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Original Research

Genetic Diversity and Relationship Among Algerian, Nigerian, and Turkish Goat Breeds Using Microsatellite Markers

Hakim Tefiel[1,2,*], Mohamed Chahbar[1,2], Khaled Fantazi[3], Onur Yilmaz[4], Ibrahim Cemal[4], Benali Kidoud[2], Kheira Setti Ahmed[1], Semir Bechir Suheil Gaouar[2]

[1]Agronomy Environment Research Laboratory, Department of Agronomic, Forestry and Environmental Sciences, Institute of Natural and Life Sciences, Tissemsilt University, 38000 Tissemsilt, Algeria
[2]Laboratory of Applied Genetic in Agronomy, Ecology and Public Health (GenApAgiE), SNV/STU Faculty, University Abou Bekr Belkaid, 13000 Tlemcen, Algeria
[3]National Institute of Agronomic Research, Animal Productions Division, INRA Algeria, BP200 Hassen Badi, El-Harrach 16200 Algiers, Algeria
[4]Department of Animal Science, Faculty of Agriculture, Aydın Adnan Menderes University, 09100 Aydın, Türkiye
*Correspondence: hakimtefiel@yahoo.fr; tefiel.hakim@univ-tissemsilt.dz (Hakim Tefiel)
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Abstract

Background: This study was conducted to identify genetic diversity among goat breeds in Algeria, Türkiye, and Nigeria, which is believed to have arisen due to historical influences, trade networks, and environmental adaptations, using 12 microsatellite markers. Additionally, the study provided insights into the population structure and kinship relationships among the breeds. **Methods**: The animal material of the study consisted of 514 goats from eight breeds: four Algerian (n = 224), two Turkish (n = 140), and two Nigerian (n = 150) native goat breeds. The quality and quantity control of DNA obtained from blood samples was determined using the Nanodrop 2000 device. In the study, 12 microsatellite markers were used. Capillary electrophoresis was used to separate polymerase chain reaction (PCR) fragments labeled with fluorescent dye in the Beckman Coulter GeXP Genetic Analyzer. Statistical analyses were used to calculate molecular genetic parameters, F-statistics, and genetic distances. Factorial correspondence analysis, structure analysis, and dendrogram construction were used to explore population structure. **Results**: The study used microsatellite markers to analyze genetic diversity in various breeds, revealing 149 alleles with a mean of 12.41 per locus. Positive inbreeding coefficient within subpopulations (F_{IS}) values indicated a heterozygote deficiency, suggesting potential breeding strategies. Population structure analyses revealed distinct genetic clusters and relationships, providing insights into genetic variation within populations. **Conclusion**: The study provides a detailed analysis of goat populations in Algeria, Türkiye, and Nigeria, revealing the presence of heterozygote deficiency and the need for strategic breeding interventions to preserve genetic diversity. The findings also reveal distinct genetic clusters and relationships with historical influences, particularly the role of the Mediterranean Sea, adding depth to our understanding. The research offers practical guidance for the sustainable management of these valuable genetic resources, emphasizing adaptive strategies to ensure the resilience and adaptability of goat populations. The findings are crucial for informed decision-making in conserving and utilizing diverse livestock breeds, urging further exploration of goat populations' genetic landscapes.

Keywords: genetic diversity; Algerian goat breeds; Turkish goat breeds; Nigerian goat breeds; microsatellites; population genetic structure

1. Introduction

Goats are essential for rural life in developing economies, contributing to food security and poverty alleviation. Climate change, market dynamics, and the movement of people and animals influence the genetic diversity of goat populations. The Mediterranean Sea has been a significant conduit for trade between Africa, Europe, and Asia, influencing the genetic makeup of goat breeds. However, there is a gap in understanding regarding the genetic relationships between goat breeds from Algeria, Türkiye, and Nigeria. This study aimed to explore the genetic diversity, population structure, and interbreed relationships among these breeds using twelve microsatellite markers to investigate the genetic tapestry woven by centuries of trade, travel, and environmental adaptations.

Preserving biological diversity is essential for future breeding options and livestock genetic resources, which are crucial for adapting to changing climates and markets [1]. A previous study by Cañón *et al.* [2] highlighted the importance of the Mediterranean Sea as a pathway for the movement of people and animals within a vibrant web of commerce. The transcontinental commerce of products, plants, and animals between Africa, Europe, and Asia is typically associated with Africans; however, Arabs also experienced significant population shifts and were frequent travelers due to their role as extensive traders. Over the Mediter-

Table 1. Number of sampled animals and herds.

