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Molecular Assessment of Genetic Diversity and Bottleneck in Hair Goat Reared in Türkiye

ABSTRACT

Objective: Being the most preferred and geographically distributed in Türkiye, the Hair goat was screened at a molecular level to evaluate genetic diversity and population structure via microsatellite DNA markers. This paper also aimed to investigate the effects of genetic bottleneck to evaluate whether the Hair goat has maintained its effective population size in recent past.

Material and Methods: A total of 411 Hair goats were sampled from farms participating in the "Hair Goat Breeding" project, initiated by the General Directorate of Agricultural Research and Policies in Aydın and Denizli provinces. Sampled animals were genotyped with 18 microsatellite loci to assess genetic diversity, population structure, and genetic bottleneck.

Results: A total of 341 different alleles were observed across 18 microsatellite loci in which the highest number of alleles (26) and effective alleles (10.18) were detected in INRA005 and HSC loci, respectively. The average observed heterozygosity (0.73) was lower than the expected value (0.83), whereas all loci turned out to be highly informative (PIC>0.50). Factorial correspondence analysis separated animals into two groups, while a genetic admixture was detected between these groups. STRUCTURE analysis, on the other hand, confirmed that 411 animals were derived from three ancestral populations in which the third group is drawn due to admixed individuals. The Wilcoxon test and mode-shift indicator detected a lack of genetic bottleneck indicating that Hair goats reared in Türkiye have maintained their effective population size in recent past.

Conclusion: This study validates that used microsatellite markers are highly polymorphic and could be utilized for revealing genetic diversity in different local goat breeds. The findings recovered in this study could be integrated into breeding and conservation programs, while further studies should adopt SNP array technologies and next-generation sequencing platforms to reveal deeper knowledge about the genetic diversity and population structure of Anatolian goat breeds.

Keywords: Genetic variability, genetic variation, small ruminants, SSR markers

Türkiye'de Yetistirilen Kıl Keçilerinde Genetik Çesitlilik ve Darbogazın Moleküler Degerlendirmesi

ÖZ

Amaç: Türkiye'de en çok yetiştirilen ve coğrafi dağılıma sahip olan Kıl keçisi, mikrosatellit DNA belirteçleri aracılığıyla genetik çeşitliliği ve popülasyon yapısını değerlendirmek için moleküler düzeyde taranmıştır. Bu çalışma aynı zamanda Kıl keçisinin yakın geçmişte etkin popülasyon büyüklüğünü koruyup korumadığını değerlendirmek için genetik darboğazın etkilerini araştırmayı amaçlamıştır.

Materyal ve Methot: Aydın ve Denizli illerinde Tarımsal Araştırmalar ve Politikalar Genel Müdürlüğü tarafından başlatılan "Kıl Keçisi Islahı" projesine katılan çiftliklerden toplam 411 Kıl keçisi örneklenmiştir. Örneklenen hayvanlar, genetik çeşitlilik, populasyon yapısı ve genetik darboğazın değerlendirilmesi için 18 mikrosatellit lokusu ile genotiplendirilmiştir.

Bulgular: 18 mikrosatellit lokusundan toplam 341 farklı alel gözlenmiş olup, en yüksek alel sayısı (26) ve etkin alel sayısı (10.18) sırasıyla INRA005 ve HSC lokuslarında tespit edilmiştir. Gözlenen ortalama heterozigotluk (0.73) beklenen değerden (0.83) daha düşükken, tüm lokusların oldukça bilgilendirici olduğu ortaya çıkmıştır (PIC>0.50). Faktöriyel ilişki analizi hayvanları iki gruba ayırırken, bu gruplar arasında genetik bir karışım tespit edilmiştir. Öte yandan STRUCTURE analizi, 411 hayvanın üç atasal populasyondan türediğini ve üçüncü grubun karışmış bireylerden oluştuğunu doğrulamıştır. Wilcoxon testi ve mod kayması grafiği, Türkiye'de yetiştirilen Kıl keçilerinin yakın geçmişte etkin populasyon büyüklüğünü koruduğunu ve populasyonlarda herhangi bir genetik darboğazın bulunmadığını ortaya koymuştur.

