Kafkas Univ Vet Fak Derg
19 (2): 207-213, 2013
DOI: 10.9775/kvfd.2012.7475

Journal Home-Page: http://vetdergi.kafkas.edu.tr
Online Submission: http://vetdergikafkas.org

RESEARCH ARTICLE

Genetic Diversity of Three Native Goat Populations Raised in the South-Eastern Region of Turkey [1]

Şükrü GÜRLER * Faruk BOZKAYA *

[1] *This work was supported by Harran University Scientific Research Projects Coordination (HUBAK-65)*

* Harran Üniversitesi, Veteriner Fakültesi, Genetik Anabilim Dalı, TR-63100 Eyyübiye, Şanlıurfa - TÜRKİYE

Makale Kodu (Article Code): KVFD-2012-7475

Summary

The aim of this study was to investigate the genetic variability of three goat populations raised in the Southeastern region of Turkey by using microsatellite loci defined in gazelle *(Gazella granti)*. DNA was isolated from 120 blood samples collected from goats raised in Sanliurfa (n = 40), Kilis (n = 40) and Siirt (n = 40) provinces. Eight microsatellite loci (33HDZ8, 33HDZ290, 33HDZ433, 33HDZ496, 33HDZ593, 33HDZ692, 33HDZ749, 33HDZ974) were used for amplification with polymerase chain reaction (PCR). Fragment lengths of the amplifed loci were analysed using a capillary electrophoresis system. Six of the eight loci (75%) were successfully amplified and four (66.7%) of them were polymorphic. Three of the polymorphic loci (33HDZ496, 33HDZ749 ve 33HDZ974) were used for estimating genetic parameters. A total of 40 alleles were detected. Number of alleles and polymorphism information contents (PIC) for the loci 33HDZ496, 33HDZ749 and 33HDZ974 were 13, 15 and 12 and 0.836, 0.821 and 0.817, respectively. The mean number of alleles was 10.33±1.15, 10.67±2.08 and 11.33±0.58 and effective number of alleles was 6.131±1.42, 5.823±0.23 and 5.870±0.75 for Sanliurfa, Kilis and Siirt populations, respectively. The mean observed and expected heterozygosities for Sanliurfa, Kilis and Siirt populations were 0.827±0.083, 0.808±0.044 and 0.895±0.069 as well as 0.843±0.043, 0.841±0.007 and 0.838±0.023 respectively. For the 33HDZ496, 33HDZ749 and 33HDZ974 loci FIS values were 0.0164, 0.0245 and 0.0240, respectively. The FST values (0.009) showed that about 99% of the genetic variation was due to variation among individuals. The results have suggested that the three populations studied have a high genetic variability and the loci, 33HDZ496, 33HDZ749, 33HDZ974, can be used as markers due to their high number of alleles (≥12) and PIC (>0.81) values.

Keywords: *Goat, Microsatellite, Genetic diversity*

Güney Doğu Anadolu Bölgesi'nde Yetiştirilen Üç Keçi Populasyonunda Genetik Çeşitlilik