Country	Name of breeds	Breed abbreviation	Sampling location	Number of samples	Total
Algeria	Arbia	AR	Tissemsilt	79	224
	Mekatia	ME	Laghouat	51	
	Naine of Kabylie	NK	Bejaïa	59	
	M'zabite	MO	Ghardaïa	35	
Türkiye	Hair Goat	HG	Aydın	100	140
	Damascus	DA	Gaziantep	40	
Nigeria	Red Sokoto	RS	Itoko, Bodija	48	150
	West African Dwarf	WAD	Itoko, Bodija	55	
	Sahel	SA	Itoko, Bodija	47	
Total					514

ranean region, these movements relocated both people and their animals [3]. Microsatellite markers exhibit a high degree of polymorphism, random distribution throughout the genome, co-dominance, automated genotype scoring capabilities, and selection neutrality, making them extremely significant and useful tools in previous diversification study [4]. A thorough understanding of the current genetic diversity in domestic animals and how that variability is distributed among breeds is a prerequisite for both the conservation and use of that biodiversity [5]. However, no prior analysis exists of the link between Algerian, Turkish, and Nigerian breeds.

Meanwhile, microsatellite marker studies on these breeds have revealed significant genetic variability within and between them [6–11]. However, most of this research concentrated on the variety and relationships between goat breeds at the national level, with relatively little data available at the regional level. Therefore, this current study was designed to examine the genetic diversity, population structure, and genetic relationships among four breeds of goats in Algeria (M'zabite, Naine of Kabylie, Mekatia, and Arbia), two Turkish goat breeds (Damascus and Hair goat), and three Nigerian goat breeds (West African Dwarf, Red Sokoto, and Sahel) using twelve microsatellite markers.

2. Materials and Methods

2.1 DNA Extraction of Samples

The animal material used in the study consisted of 514 goats from eight breeds: four Algerian (n = 224), two Turkish (n = 140), and two Nigerian (n = 150) native goat breeds (Table 1). Blood samples were collected into a vacutainer tube filled with K3EDTA (Fisher Scientific, Arendalsvägen, Göteborg, Sweden) from the jugular vein of each animal. Next, DNA quantification and qualification of all samples were performed using a NanoDrop 2000 (Thermo Scientific, Waltham, MA, USA). The protocol was approved by the University of Abou Bekr Belkaid, Tlemcen Ethics Committee (approval number: 32/2022), and the type approval number was 16/10/2022 EDCTU.

2.2 PCR, Fragment Analysis

This study used 12 microsatellite markers recommended by the Food and Agriculture Organization (FAO) of the United Nations [12]. Three multiplex groups were formed using the microsatellites (Table 2, Ref. [12]). Approximately 50 ng of DNA was utilized for the polymerase chain reaction (PCR). A PCR master mix was prepared, consisting of 0.10 µM primers, 0.20 mM dNTPs, 2.0 mM $MgCl_2$, 1× PCR buffer, and 1 unit of Taq DNA polymerase (Thermo Scientific, Waltham, MA, USA), resulting in a total volume of 25 µL (Table 3). Capillary electrophoresis was used to separate PCR fragments labeled with fluorescent dye in the Beckman Coulter GeXP Genetic Analyzer (Beckman Coulter, Inc., Pasadena, CA, USA).

2.3 Statistical Analysis

The following values were calculated using GenAlEx 6.5.01 (https://biology-assets.anu.edu.au/GenAlEx/Welcome.html) [13], POPGENE 1.32 (Molecular Biology and Biotechnology Center, University of Alberta, Edmonton, Canada) [14], and CERVUS 3.0.3 (www.fieldgenetics.com) [15,16]: the number of alleles per locus (Na), the mean number of alleles (MNa), effective number of alleles (Ne), polymorphic information content (PIC), observed heterozygosity (Ho), expected heterozygosity (He), average heterozygosity ($\hat{H}$), Hardy–Weinberg equilibrium (HWE), Wright's F-statistics (total inbreeding coefficient (F_{IT}), inbreeding coefficient within subpopulations (F_{IS}), fixation index (F_{ST})) [17,18], and null allele frequencies. The robustness of the dendrogram topology was tested using the bootstrap resampling methodology (1000 replicates) and Nei's minimum genetic distance matrix [19]. FSTAT 2.9.3 (Institute of Ecology, University of Lausanne, Lausanne, Switzerland) [20] was used to calculate Nei's gene diversity (H_T), diversity between breeds (D_{ST}), and coefficient of gene differentiation (G_{ST}) values. Factorial correspondence analysis was carried out using the GENETIX V4.0.5 (CNRS UMR 5000, University of Montpellier II, Montpellier, France) [21] software's "AFC populations" program to test for potential admixtures that

Table 2. Details of considered microsatellite loci [12].

