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RESEARCH ARTICLE

# Polymorphism Analysis of Milk Yield Candidate Genes in Turkish Native Goats: Honamlı and Hair Breeds

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**Abstract**

This study examined polymorphisms of nine genes (ADFP, AGPAT6, FOLR1, LHX3, PITX1, PITX2, PRLR, PROP1, and STAT5A) in Honamlı and Hair goats and compared allele and genotype frequencies with those reported in other breeds. A total of 200 goats (100 Honamlı, 100 Hair) were genotyped using PCR–RFLP. Allele and genotype frequencies were calculated, and deviations from Hardy–Weinberg equilibrium (HWE) were tested. Polymorphisms were identified in ADFP, AGPAT6, FOLR1, LHX3-1, LHX3-3, PITX1, PITX2-1, PRLR, and PROP1, whereas LHX3-2, PITX2-2, and STAT5A were monomorphic. ADFP showed C-allele/CC predominance with significant HWE deviation in both breeds. AGPAT6 (C-allele/CC) conformed to HWE, while FOLR1 (C-allele/CC) deviated only in pooled data. LHX3-1 (A-allele) was in HWE, whereas LHX3-3 (C-allele) deviated in both breeds. PITX1 (G-allele) was in HWE, while PITX2-1 (T-allele) was in HWE in Honamlı but deviated in Hair and pooled populations. PRLR (T-allele/TT) was in HWE, while PROP1 (C-allele/CC) deviated in Hair and pooled groups. STAT5A was fixed for CC. Turkish goats reveals allele predominance patterns and HWE deviations, suggesting effects of selection and population structure. These results enrich global goat genetic resources and support marker-assisted selection for milk traits.

**Keywords:** Candidate genes, Goat, Honamlı, Hair, Milk yield traits, Polymorphism

## INTRODUCTION

Milk trait is one of the economically important traits of goats. Due to the aspect of the quantitative traits, milk traits are determined by many genes and environmental factors [1-3]. There are many genes affecting milk traits in goats. Genetic polymorphisms occurring in genes determining milk traits may result in differences in milk traits of individuals within the population [2,4]. Depending on the variations, significant differences may occur in the milk phenotypes such as milk yield, milk fat, and milk [2,4-9].

Adipose differentiation-related protein (ADFP also known as PLIN2) is a member of the perilipin protein family and is involved in the transport and storage of neutral lipids in multiple cell types [10]. This protein family regulates body fat distribution and is found on the surface of lipid droplets in different tissues [11]. Several single nucleotide polymorphisms (SNP) were reported in the ADFP gene related to milk fat and total solid in Chinese dairy goats [10]. 1-acylglycerol-3-phosphate O-acyltransferase 6 (AGPAT6) is an important gene family that plays a role in the synthesis pathway of triglycerides in different cell types. AGPAT6 is one of the important genes in this family that plays a role in milk fat production in the mammary gland [12]. A SNP in the exon 4 of the AGPAT6 gene, 9263C>G, is associated with milk yield, milk protein, milk lactose, and milk fat revealing a favorable G allele in dairy goats [13,14]. The folate receptors (FOLR) bind folic acids with high affinity and consists of four members (FOLR1, FOLR2, FOLR3, FOLR4) [15,16], is an important regulator of folate metabolism for milk protein synthesis in the mammary gland. A potential SNP, 7884A>C, in exon 3 of the FOLR1 gene was reported in dairy Xinong Saanen and Guanzhong goat breeds [4]. The LHX3 (LIM homebox3) gene, a member of the LIM-homedomain gene family, plays a role in pituitary gland and nervous system development [8]. This gene affects milk traits by regulating the expression of genes related to milk production [17-19]. Several SNP in the intron2, exon 3, and exon 6 related to milk yield were reported in dairy Xinong Saanen goat.