Özet

Bu çalışma bir ceylan türünde *(Gazella granti)* tanımlanmış sekiz mikrosatelit lokusunu kullanarak Güneydoğu Anadolu Bölgesinde yetiştirilen üç keçi populasyonunu genetik çeşitlilik yönünden değerlendirmek amacıyla yapılmıştır. Bu amaçla, Şanlıurfa (n = 40), Kilis (n = 40) ve Siirt (n = 40) illerinde yetiştirilen üç keçi populasyonundan toplam 120 adet kan örneği alınmış ve bu örneklerden DNA izole edilmiştir. İzole edilen DNA'lar sekiz mikrosatelit lokusuna (33HDZ8, 33HDZ290, 33HDZ433, 33HDZ496, 33HDZ593, 33HDZ692, 33HDZ749, 33HDZ974) ait primerler kullanılarak PCR ile çoğaltılmış ve PCR ürünleri kapillar elektroforeze tabi tutularak fragman uzunluğu analizi gerçekleştirilmiştir. Sekiz lokustan altısı (%75) PCR ile amplifiye olmuş ve bunlardan dördü (%66.7) polimorfik bulunmuştur. Polimorfik lokusların üçü (33HDZ496, 33HDZ749 ve 33HDZ974) genetik parametrelerin hesaplanmasında kullanılmıştır. Çalışmada toplam 40 allel tespit edilmiştir. 33HDZ496, 33HDZ749 ve 33HDZ974 lokusları için sırasıyla 13, 15 ve 12 allel gözlenmiş olup, herbir lokus için hesaplanan polimorfizm bilgi içeriği (PIC) aynı sırayla 0.836, 0.821 ve 0.817 olarak belirlenmiştir. Şanlıurfa, Kilis ve Siirt populasyonları için ortalama allel sayıları sırasıyla 10.33±1.15, 10.67±2.08 ve 11.33±0.58, etkili allel sayıları ise yine aynı sıra ile 6.131±1.42, 5.823±0.23 ve 5.870±0.75 olarak bulunmuştur. Şanlıurfa, Kilis ve Siirt populasyonları için ortalama gözlenen heterozigotluk oranları sırasıyla 0.827±0.083, 0.808±0.044 ve 0.895±0.069, beklenen heterozigotluk oranları ise yine aynı sıra ile 0.843±0.043, 0.841±0.007 ve 0.838±0.023 olarak belirlenmiştir. 33HDZ496, 33HDZ749 ve 33HDZ974 lokusları için hesaplanan FIS değerleri sırasıyla 0.0164, 0.0245 ve 0.0240 olarak bulunmuştur. Tüm populasyonlar için hesaplanan FST değeri (0.009) incelenen populasyonda gözlenen genetik çeşitliliğin %99'unun bireyler arasındaki farklılıktan kaynaklandığını göstermiştir. Çalışma sonuçları incelenen keçi populasyonunun oldukça yüksek bir genetik çeşitliliğe sahip olduğunu göstermiştir. Çalışma sonuçları ayrıca, sahip oldukları yüksek allelik zenginlik (≥12) ve PIC (>0.81) değerleri nedeniyle incelenen sekiz mikrosatelit lokusundan üçünün (33HDZ496, 33HDZ749, 33HDZ974) keçilerde moleküler belirteç olarak kullanılabileceğini göstermiştir.

Anahtar sözcükler: *Keçi, Mikrosatelit, Genetik çeşitlilik*

İletişim (Correspondence)
+90 414 3183906
gurler@harran.edu.tr

INTRODUCTION

Goats were domesticated about 10.000 years ago in the region defined as Fertile Crescent [1-4] partially including the Southeastern Anatolia. Goats are able to utilize roughage of lower quality and are adapted to various environmental conditions [5]. Although goat breeding has a lower proportion in the food production of animal origin in the world, still preserves its importance, especially for developing countries [6,7]. While presence of goats increased approximately three-fold between 1970 and 2010 in the world, the number of goats in Turkey decreased from 20 to 5 million [8,9]. On the other hand extensive goat breeding in South-eastern Anatolia still plays an important role in the regional economy.

Using a limited number of animals with high breeding values has resulted in a decrease of the number of local breeds or their extinction. This leads to a dramatic decline in the genetic variablity within local breeds. Therefore programs of national and international levels have been developed in order to maintain the genetic variability of livestock and several strategy papers have been published by the Food and Agriculture Organization [10,11]. The first step towards maintaining the genetic variability of local genetic resources is to assess their genetic potential in terms of genetic diversity [12]. Microsatellites are most common genetic markers used for determining genetic variabiliy, due to their high polymorphism, abundance in the genome and quasi neutral nature in terms of selection [13].

Primer binding regions of some microsatellite loci are highly conserved, which allows the use of same microsatellite markers in closely related species such as cattle, sheep and goat. For example, about 70-73% and 60% of the bovine derived microsatellites can be amplified with 60% and 40% of these are polymorphic in sheep and goat, respectively [14-17].

The purpose of this study was to investigate the utility of eight microsatellite loci defined in gazelle [18] *(Gazella granti)* as a molecular marker of genetic diversity in three goat populations raised in the Southeastern Anatolia Region of Turkey.