Multiplex groups	Microsatellites	Primer Sequences (5′–3′)	Allelic range (bp)
M1	CSRD0247	F: GGACTTGCCAGAACTCTGCAAT	220–247
		R: CACTGTGGTTTGTATTAGTCAGG	
	McM0527	F: GTCCATTGCCTCAAATCAATTC	165–187
		R: AAACCACTTGACTACTCCCCAA	
	SRCRSP0005	F: GGACTCTACCAACTGAGCTACAAG	158–180
		R: TGAAATGAAGCTAAAGCAATGC	
	SRCRSP0023	F: TGAACGGGTAAAGATGTG	85–123
		R: TGTTTTTAATGGCTGAGTAG	
	HSC	F: CTGCCAATGCAGAGACACAAGA	267–301
		R: GTCTGTCTCCTGTCTTGTCATC	
M2	INRA063	F: GACCACAAAGGGATTTGCACAAGC	164–186
		R: AAACCACAGAAATGCTTGGAAG	
	MAF0065	F: AAGGCCAGAGTATGCAATTAGGAG	123–157
		R: CCACTCCTCCTGAGAATATAACATG	
	SRCRSP0008	F: TGCGGTCTGGTTCTGATTTCAC	209–235
		R: CCTGCATGAGAAAGTCGATGCTTAG	
	SRCRSP0024	F: AGCAAGAAGTGTCCACTGACAG	139–175
		R: TCTAGGTCCATCTGTGTTATTGC	
M3	INRA0005	F: CAATCTGCATGAAGTATAAATAT	135–149
		R: CTTCAGGCATACCCTACACC	
	ILST0019	F: AGGGACCTCATGTAGAAGC	144–158
		R: ACTTTTGGACCCTGTAGTGC	
	BM1818	F: AGCTGGGAATATAACCAAAGG	248–278
		R: AGTGCTTTCAAGGTCCATGC	

F, forward primer; R, reverse primer.

Table 3. The used touchdown PCR protocol.

Multiplex group	First denaturation	Denaturation	Annealing	Extension	Cycle	Final extension
M1, M2, and M3	95 °C (5 min)	95 °C (40 sec)	60–50 °C (40 sec)	72 °C (1 min)	30	72 °C (10 min)

PCR, polymerase chain reaction.

may have occurred between the populations. Using this structure, cluster techniques based on the Bayesian approach were employed to analyze the population structures [22–25]. The analysis used independent allele frequencies and an admixture model with a burn of 20,000 length and 100.000 Markov chain Monte Carlo iterations for each from K = 2 to 10. There were 20 replication runs for each K. Using ΔK, the right number of clusters was determined based on the change rate in the log probability of the data, according to Evanno's method [26]. STRUCTURE HARVESTER was used to determine the ideal K values [27].

3. Results and Discussion

This study uses 12 microsatellite markers to explore the genetic diversity, population structure, and interbreed relationships among Algerian, Turkish, and Nigerian goat breeds. The results (Table 4, Ref. [18,28]) reveal high variability in alleles, effective alleles, and polymorphic information content, with observed heterozygosity and expected heterozygosity values providing nuanced understanding. Positive F_{IS} values suggest a heterozygote deficiency, indicating potential implications for breeding strategies and population dynamics. Population structure analyses reveal genetic relationships and distinct clusters among the breeds. These findings contribute to the scientific understanding of goat genetics and offer practical implications for conservation and breeding strategies in changing climates and markets.

The selected microsatellite panel performed well in the diversity study, focusing on loci with at least four alleles based on identified alleles, gene diversity, PIC, and F_{IS} values [29]. Every locus examined in this study had four or more alleles, proving that every marker was suitable for examining genetic diversity. A total of 149 alleles were identified from the 12 microsatellites utilized in this study. The number of alleles observed was greater than that reported for West African goats (120) [30], West Himalayan goats (135) [31], West Java goats (96) [32], and Benin goats [11]. The allele numbers obtained in the present study were lower

Table 4. Genetic polymorphism parameters of the twelve investigated loci in NK, AR, ME, MO, RS, WAD, SA, HG, and DA goat breeds.