Pituitary homeobox 1 (PITX1) and PITX2 are involved in several developmental pathways such as cell proliferation, differentiation, hematopoiesis, and organogenesis [9,20] and regulate milk traits in goats [7,9,21]. A novel 201G>A transition in the intron 1 of the PITX1 gene affected milk fat, protein, and milk yield in Guanzhong dairy goat [7]. Similar to PITX1 polymorphism, a novel SNP affecting milk yield, milk fat, and mil lactose was reported in Chinese dairy goats [9]. Prolactin is one of the most important genes that regulate milk traits [4]. Through its receptor, prolactin receptor (PRLR) which belongs to the growth hormone receptor family, this hormone promotes the development of the mammary glands and stimulates it to produce milk, lactose, fat, and proteins [22]. A C>T transition in the 3' UTR of the PRLR gene is associated with average milk yield in dairy goats [4]. Prophet of PIT-1 (PROP1) is expressed in the pituitary gland. It also controls the expression of growth hormone, prolactin, and thyroid-stimulating hormone subunits [2]. Alterations in the PROP1 gene can influence the expression of the POU1F1 gene [23]. Consequently, the PROP1 gene emerges as a promising candidate gene in farm animals. Studies indicate that PROP1 affects milk traits [2,24] and growth traits [25,26] in goats. In Malabadi goat, a SNP in exon 2 of the PROP1 is associated with yield, milk fat, and milk protein gene [2]. Signal transducers and activators of transcription (STATs), a family of transcription factors, regulate the effects of various hormones and cytokines. STAT5 can also be described as mammary gland factor [27]. STAT5A, one of the components of the STAT5 protein, is an important mediator of prolactin signaling and activates the transcription of milk protein genes in response to prolactin. Polymorphism in the STAT5A gene is associated with milk yield and milk fat in goats [5] and cattle [28]. Accumulative findings in the goat show that polymorphisms in these genes affect many milk traits such as milk yield, milk fat, milk protein, and lactose content [2,5,7-10,13,14,22,24].

Türkiye is one of the leading countries in Europe with its goat population. Novel data indicates that Türkiye has 10.8 million head goats from different breeds [29]. And, this number is higher than goat population of the all EU countries [30]. Hair, Honamlı, Angora, Kilis, and Norduz goats are the native goat breeds of Türkiye. However, the predominant goat breed is the Hair goat and extensively bred throughout the Anatolian region. Hair goat is a multipurpose breed and is raised for its meat, milk, and hair [31]. On the other hand, Honamlı goat is raised in a region compromise Burdur, Antalya, and Isparta provinces. Similar to the Hair goat, the Honamlı goat is raised for meat, milk, and hair [31,32]. While numerous studies have examined genetic regions potentially linked to economically important traits in Turkish goat breeds, research on this subject concerning Honamlı and Hair goat breeds is limited [33-35].

Considering this background, this study aimed to investigate the presence and distribution of polymorphisms in ADFP, AGPAT6, FOLR1, LHX3, PITX1, PITX2, PRLR, PROP1, and STAT5A genes, which can be used as genetic markers in further selection programs in Honamlı and Hair goats, two important native Turkish breeds.

## Material and Methods

### Ethical Statement

All experimental procedures were approved by the Burdur Mehmet Akif Ersoy University Animal Experiments Local Ethics Committee (Approval No: 713, dated 13.01.2021). Hair goats (n=100) and Honamlı goats (n=100) were used as animal materials in the study. All procedures were conducted in accordance with Directive 2010/63/EU on the protection of animals used for scientific purposes.

### Animal Material and Sampling

In the study, a total of 200 goats including Turkish Hair goats (n=100) and Honamlı goats (n=100) were used as animal material. Blood samples from the goats collected aseptically from the jugular vein were placed into 10 mL $K_3$-EDTA tubes for DNA isolation.

### DNA Isolation and DNA Quality Controls

Genomic DNA isolation from the collected blood samples was performed using a kit (GeneJET Genomic DNA Purification Kit) according to the instructions of the company. The purify and quantity of genomic DNA were evaluated according to the optical density values at 260/280 nm wavelength in Nanodrop 2000 (Thermo Scientific). The integrity of genomic DNA stained with ethidium bromide was evaluated on the 0.8% agarose gel under UV transilluminator.