Sonuç: Bu çalışma, kullanılan mikrosatellit belirteçlerin oldukça polimorfik olduğu ve farklı yerel keçi ırklarındaki genetik çeşitliliği ortaya çıkarmak için kullanılabileceği ortaya konmuştur. Bu çalışmadan elde edilen bulgular ıslah ve koruma programlarına entegre edilebilme özelliğine sahip olup, ileriki çalışmalarda Anadolu keçi ırklarının genetik çeşitliliği ve populasyon yapısı hakkında daha derin bilgi edinmek için SNP dizi teknolojileri ve yeni nesil dizileme platformları kullanılmalıdır.

Anahtar Kelimeler: Genetik çeşitlilik, genetik varyasyon, küçükbaş, SSR markörleri

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INTRODUCTION

Although small ruminant rearing is mostly practiced in a traditional way by smallholder farmers in Türkiye, it plays a significant role in the agricultural sector in producing animal-derived products such as milk and meat. According to Food and Agriculture Organization of the United Nations (FAO) statistics, the goat population in Türkiye for 2022 is 11,577,862 individuals (FAOSTAT, 2022). Although the intensity varies according to the regions, Hair goat, which is bred almost throughout the country, has a numerical superiority with a ratio of over 90%. Other local (Ankara, Norduz, Kilis, Aleppo, Gökçeada, Honamlı, Mahalli, İspir, Abaza, Kaçkar, Georgian, etc.) and exotic (Saanen, Maltiz, etc.) goat breeds and their crosses make up the remaining 10%.

While the number of goats in Türkiye was estimated at 24.6 million in the 1960s, this number decreased to 7.1 million in 2011 (Semerci and Çelik, 2016; Günlü and Mat, 2021). The "Goat Damage Reduction Action Plan" (Anonymous, 2008), prepared by the Ministry of Environment and Forestry and targeting goat species, especially the Hair goat breed, played a major role in this rapid numerical decrease. In the following years, due to the positive measures implemented by the public sector, the number of goats increased slightly to just above 10 million heads, but it did not reach the levels of the previous decades.

Local goat breeds are expected to be well-adapted to their reared climatic zones due to most probably developing adaptation against environmental stressors over generations via the natural selection (Demir et al. 2022). Hair goat breeding, which is carried out in a traditional structure throughout Türkiye, has an extensive structure (Cedden et al., 2020). Hair goats play a significant role in meeting the livelihood and food needs of the rural population residing in mountain villages near forests. In almost all regions of Türkiye, goat breeding is widely practiced in mountainous, forested, and maquis areas under extensive conditions. It is considered that there is uncontrolled mating in traditional extensive breeding, leading to populations seriously interbreeding.

Many studies (Daskiran et al., 2018; Elmaz et al., 2020; Demiraslan et al., 2021; Varol and Demirhan, 2022; Karaşahin et al., 2023) have revealed a wide phenotypic variation in Hair goat populations. The high phenotypic variation revealed by these studies is also an important indicator of genetic variation (Gül et al., 2020; Demiray et al., 2024). Therefore, it is also necessary to concretely demonstrate the genetic diversity in the population using molecular genetic techniques.

Objective identification of the genetic structure of existing animal populations is of great importance for breeding, conservation, and sustainable use of genetic resources. In Türkiye, several phenomena such as reduction in population size, migration, non-systematic mating, topological differences among regions, and farmer's preferences are of potential to directly affect genetic diversity and population structure in livestock species.

Therefore, this study aimed to investigate the genetic diversity in the Hair goat, which is the predominant goat breed in Türkiye, using microsatellite DNA markers at the molecular level. The study also aimed to assess the population for genetic bottlenecks and to identify any genetic changes that may have occurred in population structures.

MATERIAL and METHOD

Material

The animal material for the study comprised 411 hair goats from farms participating in the "Hair Goat Breeding" project, initiated by the General Directorate of Agricultural Research and Policies in Aydın and Denizli provinces. The distribution of the animal material sampled is provided in Table 1.

Table 1. Geographic distribution of sampling strategy
Tablo 1. *Örneklem stratejisine ait coğrafik dağılım*

Province	District	Farms	N
Aydın	Bozdoğan	9	84
	Çine	5	27
	Karacasu	13	130
	Kuyucak	1	33
Denizli	Babadag	1	18
	Cal	1	18
	Honaz	2	101
		Total	**411**

Method

DNA Extraction

DNA isolation from blood samples taken from the jugular vein into vacuum tubes containing K3-EDTA was performed using the salt precipitation method (Miller et al., 1988). After DNA isolation, the quantity and quality of DNA were determined using NanoDrop 2000 (Thermo Scientific, USA).