Markers	Allelic range (bp)	Na	Ne	PIC	F_{IS}*	FI_T*	F_{ST}*	Ho	He	F (Null)	DS_T	G_{ST}	HT	Nm*	HWE
INRA005	120–203	13	6.718	0.921	0.093	0.267	0.192	0.672	0.741	0.1734	0.168	0.183	0.917	1.055	***
ILTS0019	124–170	11	6.385	0.872	0.059	0.203	0.153	0.698	0.741	0.1199	0.127	0.145	0.876	1.386	***
BM1818	218–298	13	7.512	0.921	0.061	0.125	0.068	0.807	0.859	0.0710	0.055	0.059	0.923	3.418	***
CSRD0247	96–246	11	6.967	0.968	0.055	0.169	0.121	0.803	0.850	0.0854	0.109	0.113	0.968	1.812	***
McM0527	147–213	10	7.134	0.957	0.094	0.209	0.127	0.759	0.838	0.1124	0.113	0.118	0.960	1.724	***
SRCSRP0023	81–133	13	6.757	0.934	0.044	0.146	0.106	0.803	0.840	0.0648	0.092	0.098	0.941	2.102	***
HSC	259–309	14	9.136	0.962	0.066	0.140	0.080	0.828	0.887	0.0697	0.068	0.071	0.965	2.881	***
INRA063	141–217	12	7.619	0.924	0.180	0.287	0.130	0.660	0.805	0.1803	0.112	0.121	0.927	1.671	***
SRCRSP0008	201–259	14	9.299	0.947	0.038	0.144	0.110	0.811	0.843	0.0789	0.096	0.101	0.948	2.024	***
SRCRSP0024	129–187	14	8.367	0.924	0.134	0.231	0.112	0.711	0.822	0.1288	0.095	0.102	0.926	1.990	***
MAF0065	105–205	12	6.940	0.948	0.105	0.203	0.109	0.758	0.846	0.1122	0.095	0.100	0.951	2.034	***
SRCSRP005	148–208	12	7.548	0.953	0.114	0.211	0.110	0.752	0.849	0.1132	0.097	0.101	0.955	2.024	***
Mean		12.42	7.532	0.936	0.087	0.194	0.118	0.755	0.827	0.1091	0.102	0.109	0.938	2.010	

*Wright's statistics according to Weir and Cockerham (1984) [18]; *$p < 0.05$, ***$p < 0.001$. Na, number of alleles; Ne, the effective number of alleles; PIC, polymorphic information content; F_{IT}, F_{IS}, F_{ST}, Wright's F-statistics; Ho, observed heterozygosity; He, expected heterozygosity; HWE, Hardy–Weinberg equilibrium; F (Null), null allele frequency; H_T, Nei's gene diversity; D_{ST}, the diversity between breeds; G_{ST}, coefficient of gene differentiation; Nm, gene flow estimate ($Nm = 0.25 (1 – F_{ST})/F_{ST}$ [28]).

Table 5. Genetic polymorphism parameters according to studied goat breeds across 12 loci.

Breeds	MNA	Mean heterozygosity		NPA		Total
		Ho	He	Frequencies		
		(SE)	(SE)	≥5%	<5%	
ME	13.750	0.81 (0.029)	0.89 (0.013)	6	5	11
MO	12.833	0.80 (0.025)	0.88 (0.012)	7	4	11
AR	16.417	0.81 (0.017)	0.90 (0.007)	6	10	16
NK	15.917	0.87 (0.015)	0.90 (0.005)	10	8	18
RS	8.000	0.65 (0.041)	0.70 (0.045)	-	4	4
WAD	9.083	0.65 (0.043)	0.75 (0.027)	2	7	9
SA	8.250	0.66 (0.041)	0.71 (0.043)	-	5	5
HG	14.167	0.75 (0.05)	0.83 (0.019)	7	9	16
DA	15.333	0.80 (0.021)	0.88 (0.006)	16	18	34

AR, Arbia; ME, Mekatia; NK, Naine of Kabylie; MO, M'zabite; HG, Hair Goat; DA, Damascus; RS, Red Sokoto; WAD, West African Dwarf; SA, Sahel, MNA, mean number of alleles; Ho, mean observed heterozygosity; He, mean expected heterozygosity; NPA, number of private alleles.