### PCR-RFLP

*Table 1* shows primer pairs used for amplification of relevant gene regions and PCR conditions. PCR reaction was performed in 25 µL total volume with optimized concentration of 1X buffer, $MgCl_2$, dNTP, primers, and Taq DNA polymerase. Annealing temperature was optimized for PCR amplification of each gene region *(Table 1)*. Following PCR amplification, PCR products were evaluated on the 2% agarose gel under UV transilluminator.

PCR products of relevant genes were digested with restriction enzymes represented in *Table 1* according to the manufacturers' instructions (Thermo Scientific™). Following RFLP reaction, digested PCR products were visualized on the 3-4% agarose gel and evaluated for detection of genotypes.

***Table 1.*** *Primer pairs used, PCR product sizes, and restriction patterns of genes in the study*

| Gene | Primers (5'→3') | PCR Product Size (bp) | Enzyme | Restriction Pattern | Reference |
|---|---|---|---|---|---|
| ADFP | F: GTTTCCAATCGACCCCAGACG<br>R: TACACAAAACAGCCTCACTGG | 224 | *Hpy188I* | TT: 165+59<br>TC: 165+140+59+25<br>CC: 140+59+25 | [7] |
| AGPAT6 | F: ATCTGGCATTTTCACACATT<br>R: CTGACTCCATCTAAGAGCCT | 241 | *NcoI* | CC: 241<br>CG: 241+130+111<br>GG: 130+111 | [13] |
| FOLR1 | F: GTCCCTCCACCTGATGTT<br>R: CCTCCTCAGACCAGAATT | 414 | *SfaNI* | AA: 414<br>AC: 414+229+185<br>CC: 229+185 | [4] |
| LHX3 (1-2-3) | F: GCGTAACCAAGTCTGGAGCC<br>R: R:CAACACGAAGAGAGAGCACG | 205 | *DraI* | TT: 205<br>AT: 205+114+91<br>AA: 114+91 | Primers Designed in this study |
| | F: CTGCCCTTCCGAATTCACCTC<br>R: ATGAGATAGAACTCGTCGCCC | 381 | *HinfI* | CC: 381<br>CT: 381+285+96<br>TT: 285+96 | |
| | F: CCCTTCCTATCCAGCTTGGTG<br>R: GGTCCACCTCGTCCAACCAG | 187 | *MspI* | TT: 153+34<br>TC: 153+123+64+34<br>CC: 123+64 | |
| PITX1 | F: CCGCCTTCCACCTAGCCCGCAC<br>R: GCGTCCATGTCCACGTTCATCG | 230 | *MspI* | AA: 230<br>GA: 230+121+109<br>GG: 121+109 | [7] |
| PITX2 | F: TCGTCCATGAACTGCATGAAAGGC<br>R: AAAGGAAGGGAGGTCAGGGTCGTAAT | 432 | *RsaI* | TT: 432<br>TC: 432+319+113<br>CC: 319+113 | [9] |
| | F: TGGCCATGGCTTCGGTCCTGGCTCC<br>R: AAAGGAAGGGAGGTCAGGGTCGTAAT | 326 | *SmaI* | CC: 301+25<br>CG: 326+301+25<br>GG: 326 | |
| PRLR | F: AGTGAGAGTTATGGAAGGATG<br>R: AAGGTTAAGCAACTGGTCTT | 443 | *RsaI* | TT: 443<br>CT: 443+383+60<br>CC: 383+60 | [7] |
| PROP1 | F: GATGGATGGATGGGTCTCTG<br>R: TGGTGAAGGTTTGGGTTGG | 403 | *Hin6I* | CC: 223+152+28<br>CT: 251+223+152+28<br>TT: 251+152 | [2] |
| STAT5A | F: CTGCAGGGCTGTTCTGAGAG<br>R: TGGTACCAGCACTGTTAGCACAT | 215 | *Eco81I* | CC: 162+53<br>CT: 162+126+53+36<br>TT: 126+53+36 | [5] |

