **33**, 167-173.

Behrem, S (2021) Effects of environmental factors growth traits of Akkaraman sheep in Çankırı province. *Livestock Studies* **61**, 22-27.

Besufkad, S, Goshme, S, Bisrat, A, Abebe, A, Abebe, A, Getachew, T, Areaya, A, Zewdie, T, Gizaw, S (2024) Estimation of genetic parameters for growth traits and kleiber ratio in dorper sheep breed. *Heliyon* **10**,

Cases, S, Smith, SJ, Zheng, Y-W, Myers, HM, Lear, SR, Sande, E, Novak, S, Collins, C, Welch, CB, Lusis, AJ (1998) Identification of a gene encoding an acyl CoA: diacylglycerol acyltransferase, a key enzyme in triacylglycerol synthesis. *Proceedings of the National Academy of Sciences* **95**, 13018-13023.

Cerit, H, Demir, H (2016) Detection of diacylglycerol acyltransferase 1 (DGAT1) Gene polymorphism in Imroz and Chios sheep breeds in Turkey using PCR-RFLP method. *Kafkas Üniversitesi Veteriner Fakültesi Dergisi* **22**,

Cheng, J, Wang, W, Zhang, D, Zhang, Y, Li, X, Zhao, Y, Xu, D, Zhao, L, Li, W, Wang, J (2023) Identification of polymorphic loci in OSMR and GHR genes and analysis of their association with growth traits in sheep. *Animal Biotechnology* **34**, 2546-2553.

Dai, R, Zhou, H, Fang, Q, Zhou, P, Yang, Y, Jiang, S, Hickford, JG (2022) Variation in Ovine DGAT1 and Its Association with Carcass Muscle Traits in Southdown Sheep. *Genes* **13**, 1670.

Doğan, İ, Doğan, N (2019) Allel Sayılarının ve Allel Frekanslarının Heterozigotluk ve Polimorfizm Bilgi İçeriği Üzerine Etkilerinin Değerlendirilmesi.

Ertuğrul, M (1996) Küçükbaş Hayvan Yetiştirme Uygulamaları (II. Baskı). *Ders Kitabı. Ank. Üniv. Zir. Fak., Yayın*

Grisart, B, Coppieters, W, Farnir, F, Karim, L, Ford, C, Berzi, P, Cambisano, N, Mni, M, Reid, S, Simon, P (2002) Positional candidate cloning of a QTL in dairy cattle: identification of a missense mutation in the bovine DGAT1 gene with major effect on milk yield and composition. *Genome research* **12**, 222-231.

Kleiber, M (1947) Body size and metabolic rate. *Physiological reviews* **27**, 511-541.

Malewa, A, Hakim, L, Maylinda, S, Husain, M (2014) Growth hormone gene polymorphisms of Indonesia fat tailed sheep using PCR-RFLP and their relationship with growth traits. *Livestock Research for Rural Development* **26**, 115.

Martin, P, Palhière, I, Maroteau, C, Bardou, P, Canale-Tabet, K, Sarry, J, Woloszyn, F, Bertrand-Michel, J, Racke, I, Besir, H (2017) A genome scan for milk production traits in dairy goats reveals two new mutations in Dgat1 reducing milk fat content. *Scientific reports* **7**, 1872.

Miller, SA, Dykes, D, Polesky, H (1988) A simple salting out procedure for extracting DNA from human nucleated cells. *Nucleic acids res* **16**, 1215.

Mohammadi, K, Rashidi, A, Mokhtari, M, Nassiri, MB (2011) The estimation of (co) variance components for growth traits and Kleiber ratios in Zandi sheep. *Small Ruminant Research* **99**, 116-121.

Molabe, KM (2023) Investigation of single nucleotide polymorphisms of the growth hormone gene and its association with the growth traits of Dorper sheep. University of Limpopo.

Mukanova, L, Kırıkçı, K, Sadykulov, T, Baimazhi, Y, Zhumagaliyeva, G, Adylkanova, S (2024) Effect of DGAT1 gene polymorphisms in coarse-haired fat-tailed lambs of different genotypes. *Brazilian Journal of Biology* **84**, e285041.