Polymerase Chain Reaction (PCR) and Genotyping

In this study, a total of 411 animals were genotyped with 18 FAO (2011) recommended microsatellite markers which were amplified as three multiplex groups (Table 2). Approximately 50 ng of DNA was used for the PCR in which 0.10 µM primer, 0.20 mM dNTPs, 2.0 mM MgCl2, 1X PCR buffer, and 1 unit of Taq DNA polymerase was used. The Touch-Down PCR method was used because the microsatellites in the multiplex groups formed in the study had different annealing temperatures (Table 2).

Table 2. Thermal cycler conditions according to the touchdown PCR method

Tablo 2. *Touchdown PCR yöntemine göre termal döngüleyici koşulları*

Multiplex Grup	Primer Name	First Denat.	Denat.	Annealing	Extension	Cycle	Final Extention
M1	INRA0023 INRA0005 OarFCB20 ILST0019 BM1818 INRA0132	95 °C (5 dk)	95 °C (40 sn)	60-50 °C (40 sn)	72 °C (1 dk)	30	72 °C (10 dk)
M2	CSRD0247 McM0527 SRCRSP0005 ILSTS0087 SRCRSP0023 HSC BM1329	95 °C (5 dk)	95 °C (40 sn)	60-50 °C (40 sn)	72 °C (1 dk)	30	72 °C (10 dk)
M3	INRA063 MAF0065 SRCRSP0008 SRCRSP0024 BM1258	95 °C (5 dk)	95 °C (40 sn)	63-50 °C (40 sn)	72 °C (60 sn)	30	72 °C (10 dk)

Statistical Analysis

GenAlEx (Peakall and Smouse, 2012) was used to calculate number of alleles (Na), mean number of alleles (MNa), number of effective alleles (Ne), observed heterozygosity (Ho), expected heterozygosity (He) values, and to perform chi-square ($\chi 2$) tests for Hardy-Weinberg equilibrium. The CERVUS 3.0.3 program (Kalinowski et al., 2007) was utilized to compute polymorphic information content (PIC) and null allele frequencies. FSTAT 2.9.3 (Goudet, 2002) was used to calculate Wright's F-statistics (Weir and Cockerham, 1984; Wright, 1990), the difference between breeds (DST), and the coefficient of gene difference (GST) parameters. Gene flow between populations and population dynamics were determined through factorial relationship analysis using the "AFC sur populations" module in GENETIX v4.05 (Belkhir, 2004).

The STRUCTURE program (Falush et al., 2003, 2007; Hubisz et al., 2009; Pritchard et al., 2010), which models a set of probability distributions using the Bayesian approach, was utilized to describe how populations are genetically structured and their relationships among each other. This approach helps the analysis produce more reliable results by considering uncertainties. Independent allele frequencies and admixture models, which are crucial for determining genetic variation and complexity within populations, were utilized in the analysis conducted using the STRUCTURE program. In order to obtain reliable results in the STRUCTURE analysis, the number of iterations was set to 20,000, and the number of Markov Chain Monte Carlo (MCMC) iterations used to estimate the posterior distribution was set to 100,000. Different cluster values (K=2-7) were analyzed with 20 replications. CLUMPAK (Kopelman et al., 2015) was used to visualize the results obtained from STRUCTURE. The optimal cluster (K) value was determined using the STRUCTURE HARVESTER program (Earl and Vonholdt, 2012) with the formula $\Delta K = m|L''(K)| / s[L(K)]$, as proposed by Evanno et al. (2005).

The obtained dataset was tested for genetic bottlenecks using 1000 simulations with Sign, Standardized, and Wilcoxon tests under the Infinite Allele Model (IAM), Stepwise Mutation Model (SMM), and Two-Phase Mutation Model (TPM) using Bottleneck 1.2.0.2 (Piry et al., 1999).

RESULTS

The microsatellite-based genetic polymorphism statistics for Hair goats reared in Aydın and Denizli provinces, which constitute the animal material of the study, are given in Table 3.