***ADFP:*** *Adipose Differentiation-Related Protein,* ***AGPAT6:*** *1-Acylglycerol-3-Phosphate O-Acyltransferase 6,* ***FOLR1:*** *Folate Receptor 1,* ***LHX3 (1-2-3):*** *LIM Homeobox 3,* ***PITX1:*** *P Pituitary homeobox 1,* ***PITX2:*** *Pituitary homeobox 2,* ***PRLR:*** *Prolactin Receptor,* ***PROP1:*** *Prophet of PIT1,* ***STAT5A:*** *Signal Transducer and Activator of Transcription 5A*

### Statistical Analyses

For each gene, allele and genotype were calculated frequencies using PopGene32 [36]. The chi-square test ($\chi^2$) was applied to determine whether the populations conformed to Hardy-Weinberg equilibrium.

## Results

### Allelic and Genotypic Distributions

In this study, polymorphisms in ADFP, AGPAT6, FOLR1, LHX3, PITX1, PITX2, PRLR, PROP1, and STAT5A genes were investigated in Honamlı and Hair goat breeds using PCR-RFLP. A total of 200 goats (100 Honamlı and 100 Hair goats) were genotyped, and allelic as well as genotypic distributions were determined *(Table 2)*. Successful amplification of target gene regions was confirmed by agarose gel electrophoresis.

For the ADFP gene *(Hpy188I),* three genotypes (TT, TC, CC) and two alleles (T and C) were identified in both Hair and Honamlı goats. Similarly, the AGPAT6 gene *(NcoI)* revealed three genotypes (CC, CG, GG) and two alleles (C and G) in both breeds. In the FOLR1 gene *(SfaNI),* AA, AC, and CC genotypes were detected with two alleles (A and C) *(Fig. 1)*. The LHX3-1 *(DraI)* locus showed polymorphism with TT, AT, and AA genotypes, while the LHX3-3 *(MspI)* locus exhibited TT, TC, and CC genotypes *(Fig. 1)*. However, the LHX3-2 *(HinfI)* locus was monomorphic in both breeds.

For the PITX1 gene *(MspI),* three genotypes (AA, GA, GG) and two alleles (A and G) were observed, whereas the PITX2-1 gene *(RsaI)* revealed TT, TC, and CC genotypes