MATERIAL and METHODS

Sampling of Animals

A total of 120 blood samples were collected from goats raised in Kilis (n = 40), Sanliurfa (n = 40), and Siirt (n = 40) provinces of Turkey. Kilis goat has been developed by crossing native Hair goats with Aleppo goats and by subsequent interbreeding among the crossbred generations. This goat has been considered a separate breed. Kilis goats are distributed especially in the Kilis province and also raised in the provinces along the Syrian border of Turkey. They are kept in small flocks of 2 to 10 goats primarily for milk production. The samples collected from the Sanliurfa province included Aleppo goats, hair goats and the crossbred animals of these two breeds. The samples from the Siirt province included native hair goats and their crossbred animals with Angora goats.

DNA Analysis

DNA was isolated using Proteinase-K digestion and phenol-chloroform extraction according to Sambrook et al.[19]. DNA was purified using ethanol precipitation and the concentration of DNA was measured spectrophotometrically. The DNA samples were diluted to an end concentration of 100 ng/µl.

Eight microsatellite loci were amplified using primer pairs designed by Huebinger et al.[18] in *Gazella granti*. Polymeraze chain reaction (PCR) conditions were optimized by changing $MgCl_2$ concentrations and annealing temperatures. One of the primers of the loci successfully amplified was labeled with a fluoresecent dye for fragment length analysis. Fragment lengths of the PCR products were analyzed by using a capillary electrophoresis (Applied Biosystems, 3130xl Genetic Analyzer, Foster City CA). For detecting the alleles, peak scanner software v1.0 (Applied Biosystems) was used.

Data Analysis

Number of alleles (NA), allele frequencies, number of population specific alleles, observed (Ho) and expected heterozygosities (He) and probability of exclusion (PE) were calculated by using GenAlEx.6 software package [20]. Polymorphism information content (PIC) was calculated according to Botstein et al.[21]. Expected heterozygosities [22] (He), effective allele numbers [23] (NE), F statistics [24], exact test for deviations from Hardy-Weinberg equilibrium (HWE), genetic differentiation between populations and pair-wise linkage disequilibrium were estimated using GENEPOP [25] package (version 3.1). The program performs a probability test using a Markov Chain (dememorization 1000, batches 100, iterations per batch 1000) method. Presence of putative null alleles was tested by using Expectation Maximization (EM) algorithm [26] in FreeNA [27] program. Nei's original measures of genetic distance among populations [28] and gene flow (Nm) were computed by POPGENE [29] (version 1.31). Analysis of molecular varians (AMOVA), and pairwise F_{ST} differences were computed using ARLEQUIN [30]. FSTAT [31] (version 1.2) was used for calculating allelic richness (AR) (number of alleles in sample of standardized size was 31).

RESULTS

Using PCR method six loci were successfully amplified while two loci (33HDZ290 and 33HDZ433) yielded no PCR product. The optimized PCR conditions, size ranges of the PCR products and the fluorescent dye used for each loci are shown in *Table 1*.

Table1. *Details of microsatellite marker loci and PCR conditions*
Tablo 1. *Mikrosatelit belirteçleri ve PCR koşulları*

Loci	Template DNA (µl)	$MgCl_2$ (mM)	dNTP (mM)	Primers (µM)	Taq DNA Pol. (IU)	Annealing Temp. (°C)	Size Range (bp)	Florescent Label
33HDZ8	1	2	0.2	0.4	1.0	58	150-190	(NED)
33HDZ496	2	2	0.2	0.4	0.5	58	230-300	(FAM)
33HDZ593	1	2	0.2	0.4	0.5	58	200-210	(FAM)
33HDZ692	1	2	0.2	0.4	0.5	58	200-250	(NED)
33HDZ749	1	2.5	0.2	0.8	1.0	50	180-190	(HEX)
33HDZ974	1	2	0.2	0.4	0.5	58	270-290	(HEX)

One of the loci (33HDZ593) was monomorphic. For the 33HDZ8 locus two fragments of 165 and 169 bp length were observed, while for the 33HDZ692 locus PCR products of four different fragment lengths ranging from 267 to 270 bp were observed. Since 33HDZ8 and 33HDZ692 loci exhibited numerous non specific PCR products they were not included in the further analyses.