Table 3. Polymorphism statistics of microsatellite loci

Tablo 3. Mikrosatellit lokuslarına ait polimorfizm istatistikleri

Loci	Na	Ne	Ho	He	PIC	Wright's F-statistics			D_{ST}	G_{ST}	HWE	F(Null)
						F_{IS}	F_{IT}	F_{ST}				
INRA005	26	3.34	0.62	0.70	0.67	0.487	0.500	0.025	0.053	0.070	***	0.042
INRA0023	17	9.35	0.73	0.89	0.88	0.191	0.203	0.015	0.040	0.044	***	0.126
OARFCB20	25	6.74	0.84	0.85	0.84	-0.012	0.010	0.021	0.028	0.032	***	-0.010
ILTS0019	12	4.23	0.65	0.76	0.74	0.307	0.311	0.006	0.013	0.016	***	0.155
INRA0132	20	5.32	0.68	0.81	0.79	0.148	0.162	0.016	0.021	0.026	***	0.099
BM1818	17	7.47	0.76	0.87	0.85	0.108	0.115	0.007	0.029	0.034	***	0.070
BM1329	18	5.80	0.62	0.83	0.81	0.214	0.217	0.004	0.027	0.031	***	0.106
HSC	24	10.18	0.74	0.90	0.90	0.139	0.145	0.008	0.021	0.023	***	0.097
CSRD0247	21	7.13	0.92	0.86	0.85	-0.069	-0.056	0.012	0.061	0.070	***	-0.041
McM0527	15	6.54	0.72	0.85	0.83	0.130	0.146	0.018	0.046	0.054	***	0.104
SRCSRP0023	23	5.60	0.94	0.82	0.81	-0.163	-0.154	0.008	0.028	0.034	***	-0.107
ILTS0087	15	6.15	0.75	0.84	0.82	0.080	0.087	0.008	0.019	0.022	***	0.028
SRCSRP005	16	9.07	0.79	0.89	0.88	0.113	0.119	0.006	0.024	0.027	***	0.064
BM1258	18	8.97	0.60	0.89	0.88	0.296	0.299	0.005	0.029	0.032	***	0.021
SRCRSP0024	21	4.20	0.65	0.76	0.73	0.452	0.456	0.008	0.035	0.045	***	0.035
SRCRSP0008	21	5.59	0.69	0.82	0.80	0.270	0.282	0.016	0.029	0.035	***	0.178
INRA063	12	3.62	0.65	0.72	0.68	0.525	0.531	0.014	0.024	0.032	***	0.014
MAF0065	20	8.57	0.70	0.88	0.87	0.195	0.199	0.005	0.047	0.054	***	0.090
Mean	**18.94**	**6.55**	**0.73**	**0.83**	**0.81**	**0.182**	**0.191**	**0.011**	**0.032**	**0.038**		

Na: number of alleles, Ne: effective number of alleles, PIC: polymorphic information content, Ho: observed heterozygosity, He: expected heterozygosity, DST: the diversity between breeds, GST: coefficient of gene differentiation, HWE: Hardy-Weinberg Equilibrium, F(Null): null allele frequency, * p<0.05, ** p<0.01, *** p<0.001

A total of 341 alleles were observed in 18 microsatellite loci. The highest number of alleles was observed at the INRA005 (26), while the highest effective alleles were found at the HSC (10.18). PIC values, which are important indicators for understanding genetic diversity and population structure, varied between 0.67 (INRA005) and 0.90 (HSC). The average Ho value, which represents the ratio of heterozygous individuals in relation to the microsatellites studied, was 0.73. The overall averages of Wright's F-statistic values were 0.182, 0.191, and 0.011 for FIS, FIT, and FST, respectively. The mean value of GST, which indicates the level of genetic variation and is defined as the coefficient of gene variation, was 0.038 in the study. The overall mean of the coefficient of variation between races (DST) was 0.032. All microsatellites used in the study deviated from Hardy-Weinberg equilibrium. The null allele frequencies, which are crucial for assessing the accuracy and reliability of genetic analyses, were below 0.20. Summary of genetic diversity parameters per population is given in Table 4.

Table 4. . Polymorphism statistics, the number of alleles not in Hardy-Weinberg equilibrium, and the number of unique alleles for populations.