***Table 2.*** *Allele and genotype frequencies of candidate genes in Hair and Honamlı goat*

| Gene | Breed | n | Allele Frequency | Observed Genotypes | Ho | He | $\chi^2$ | p |
|---|---|---|---|---|---|---|---|---|
| ADFP | Honamlı | 100 | T=0.16 C=0.84 | TT=7 TC=19 CC=74 | 0.19 | 0.28 | 10.12 | 0.01* |
| | Hair | 100 | T=0.21 C=0.79 | TT=8 TC=27 CC=65 | 0.27 | 0.34 | 4.25 | 0.04* |
| | Total | 200 | T=0.19 C=0.81 | TT=15 TC=46 CC=139 | 0.23 | 0.31 | 13.11 | 0.01* |
| AGPAT6 | Honamlı | 100 | C=0.88 G=0.12 | CC=78 CG=19 GG=3 | 0.19 | 0.22 | 1.91 | 0.17 |
| | Hair | 100 | C=0.82 G=0.18 | CC=67 CG=30 GG=3 | 0.3 | 0.29 | 0.01 | 0.90 |
| | Total | 200 | C=0.85 G=0.15 | CC=145 CG=49 GG=6 | 0.24 | 0.26 | 0.6 | 0.44 |
| FOLR1 | Honamlı | 100 | A=0.16 C=0.84 | AA=5 AC=22 CC=73 | 0.22 | 0.27 | 3.54 | 0.06 |
| | Hair | 100 | A=0.11 C=0.89 | AA=3 AC=16 CC=81 | 0.16 | 0.2 | 3.64 | 0.06 |
| | Total | 200 | A=0.14 C=0.86 | AA=8 AC=38 CC=154 | 0.19 | 0.23 | 7.22 | 0.01* |
| LHX3-1 | Honamlı | 100 | T=0.35 A=0.65 | TT=13 AT=44 AA=43 | 0.44 | 0.46 | 0.14 | 0.70 |
| | Hair | 100 | T=0.39 A=0.61 | TT=19 AT=40 AA=41 | 0.4 | 0.48 | 2.7 | 0.10 |
| | Total | 200 | T=0.37 A=0.63 | TT=32 AT=84 AA=84 | 0.42 | 0.47 | 2.06 | 0.15 |
| LHX3-3 | Honamlı | 100 | T=0.20 C=0.80 | TT=10 TC=21 CC=69 | 0.21 | 0.33 | 13.16 | 0.01* |
| | Hair | 100 | T=0.28 C=0.72 | TT=13 TC=30 CC=57 | 0.3 | 0.41 | 6.84 | 0.01* |
| | Total | 200 | T=0.24 C=0.76 | TT=23 TC=51 CC=126 | 0.25 | 0.37 | 19.09 | 0.01* |
| PITX1 | Honamlı | 100 | A=0.11 G=0.89 | AA=2 GA=18 GG=80 | 0.18 | 0.2 | 0.76 | 0.38 |
| | Hair | 100 | A=0.22 G=0.79 | AA=5 GA=33 GG=62 | 0.33 | 0.34 | 0.75 | 0.78 |
| | Total | 200 | A=0.16 G=0.84 | AA=7 GA=51 GG=142 | 0.25 | 0.27 | 0.87 | 0.35 |
| PITX2-1 | Honamlı | 100 | T=0.69 C=0.31 | TT=51 TC=36 CC=13 | 0.36 | 0.43 | 2.68 | 0.10 |
| | Hair | 100 | T=0.66 C=0.34 | TT=51 TC=31 CC=18 | 0.31 | 0.45 | 9.58 | 0.01* |
| | Total | 200 | T=0.68 C=0.32 | TT=102 TC=67 CC=31 | 0.33 | 0.44 | 11.15 | 0.01* |
| PRLR | Honamlı | 100 | C=0.08 T=0.92 | CC=1 CT=14 TT=85 | 0.14 | 0.15 | 0.31 | 0.58 |
| | Hair | 100 | C=0.16 T=0.84 | CC=4 CT=24 TT=72 | 0.24 | 0.27 | 1.28 | 0.26 |
| | Total | 200 | C=0.12 T=0.88 | CC=5 CT=38 TT=157 | 0.19 | 0.21 | 2.14 | 0.14 |
| PROP1 | Honamlı | 100 | C=0.92 T=0.08 | CC=85 CT=14 TT=1 | 0.14 | 0.15 | 0.31 | 0.58 |
| | Hair | 100 | C=0.83 T=0.17 | CC=71 CT=23 TT=6 | 0.23 | 0.29 | 4.41 | 0.04* |
| | Total | 200 | C=0.87 T=0.13 | CC=156 CT=37 TT=7 | 0.18 | 0.22 | 5.92 | 0.01* |

***ADFP:*** *Adipose Differentiation-Related Protein,* ***AGPAT6:*** *1-Acylglycerol-3-Phosphate O-Acyltransferase 6,* ***FOLR1:*** *Folate Receptor 1,* ***LHX3 (1-2-3):*** *LIM Homeobox 3,* ***PITX1:*** *P Pituitary homeobox 1,* ***PITX2:*** *Pituitary homeobox 2,* ***PRLR:*** *Prolactin Receptor,* ***PROP1:*** *Prophet of PIT1,* ***STAT5A:*** *Signal Transducer and Activator of Transcription 5A*