A total of 40 different alleles were detected for the three polymorphic loci in the three populations studied *(Table 2)*. Observed allele numbers and effective allele numbers for the loci 33HDZ496, 33HDZ749 and 33HDZ974 were 13, 15 and 12 as well as 6.69, 6.168 and 6.096 respectively. The mean number of alleles per locus was 13.33. Values of PIC and PE varied from 0.817 to 0.836 and from 0.679 to 0.710, respectively *(Table 3)*. The lowest heterozygosity was observed for the 33HDZ974 locus in Sanliurfa (0.7429) and the highest was observed for the same locus in Siirt population (0.9474). The lowest and highest expected heterozygosities were estimated for the 33HDZ974 (He = 0.795) and 33HDFZ496 (He = 0.8778) , in the Sanliurfa population, respectively *(Table 3)*.

Kilis population exhibited a heterozygosity deficiency for the 33HDZ749 locus (F_{IS} = 0.051, P<0.05), while in Siirt population an excess of heterozygotes for the 33HDZ974 locus (F_{IS} = -0.108, P<0.05) was observed. When the three populations were evaluated together the F_{IS} values were not diffferent from zero (P>0.05).

Genetic parameters in the three populations estimated by considering the three loci were shown in *Table 4*. A total of 31, 32 and 34 alleles were detected in Sanliurfa, Kilis and Siirt populations, respectively. Mean number of alleles and effective allele numbers per locus were 10.33, 10.67 and 11.33 as well as 6.13; 5.82 and 5.87 Sanliurfa, Kilis and Siirt populations, respectively.

Observed and expected heterozygisities varied from 0.808 to 0.895 and from 0.838 to 0.843 respectively. Deviation from the expected heterozygosity was only observed in Siirt population due to an excess of heterozygotes. However, the overall F_{IS} value in this population was not significantly different from zero. Deviations from Hardy-Weinberg equilibrium were observed in the Kilis population for the loci 33HDZ496 and 33HDZ749 due to a deficiency of heterozygotes and in the Siirt population for the locus 33HDZ974 due to an excess of heterozygotes.

The mean F_{ST} values for the loci 33HDZ496, 33HDZ749 and 33HDZ974 were 0.003, 0.007 and 0.016 respectively *(Table 5)*. The mean F_{ST}, F_{IT} and F_{IS} values were 0.009, 0.004 and 0.006 respectively. Number of migrants estimated based on F_{ST} values was estimated to be 16.57.

Genetic differentiation among three populations was found to be significant (P<0.05) for the 33HDZ974 locus which was estimated using exact G test. F_{ST} values estimated for population pairs varied from 0.0062 to 0.0139 *(Table 6)*. In exact G test significant differentiations were oserved between Sanliurfa and Kilis for the 33HDZ496, Sanliurfa and Siirt for the 33HDZ974 and Kilis and Siirt for the 33HDZ749 loci (P<0.05). Differentition between population pairs estimated by including the three loci was insignificant (P>0.05). AMOVA results showed that 0.9% of the total variance was explained by the variation among populations *(Table 7)*. Significant linkage disequilibrium was observed only in Siirt population between the loci 33HDZ496 and 33HDZ749. Presence of null alleles was not detected.

DISCUSSION

In this study six of eight loci (75%) were successfully amplified and four of these six loci (66.6%) were polymorphic. These findings are similar to those reported by other researchers who used microsatellite loci in different species [14,16,17]. Fragment lengths of the loci 33HDZ496, 33HDZ749 and 33HDZ974 in *Gazella granti* varied from 231 to 247, from 187 to 237 and from 253 to 255, respectively [18]. Number of alleles and the heterozygosities for 33HDZ496, 33HDZ749 and 33HDZ974 loci in *Gazella granti* have been reported to be 8, 12 and 2 as well as 0.815, 0.79 and 0.224, respectively [18]. The differences can be attributed to species differences.