Tablo 4. *Populasyonlara ait polimorfizm istatistikleri, FIS değerleri, Hardy-Weinberg dengesinde olmayan allel sayısı ve özgün allel sayıları*

Population	MNA	Heterozygosity		F_{IS}	HWE	NPA	
		Ho (SE)	He (SE)			(>%5)	(<%5)
Aydın	16.89	0.66 (0.042)	0.82 (0.016)	0.194	18	-	75
Denizli	14.78	0.69 (0.045)	0.83 (0.014)	0.176	17	-	37

MNA: Mean number of alleles, HWE: Hardy-Weinber Equilibrium, NPA: number of private alleles

Allelic diversity is an indicator of genetic diversity within a breed. The highest average allele number was observed in the Aydın Hair goat population (16.89). When the FIS values, which are defined as the inbreeding coefficient, were analyzed, there was no loss of heterozygosity in two different populations. The χ2 test results for Hardy-Weinberg equilibrium showed that 18 and 17 microsatellite loci were not in equilibrium in the Aydın and Denizli populations, respectively. The Aydın population exhibited the highest number of unique alleles the frequencies of which were lower than 5%. The graph of the factorial correspondence analysis (FCA) performed to visualize the genetic relationships and structure among populations is shown in Figure 1.

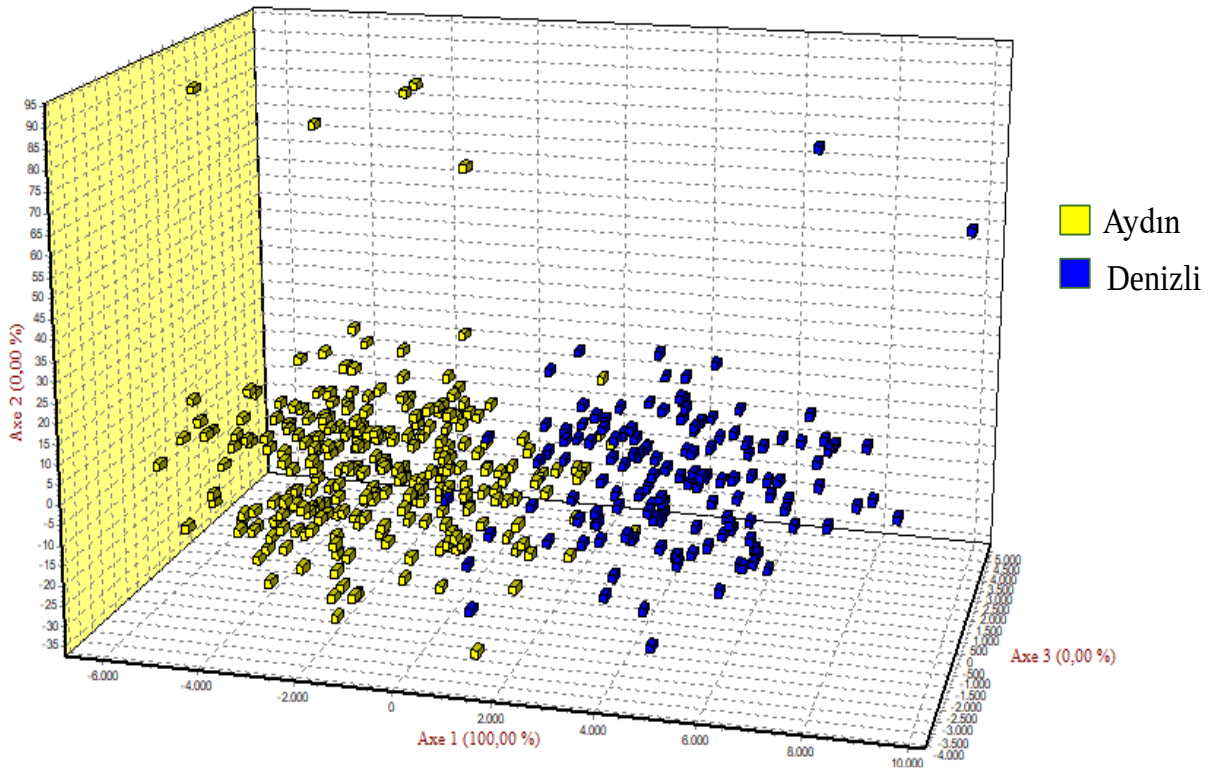

Figure 1. Factorial Correspondence Analysis (FCA) graph illustrating the relationship between hair goat populations in two distinct provinces

Şekil 1. *İki farklı ilde yetiştirilen Kıl keçi populasyonları arasındaki ilişkiyi gösteren Faktöriyel İlişki Analizi (FCA) grafiği*

In the FCA graph, it is noteworthy that the hair goat populations raised in Aydın and Denizli provinces are somewhat intertwined. STRUCTURE analysis results, including different clustering numbers (K=2-7), are presented in Figure 2. The findings also include the estimation of posterior probabilities ([Ln Pr(X|K)]) for clustering numbers (K) and ΔK values, as shown in Table 5.