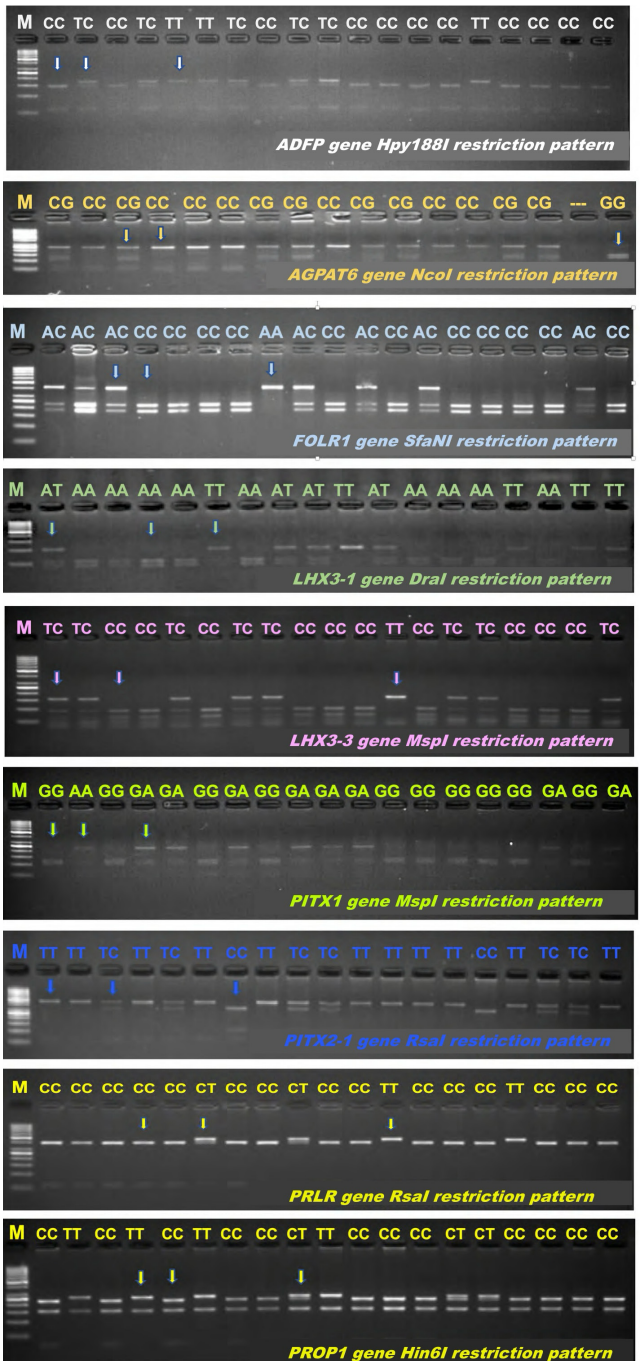


**Fig 1.** Restriction pattern of ADFP, AGPAT6, FOLR1, LHX3, PITX1, PITX2, PRLR and PROP1 genes. M: 100 bp DNA ladder

with T and C alleles *(Fig. 1)*. The PITX2-2 *(SmaI)* locus was found to be monomorphic. In the PRLR gene *(RsaI)*, CC, CT, and TT genotypes were identified, with C and T alleles segregating in both breeds. For the PROP1 gene *(Hin6I)*, CC, CT, and TT genotypes were also observed *(Fig. 1)*. Finally, the STAT5A gene *(Eco81I)* was found to be monomorphic in Honamlı and Hair goats.

Allele and genotype frequencies of each locus were also tested for Hardy-Weinberg equilibrium (HWE). While most loci were consistent with HWE, deviations were observed in some gene loci, suggesting selective pressures or breed-specific effects *(Table 2)*.