The PIC values obtained in this study were similar to or higher than those reported for most of the loci [32-37]. Therefore the loci examined in this study were highly informative. The mean number of alleles per loci (13.33) were higher than those reported by Saitbekova et al.[38], Agha et al.[39], Araujo

Table 2. *Allele frequencies*
Tablo 2. *Alel frekansları*

Loci	Allele (bp)	Population			
		Sanliurfa (N=33)	Kilis (N=34)	Siirt (N=38)	All (N=105)
HDZ496	232	0.076	0.000	0.026	0.033
	234	0.045	0.176	0.145	0.124
	236	0.045	0.015	0.053	0.038
	238	0.121	0.059	0.066	0.081
	240	0.076	0.118	0.105	0.1
	242	0.258	0.279	0.316	0.286
	244	0.106	0.206	0.105	0.138
	246	0.121	0.029	0.079	0.076
	248	0.106	0.088	0.079	0.090
	250	0.015	0.000	0.013	0.01
	252	0.000	**0.015**	0.000	0.005
	254	0.030	0.000	0.013	0.014
	256	0.000	**0.015**	0.000	0.005
HDZ749	**Allele (bp)**	**(N=35)**	**(N=31)**	**(N=38)**	**(N=104)**
	139	0.000	**0.016**	0.000	0.005
	141	0.271	0.339	0.276	0.293
	143	0.114	0.113	0.184	0.139
	147	0.000	0.000	**0.013**	0.005
	149	0.057	0.000	0.079	0.048
	151	0.171	0.113	0.276	0.192
	153	0.171	0.081	0.053	0.101
	155	0.043	0.048	0.013	0.034
	157	0.000	**0.032**	0.000	0.01
	159	0.029	0.081	0.026	0.043
	161	0.029	0.065	0.013	0.034
	163	0.043	0.048	0.039	0.043
	165	0.043	0.016	0.013	0.024
	167	0.000	**0.032**	0.000	0.01
	169	0.029	0.016	0.013	0.019
HDZ974	**Allele (bp)**	**(N=35)**	**(N=34)**	**(N=38)**	**(N=107)**
	193	0.043	0.015	0.053	0.037
	197	0.200	0.103	0.105	0.136
	199	0.000	0.000	**0.013**	0.005
	203	0.343	0.265	0.145	0.248
	205	0.057	0.147	0.066	0.089
	207	0.086	0.074	0.079	0.079
	209	0.000	0.074	0.171	0.084
	211	0.214	0.235	0.276	0.243
	213	0.029	0.044	0.053	0.042
	215	0.014	0.044	0.026	0.028
	219	**0.014**	0.000	0.000	0.005
	227	0.000	0.000	**0.013**	0.005

Private alleles are given in bold

et al.[40], Fatima et al.[41], Oliveira et al.[42], Qi et al.[43], lower than those reported by Serrano et al.[33], Cañón et al.[44] and similar to those reported by Missohou et al.[37], Barker at al.[45], Chenyambuga et al.[46], Hassen et al.[47] and Li et al.[48]. The mean number of alleles/locus/breed found in this study (between 10.33 and 11.33) were similar to those found by Bozkaya et al.[49], Korkmaz-Ağaoğlu and Ertuğrul [50] and higher than those reported by Behl et al.[35], Saitbekova et al.[38], Agha et al.[39], Barker et al.[45], Li et al.[48], Gour et al.[51], Jandurova et al.[52], Ganai et al.[53] and Di et al.[54].

Several studies have indicated that allele numbers per population are generally lower in European breeds [44,46]. The reason for the higher allelic diversity observed in this study might be due to the lack of in the studied populations any selection program and that they were raised in a region considered to be the center of domestication. Thus, a higher genetic diversity was expected [1,3].

Barker [55] and Takezaki and Nei [56] have stated that the loci used for genetic diversity studies should have at least four alleles in order to reduce the standard error. Botstein et al.[21] have reported that the loci having a PIC value over 0.5 can be considered informative. The mean number of alleles (13.33±1.52) and PIC (0.809±0.03) values in the present study are indicative of adequate polymorphism and their appropriateness of selected loci for assessing genetic variation.