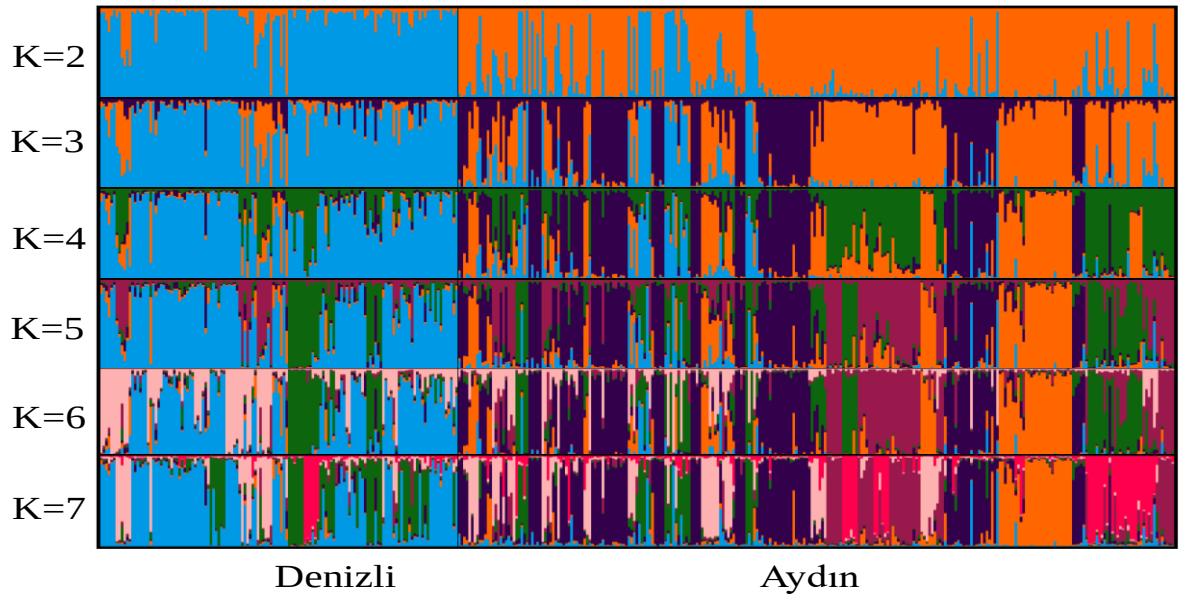

Figure 2. STRUCTURE analysis results of goat hair populations bred in two different provinces (K=7)

Şekil 2. *İki farklı ilde yetiştirilen Kıl keçi popülasyonlarındaki STRUCTURE analiz sonuçları (K=2-7)*

The results of STRUCTURE analysis revealed that the studied populations were partially admixed. The optimal number of ancestral populations, based on the ΔK value obtained using the method proposed by Evanno et al. (2005), was 3 (Table 5).

Table 5. . Estimated posterior probabilities [Ln Pr(X|K)], (K), and ΔK statistics for STRUCTURE analysis

Tablo 5. *STRUCTURE analizine ait tahmini posterior olasılıkları [Ln Pr(X|K)], (K), ve ΔK istatistikleri*

K	[Ln Pr(X|K)]	ΔK
2	-30098.20000	-
3	**-29622.51000**	**49.60589**
4	-29371.16000	0.30711
5	-29097.04500	0.22660
6	-28793.16000	4.01587
7	-28646.71000	-

The obtained dataset was tested using three different mutation models: the Infinite Allele Model (IAM), Stepwise Mutation Model (SMM), and Two-Phase Model of Mutation (TPM) as reported by Cornuet and Luikart (1996), Luikart and Cornuet (1998), and Piry et al. (1999) (Table 6).

Table 6. . Bottleneck analysis results based on three different mutation models

Tablo 6. *Üç farklı mutasyon modeline göre gerçekleştirilen darboğaz analiz sonuçları*

Breeds	Mutation	Sign test				Standardized differences test		Wilcoxon rank test (one tail for H excess)
		Hee	Hed	He	P	T2	P	P
Hair Goat (Aydın)	IAM	10.95	2	16	0.00988	2.482	0.00654	0.00168
	TPM	10.61	10	8	0.15564	-3.535	0.00020	0.87690
	SMM	10.43	17	1	0.00000	-16.953	0.00000	1.00000
Hair goat (Denizli)	IAM	10.87	2	16	0.00897	3.191	0.00071	0.00005
	TPM	10.61	8	10	0.47231	-0.940	0.17365	0.60065
	SMM	10.51	16	2	0.00005	-10.257	0.00000	0.99999