## Discussion

In this study, TT, TC, and CC genotypes of the ADFP gene were identified in the 5′UTR region of both Honamlı and Hair goat breeds. The $\chi^2$ test revealed a significant deviation from Hardy-Weinberg equilibrium ($P<0.05$), suggesting that selection, genetic drift, or population substructure might be influencing this locus. In contrast, polymorphisms at the same SNP locus were reported in Chinese dairy goats [10]. At the *Hpy188I* site in Xinong Saanen goats, TT, TC, and CC genotypes occurred at frequencies of 0.40, 0.54, and 0.06, with allele frequencies of T 0.67 and C 0.33. In Guanzhong goats, the respective frequencies were 0.32, 0.55, and 0.13 for genotypes, and 0.60 (T) and 0.40 (C) for alleles. For Xinjiang White Cashmere goats, TT and TC genotypes were observed at 0.45 and 0.55, while allele frequencies were 0.22 (T) and 0.78 (C). These findings showed that the T allele was more common in Xinong Saanen and Guanzhong breeds, whereas the C allele was dominant in Xinjiang White Cashmere goats. In contrast, our results demonstrated that the C allele predominates in both Turkish breeds, highlighting breed-specific differences. Although milk characteristics were not examined here, TT was associated with higher milk fat and CC with higher total solids in Xinong Saanen goats [10]. Thus, the dominance of the C allele and CC genotype in Honamlı and Hair goats may have implications for milk composition, which requires further study.

For the AGPAT6 gene, CC, CG, and GG genotypes were observed in both breeds, with the C allele and CC genotype being predominant. Genotype frequencies of 0.694 (CC), 0.198 (CG) and 0.108 (GG) and allele frequencies of 0.793 (C) and 0.207 (G) were reported at the *NcoI* site in Xinong Saanen goats [13]. In Guanzhong goats, frequencies were 0.623, 0.246, and 0.132 for CC, CG, and GG, with allele frequencies of 0.746 (C) and 0.254 (G). Both studies confirmed C allele predominance. In contrast, higher G allele frequencies were reported in the Saanen and Alpine breeds (C 0.36, G 0.64), and similar trends were found in the Saanen goats (C 0.336, G 0.664) (14,34). Our findings are consistent with a previous study supporting the dominance of the C allele in Turkish goats [37]. This study also indicated that GG and CG genotypes were associated with higher milk yield and quality compared to CC. Therefore, the dominance of CC in Honamlı and Hair goats could potentially indicate breed-specific limitations and warrant further association studies [13].

Regarding the FOLR1 gene, Honamlı goats showed genotype frequencies of 0.05 (AA), 0.22 (AC), and 0.73 (CC), while Hair goats showed 0.03, 0.16, and 0.81, respectively. Allele

frequencies were 0.16 (A) and 0.84 (C) in Honamlı, and 0.11 (A) and 0.89 (C) in Hair goats. Pooled data gave allele frequencies of 0.14 (A) and 0.86 (C). A monomorphic exon 3 pattern was reported in Xinong Saanen and Guanzhong goats, while polymorphism was seen in Boer goats with genotype frequencies of 0.07 (AA), 0.63 (AC) and 0.30 (CC) and allele frequencies of 0.38 (A) and 0.62 (C) [4]. While both studies confirm C allele predominance, our populations showed much lower A allele frequencies compared to Boer goats. These differences suggest breed-specific variation in FOLR1 polymorphisms.

For the LHX3 gene, at the LHX3-1 locus, Honamlı goats had genotype frequencies of 0.43 (AA), 0.44 (AT), and 0.13 (TT), while Hair goats showed 0.41, 0.40, and 0.19, respectively. The A allele was predominant in both breeds (0.65 and 0.61). Combined analysis yielded allele frequencies of 0.63 (A) and 0.37 (T), consistent with HWE. Similar results were reported in Guanzhong, Xinong Saanen, and Inner Mongolia White Cashmere goats, although some populations deviated from the HWE [8]. Additionally, A allele dominance was observed in Shami goats [38]. Thus, our results are in line with previous studies. However, at the LHX3-2 locus, our data showed monomorphism, unlike the reported balanced C and T alleles in Chinese goats [8]. At the LHX3-3 locus, C allele predominance was observed (0.80 in Honamlı, 0.72 in Hair), with significant HWE deviations in both breeds ($P<0.05$). More balanced allele frequencies were reported in Chinese goats [8], suggesting the existence of different selective or demographic forces shaping the diversity in Turkish breeds.