Observed and expected heterozygosities estimated in this study were higher than those found in most studies [12,38,39,52,53,57-59]. The values were also higher than those reported for Abaza (0.772), Angora (0.750), Gurcu (0.751) and Hair goat breeds (0.722) raised in Turkey [43]. However the values found for Kilis population in this study were similar to those reported for Kilis goats by Korkmaz-Ağaoğlu and Ertugrul [50]. Bozkaya et al.[49] have reported an expected heterozygosity of 0.70 for Kilis goats. On the other hand Bozkaya and Gurler [60] have investigated diversity of a microsatellite locus in *CSN1S1* gene and reported expected heterozygosities of 0.687, 0.721 and 0.497 in Sanliurfa, Kilis and Siirt populations respectively. Therefore the higher values of heterozygosities obtained in this study might be due to loci used. The F_{IS} values estimated for Sanliurfa (0.019), Kilis (0.040) and Siirt (-0.068) populations were similar to those reported by Korkmaz-Agaoglu and Ertugrul [50] for some Turkish goat breeds.

When the observed allele numbers and heterozygosity values are considered it can be suggested that Sanliurfa, Kilis and Siirt populations possessed similar genetic variability. The populations studied were raised in provinces near the south eastern border of Turkey and a higher migration rate was expected due to a nomadic system.

The F_{ST} value (0.009) estimated by including the three loci and the results of AMOVA indicated that less than 1% of the total variance was explained by the variance among the populations and more than 99% was explained by the

Table 3. *Genetic parameters for the three microsatellite loci in Sanliurfa, Kilis and Siirt populations.*
Tablo 3. *Şanlıurfa, Kilis ve Siirt populasyonlarında üç mikrosatelit lokusuna ait genetik parametreler*

Populations	Loci	N	NA	NE	AR	PIC	PE	Ho	He	F_{IS}	HWE	Null
Sanliurfa	33HDZ496	33	11	7.408	10.936	0.852	0.734	0.9091	0.8778	-0.036	0.3753	0.0000
	33HDZ749	35	11	6.380	10.962	0.826	0.694	0.8286	0.8559	0.032	0.1428	0.0470
	33HDZ974	35	9	4.605	8.759	0.753	0.588	0.7429	0.7950	0.066	0.1213	0.0244
Kilis	33HDZ496	34	10	5.612	9.729	0.799	0.651	0.7647	0.8351	0.084	0.0446*	0.0497
	33HDZ749	31	13	6.063	13.00	0.821	0.964	0.8065	0.8495	0.051	0.0188*	0.0490
	33HDZ974	34	9	5.794	8.911	0.807	0.662	0.8529	0.8396	-0.016	0.8638	0.0143
Siirt	33HDZ496	38	11	6.119	10.599	0.821	0.689	0.9211	0.8467	-0.088	0.2346	0.0000
	33HDZ749	38	12	5.031	11.041	0.775	0.617	0.8158	0.8119	-0.005	0.7595	0.0202
	33HDZ974	38	11	6.461	10.598	0.829	0.698	0.9474	0.8553	-0.108	0.0488*	0.0000
All	33HDZ496	105	13	6.690	10.600	0.836	0.710	0.8666	0.8527	-0.0163	NS	0.0029
	33HDZ749	104	15	6.168	11.942	0.821	0.709	0.8173	0.8379	0.0246	NS	0.0462
	33HDZ974	107	12	6.096	9.635	0.817	0.679	0.8505	0.8306	-0.0240	NS	0.0072

N: *Sample size,* ***NA:*** *Number of alleles,* ***NE:*** *Effective number of alleles,* ***AR:*** *Allelic richness per locus and per population based on minimum sample size of 31,* ***PIC:*** *Polymorphism Information Content,* ***PE:*** *Probability of Exclusion,* ***Ho:*** *Observed Heterozygosity,* ***He:*** *Expected Heterozygosity,* ***F_{IS}:*** *Fixation indices of subpopulation,* ***HWE:*** *Deviations from Hardy-Weinberg equilibrium (Exact P value by the Markov Chain method for heterozygosity deficit or excess),* ***Null:*** *Frequency of null alleles,* ***NS:*** *Not significant (P>0.05), * P<0.05*

Table 4. *Basic parameters of genetic diversity for three goat populations.*
Tablo 4. *Üç keçi populasyonu için temel genetik çeşitlilik parametreleri*