Nanekarani, S, Kolivand, M, Goodarzi, M (2016) Polymorphism of a mutation of DGAT1 gene in Lori sheep breed. *J Adv Agri Tech* **3**,

Osman, NM, Shafey, HI, Abdelhafez, MA, Sallam, AM, Mahrous, KF (2021) Genetic variations in the Myostatin gene affecting growth traits in sheep. *Veterinary world* **14**, 475.

Örkiz, M, Fehmi, K, Çalta, H (1984) Some Important Production Traits of Akkaraman Sheep of Kangal Type. *Lalahan Animal Research Institution Journal* **24**, 15-33.

Öztürk, A (1995) Akkaramanlarda doğum ağırlığı ve gebelik süresinin tekrarlanma dereceleri. *Selçuk Üniversitesi Ziraat Fakültesi Dergisi* **6**, 188-193.

Pannier, L, Mullen, A, Hamill, R, Stapleton, P, Sweeney, T (2010) Association analysis of single nucleotide polymorphisms in DGAT1, TG and FABP4 genes and intramuscular fat in crossbred Bos taurus cattle. *Meat science* **85**, 515-518.

Rashidi, A, Mokhtari, MS, Jahanshahi, AS, Abadi, MM (2008) Genetic parameter estimates of pre-weaning growth traits in Kermani sheep. *Small Ruminant Research* **74**, 165-171.

Saleh, A, Hammoud, M, Dabour, N, Hafez, E, Sharaby, M (2020) Genetic variability in IGFBP-3 and GH genes and their association with body weight and growth performance at birth, weaning and six-month in sheep.

Souza, F, Mercadante, M, Fonseca, L, Ferreira, L, Regatieri, IC, Ayres, D, Tonhati, H, Silva, SdL, Razook, A, Albuquerque, LGd (2010) Assessment of DGAT1 and LEP gene polymorphisms in three Nelore (Bos indicus) lines selected for growth and their relationship with growth and carcass traits. *Journal of Animal Science* **88**, 435-441.

Tanış, AN, Keskin, İ (2025) Association between growth hormone gene polymorphism and some growth traits in Akkaraman and Anatolian Merino sheep. *Molecular Biology Reports* **52**, 54.

Wijayanti, D, Erdenee, S, Akhatayeva, Z, Li, H, Li, J, Cai, Y, Jiang, F, Xu, H, Lan, X (2022) Genetic polymorphisms within the ETAA1 gene associated with growth traits in Chinese sheep breeds. *Animal Genetics* **53**, 460-465.

Winter, A, Krämer, W, Werner, FA, Kollers, S, Kata, S, Durstewitz, G, Buitkamp, J, Womack, JE, Thaller, G, Fries, R (2002) Association of a lysine-232/alanine polymorphism in a bovine gene encoding acyl-CoA: diacylglycerol acyltransferase (DGAT1) with variation at a quantitative trait locus for milk fat content. *Proceedings of the National Academy of Sciences* **99**, 9300-9305.

Xu, QL, Chen, YL, Ma, RX, Xue, P (2009) Polymorphism of DGAT1 associated with intramuscular fat-mediated tenderness in sheep. *Journal of the Science of Food and Agriculture* **89**, 232-237.

Yang, J, Zang, R, Liu, W, Xu, H, Bai, J, Lu, J, Wu, J (2011) Polymorphism of a mutation of DGAT1 gene in four Chinese indigenous sheep breeds.

Yavuz, İH (2015) Akkaraman kuzularında yaşama gücü, büyüme ve vücut ölçüleri. Fen Bilimleri Enstitüsü.

Yeh, FC, Yang, R, Boyle, TB, Ye, Z, Mao, JX (1997) POPGENE, the user-friendly shareware for population genetic analysis. *Molecular biology and biotechnology centre, University of Alberta, Canada* **10**, 295-301.

Yen, C-LE, Stone, SJ, Koliwad, S, Harris, C, Farese Jr, RV (2008) Thematic review series: glycerolipids. DGAT enzymes and triacylglycerol biosynthesis. *Journal of lipid research* **49**, 2283-2301.