IAM: The infinite allele model, TPM: Two-phase mutation model, SMM: The stepwise mutation model, Hee: Expected number of loci with heterozygosity excess, Hed: heterozygosity deficiency, He: heterozygosity excess

The expected numbers of loci with heterozygous excess in the two different goat hair populations studied were found to be 10.61 (p>0.05) in the Wilcoxon rank test for the Aydın population and 10.61 (p>0.05) for the Denizli population. In order to identify potential bottlenecks in the studied populations, a mode-shift plot was generated using allele frequency classes of 18 microsatellite loci (Figure 3).

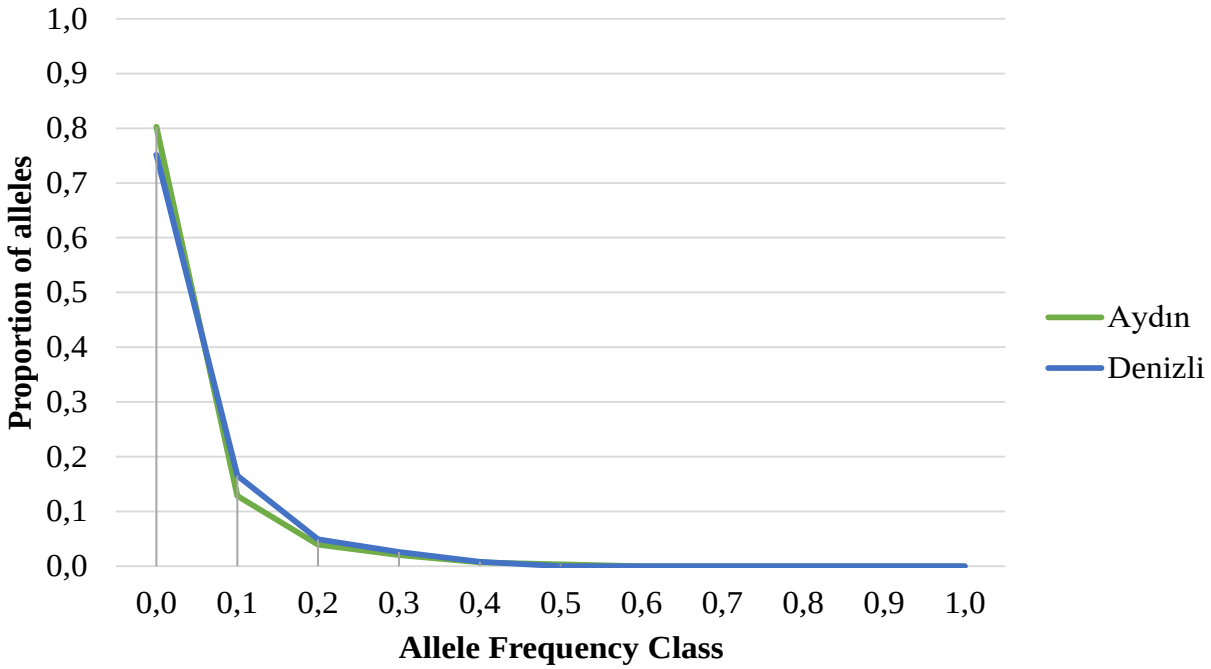

Figure 3. Mode-shift graph for the bottleneck analysis of the hair goat populations studied

Şekil 3. *Çalışılan kıl keçi popülasyonlarında gerçekleştirilen darboğaz analizine ilişkin mode-shift grafiği*

An L-shaped graph consistent with the distribution ranges of the normal frequency class was obtained from the mode-shift indicator.

DISCUSSION and CONCLUSION

The number of alleles and the average polymorphic information content obtained indicate that the 18 microsatellite loci used in the study exhibit a very high level of polymorphism. The high frequencies of observed heterozygosity and the average number of alleles at each locus are important indicators of the high genetic diversity in the studied Hair goat populations. Molecular genetic parameter values such as Na, Ne, Ho, and He obtained from the present study were higher than those reported in some studies (Agaoglu and Ertugrul, 2012; Bulut et al., 2016; El-Sayed et al., 2016; Karslı et al., 2020) and lower than those in others (Murital et al., 2015; Gül et al., 2020; Demiray et al., 2024). The Na and Ne parameters indicate that the microsatellite loci used in the studied populations are highly polymorphic. On the other hand, the average PIC value supported the reliability of this finding and was higher than the values reported in the literature (Li et al., 2008; Serrano et al., 2009; Mahmoudi et al., 2010; Wang et al., 2011; Souza et al., 2012; Murital et al., 2015). This discrepancy in the literature was attributed to variations in the breed, breeding methods, and microsatellites utilized in other studies.