Parameters	Populations			All
	Sanliurfa	Kilis	Siirt	
N ±SD	34.33±1.15	33±1.73	38±0.00	35.11±2.47
TNA	31	32	34	40
MNA±SD	10.33±1.15	10.67±2.08	11.33±0.58	10.78±1.30
NEA± SD	6.131±1.42	5.823±0.23	5.870±0.75	5.941±0.82
AR±SD	10.22±1.26	10.55±2.16	10.75±0.26	10.50±1.28
Ho± SD	0.827±0.083	0.808±0.044	0.895±0.069	0.843±0.071
He± SD	0.843±0.043	0.841±0.007	0.838±0.023	0.841±0.025
F_{IS}	0.019	0.040	-0.068	-0.0055
PA	1	5	3	9

N: *Mean sample size,* ***SD:*** *Standard daviation,* ***TNA:*** *Total number of alleles,* ***MNA:*** *Mean number of alleles,* ***NEA:*** *Mean number of effective alleles,* ***AR:*** *Mean number of allelic richness,* ***Ho:*** *Observed Heterozygosity,* ***He:*** *Expected Heterozygosity,* ***F_{IS}:*** *Fixation indices of subpopulation,* ***PA:*** *Privte alleles*

Table 5. *Wright's F-statistics and gene flow (Nm) for each locus across the all populations.*
Tablo 5. *Wright'ın F-istatistikleri ve gen akış değerleri (Nm)*

Loci	F_{IS}	F_{IT}	F_{ST}	Nm
HDZ496	-0.016371	-0.013142	0.003178	20.826
HDZ749	0.024517	0.031747	0.007412	16.633
HDZ974	-0.024006	-0.007203	0.016409	12.276
All	-0.0055	0.0036	0.009096	16.578

Table 6. *Genetic distances between populations (Above diagonals Nei's standard genetic distances. below diagonals pairwise F_{ST} values)*
Tablo 6. *Populasyonlar arası genetik mesafeler (üst diagonal: Nei'nin standart genetik mesafesi, alt diagonal: popuasyon çiftleri için F_{ST} değerleri)*

Region	Sanliurfa	Kilis	Siirt
Sanliurfa	-	0.1122	0.1447*
Kilis	0.0062	-	0.1068
Siirt	0.0139*	0.0067	-

** P<0.05*

Table 7. *AMOVA design and results (average over 3 loci)*
Tablo 7. *Moleküler varyans analizi sonuçları (tüm lokuslar için)*

Source of Variation	Degree of Freedom	Sum of Squares	Variance Component	Percentage of Variation
Among populations	3	4.117	0.01141	0.89743
Within populations	107	261.776	1.26054	99.10257
Total	110	265.893	1.27196	

variance within individuals. The mean F_{ST} value estimated in this study was similar to those reported by Bruno-de-Soussa et al.[36], Araújo et al.[40], Rout et al.[59], Martinez et al.[61], Tadlaoui-Ouafai et al.[62], and lower than that reported by Oliviera et al.[42], Hassen et al.[47], Li et al.[48], Gour et al.[51], Dixit et al.[63] and Kumar et al.[64]. Luikart et al.[1] and Naderi et al.[3] have stated that a lower F_{ST} value generally observed in goat populations results from a higher mobility of goats between different regions, which reduces a genetic differentiation between populations. The higher number of migrants (Nm = 16.58) estimated in this sutudy was in accordance with this suggestion.

The differentiation between population pairs was not significant when the three loci were considered. Bozkaya and Gürler [60] have reported that Siirt population significantly differentiated from both Sanliurfa and Kilis populations, while Sanliurfa and Kilis populations did not significantly differentiated, in accordance with the geographical distance between the populations. However Bozkaya and Gürler [60] have used a single microsatellite locus in *CSN1S1* gene, which showed a mean allele number of 4.33. In the present study each population pair showed a significant differentiation for different loci. Therefore the differences might be due to the loci used. The results indicated a different evolutionary history of different loci.

In conclusion, eight microsatellite locus origined from *Gazella granti* were tested first time in goats with this study. Three of them can be used as genetic markers in goats. The optimal PCR conditions for each of the locus were described. In addition, populations of goats reared in the Southeastern Anatolia Region were evaluated in terms of genetic diversity regarding these microsatellite loci. Despite declining numbers, studied goat populations still carry a high genetic diversity. They have significant potential in the protection of indigenous genetic resources.

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