For the PITX1 gene, the G allele (0.77) was reported to be dominant in Guanzhong goats [7]. Similarly, Honamlı and Hair goats in our study showed high G allele frequencies (0.89 and 0.79). The genotype distributions were in HWE, consistent with Guanzhong goats. Since AG and GG genotypes were previously linked with improved milk traits [7], the high G frequency in Turkish breeds may also indicate favorable milk-related traits.

At the PITX2-1 locus, our study revealed TT genotype and T allele predominance (0.69 in Honamlı, 0.66 in Hair), with TT being the most common genotype. This contradicts the study [9] reporting near fixation of the C allele in Guanzhong goats, but is closer to the findings of higher T allele frequencies in Hainan black goats [39]. While Honamlı goats conformed to HWE, Hair goats and pooled data deviated significantly, suggesting possible selective effects. Both Turkish breeds were monomorphic (GG) at the PITX2-2 locus, which was consistent with other studies, indicating conservation of this locus [7,39].

For the PRLR gene, Honamlı and Hair goats showed predominance of the TT genotype and T allele with frequencies of 0.92 and 0.84, respectively. In contrast, the A allele is dominant in Chinese breed and significant deviations from HWE have been reported [4]. Our data, however, did not deviate from HWE, suggesting different evolutionary pressures in Turkish goats.

For the PROP1 gene, Honamlı and Hair goats displayed high C allele frequencies (0.92 and 0.83), consistent with previous studies [2,7,24]. However, unlike earlier reports, TT genotypes were detected at low frequency in our populations, especially in Hair goats. While Honamlı goats were in HWE, Hair goats showed a slight deviation, suggesting possible breed-specific variation.

Finally, for the STAT5A gene, both Honamlı and Hair goats were monomorphic (CC), while earlier studies in Guanzhong [5] and Garganica [40] goats reported presence of heterozygotes. This suggests reduced variability and possible fixation of the C allele in Turkish breeds.

Within the scope of the existing literature, this study appears to be one of the early examples focusing on polymorphisms in the ADFP, AGPAT6, FOLR1, LHX3, PITX1, PITX2, PRLR, PROP1, and STAT5A genes in Honamlı and Hair goats, two important native genetic resources of Türkiye. The results revealed both polymorphic and monomorphic patterns across different loci, with clear breed-specific differences in allelic and genotypic distributions. Notably, loci such as ADFP, AGPAT6, FOLR1, LHX3, PITX1, PITX2-1, PRLR and PROP1 exhibited substantial variation, while LHX3-2 and STAT5A were found to be monomorphic, suggesting possible fixation due to historical selection or genetic drift. In addition, certain loci such as ADFP, LHX3, and PITX1 showed relatively higher heterozygosity values, indicating their potential as informative genetic markers for milk production traits in Turkish goat breeds. Overall, our findings provide novel insights into the genetic diversity of Turkish native goats and offer a potential basis for ADFP, AGPAT6, FOLR1, LHX3, PITX1, PITX2-1, PRLR, PROP1 and LHX3 gene polymorphism studies aimed at improving milk yield and composition traits in these native breeds. However, since our study did not directly assess production traits, further research integrating polymorphism data with phenotypic performance records will be essential to clarify these associations and harness the genetic potential of Honamlı and Hair goats for sustainable breeding and conservation strategies.

## Declarations

**Availability of Data and Materials:** Data and Materials are available from the corresponding author (ÖKA).

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**Ethical Statement:** All experimental procedures were approved by the Burdur Mehmet Akif Ersoy University Animal Experiments Local Ethics Committee (Approval No: 713, dated 13.01.2021).

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**Declaration of Generative Artificial Intelligence (AI):** The article and tables and figures were not written/created by AI and AI assisted technologies.

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