When the FIS values obtained are analyzed, it is noteworthy that there is a loss of heterozygosity in the studied loci OarFCB20, CSRD0247, and SRCSRP0023. The average FST value for the studied loci indicates low genetic diversity among populations. Considering that the animal material used in the study included individuals of the same breed raised in different regions, it can be said that this finding is expected. The FST value obtained was higher than reported in some literature (Li et al., 2008; Mahrous et al., 2013; Whannou et al., 2022; Demiray et al., 2024). The GST value, which indicates the rate of genetic variation, demonstrates that 96.20% of the total genetic variation can be attributed to differences among individuals. The overall average of the genetic diversity value (DST) indicates that the diversity among populations is not high. As a matter of fact, this finding also supports the previously mentioned FST and GST findings. Allele distributions of all microsatellite markers were found to deviate from Hardy-Weinberg equilibrium. Animal material was obtained from the farms participating in the breeding project. Within this context, selection practices are implemented on these farms as part of the breeding program. Given this scenario, the deviations of the studied microsatellites from the Hardy-Weinberg equilibrium seem to be a common occurrence.

The MNa and He values obtained for the populations in this study were higher than the values reported in the literature (Li et al., 2008; Afroz et al., 2010; Mahmoudi et al., 2010; Mahrous et al., 2013). When the FIS values, which represent the inbreeding coefficient, were analyzed, it was observed that there was no loss of heterozygosity in two different populations. A total of 112 unique alleles were observed in the two populations studied. The Aydın population exhibited the highest number of unique alleles. However, the frequency of all unique alleles was below 5%. In other words, the ability of the unique alleles to distinguish between populations is very weak. This is a result of working in a single breed.

When the FCA graph was analyzed, two different groups were observed. It was noted that some animals from the animal material used in the study were outside of these groups. It is noteworthy that there is no clear distinction between the two Hair goat populations, and some individuals are clustered in a separate group. As a matter of fact, a similar situation is also observed in the results of STRUCTURE analysis. The ΔK value obtained using the method described by Evanno et al. (2005) indicated that the optimal number of groups was 3. This supports the results obtained in the FCA analysis. Although studies on the determination of genetic diversity of Hair goats in different regions in Türkiye are limited, most of the studies conducted on goats in Türkiye have revealed a similar population structure (Gül et al., 2020; Karslı et al., 2020; Demiray et al., 2024). Therefore, the population structures identified in this study are consistent with those of other studies.

The IAM and SMM are known to cause inconsistent results in studies utilizing microsatellites. Therefore, the TPM has been reported to be the most useful model for testing heterozygote redundancy in bottleneck tests with microsatellites (Di Rienzo et al., 1994; Luikart et al., 1998; Piry et al., 1999). On the other hand, it has been reported that the Wilcoxon test can be used with high confidence even in studies using a limited number of loci (less than 20) for bottleneck analysis (Piry et al., 1999). In this context, the expected numbers of loci with heterozygous excess in the TPM analysis and the results of the Wilcoxon test did not reveal any genetic bottleneck in the Hair goat populations bred in Aydın and Denizli province. This is the most concrete indication that animal transfers between farms are carried out in a systematic way. A similar situation in hair goats in Türkiye (Agaoğlu and Ertugrul, 2012) also revealed a similar situation.

In conclusion, molecular genetic studies aimed at defining the variations among and within domestic goat breeds in Türkiye, particularly the Hair goat populations, which are bred in numerous regions and constitute the majority of our goat population, are limited. In this context, this study is expected to make significant contributions to the literature. The results obtained show that the diversity among individuals in the studied populations is higher than the diversity among populations. This situation can be seen as an opportunity for breeding programs and genetic resource conservation programs. The findings obtained in this study demonstrate that the microsatellite markers utilized are polymorphic and can be effectively employed in genetic diversity studies. The findings of this study clearly demonstrate that the microsatellites utilized can safely determine genetic diversity in Hair goat populations.

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