than those reported for Retinta Extremena goats in Spain [33], native goats in Türkiye [6,8], and native goat breeds in Algeria [9,10]; the average number of alleles per locus in this study was 12.41. This value was higher than reported in several related studies [30,31,33,34]. In studies conducted on various goat breeds, the number of alleles per locus was reported as 14.12, 16.48, and 16.50 for South Indian, Indian, and Indian Kerala goat breeds, respectively [35,36]. For Turkish goat breeds, the number was 15.65 [6], while Algerian breeds exhibited values of 25 and 28.39 [9,10]. On the other hand, the number of alleles per locus was reported to be 17.82 in certain goat breeds raised in Türkiye [8], 8 in East Java goats [32], and 11.25 in Benin goats [11]. According to Kumar *et al*. [37], the genetic diversity found in those populations, as measured by the mean number of alleles across a range of loci in various populations, represents a believable indicator of genetic variation within populations. The average effective number of alleles was 7.53, ranging from 6.385 (ILTS0019) to 9.3 (SRCRSP0008). This value was significantly higher than those reported by Singh *et al*. [31], Parejo *et al*. [33], and Dixit *et al*. [34]. PIC values can be used as a statistical measure of a marker's informativeness; in population genetic analyses, a genetic marker with a PIC value greater than 0.5 is typically regarded as informative [38]. The current PIC values ranged from 0.87 (ILTS0019) to 0.96 (CSRD0247), with a mean of 0.93. The values obtained for PIC were higher than those reported in several studies conducted on goats [6,8–10,31,32,39,40].

This study demonstrated that the examined microsatellites exhibited a high level of polymorphism in these populations and can be utilized with great confidence for identifying genetic diversity within them. This could be because the population's heterozygosity and allele richness levels, reliable markers of genetic polymorphism in the Algerian goats under study, were higher than average. The F_{IS} indicates the heterozygous excess or deficiency deviation between genotypic and panmictic frequencies. Positive F_{IS} values indicate heterozygote deficiency and negative values indicate heterozygote excess compared to the HWE estimations [41]. Each of the 12 loci used in this investigation had a positive F_{IS} value. Tefiel *et al.* [9] reported that only 2 of the 18 loci in their study exhibited negative F_{IS} values, indicating an excess of heterozygotes. Similar situations have been reported [33]. The average F_{IS} value obtained in this study (0.087) was higher than the values reported in studies conducted in Switzerland (0.014), Türkiye (0.037), South Africa (0.020), Spain (0.060), and among Algerian goat breeds (0.057 and 0.083) [6,9,10,32,39,42]. The general heterozygosity loss, or F_{IT} value, was between 0.125 (BM1818) and 0.287 (INRA063), with a mean of 0.194. This value exceeded the 0.08 reported by Bosman *et al.* [39], the 0.077 obtained by Parejo *et al.* [33], the 0.102 reported by Tefiel *et al.* [9], and the 0.146 obtained by Tefiel *et al.* [10]. The F_{ST} values obtained for each locus in this study indicate population differences (Table 4). While F_{ST} values ranging from 0.05 to 0.3 are commonly considered normal findings [43], it has also been noted that smaller values can be significant. The average F_{ST} value obtained (0.118) is a key indicator of genetic divergence between the studied populations, suggesting that gene flow is not entirely interrupted. However, there is still some limited gene flow between these populations. This observed level of genetic divergence is believed to result from geographical barriers, variations in reproductive behaviors, environmental adaptations, or other factors that impede gene flow between populations. In the study of the genetic structure of 45 goat breeds from Europe and the Middle East, Cañón *et al.* [2] reported that only 7% of all genetic variability could be attributed to breed differences. The mean F_{ST} value was higher than some values reported in previous research [6,9,10,44–48] and lower than others [36] for goat breeds raised in various countries. The expected and observed heterozygosity for Ho and He are provided in Table 4, with respective means of 0.75 and 0.82. The He value was greater than Ho, indicating a population heterozygote deficit. The average Ho value (0.75) was higher than those reported for Western Himalayan goat breeds [31], Indian goat breeds [35,37,40], Turkish goat breeds [6,8], and Benin goat breeds. Hence, based on these results, it can be considered that although the populations under investigation had a high level of genetic diversity, there was a slight heterozygote deficit, as shown by slightly lower Ho values. Meanwhile, high levels of genetic variation may be attributed to the admixture of populations or lower selection pressure, as reported by [31,40]. Heterozygote deficit may be linked to the use of an inadequate number of stud bucks, a small population size, insufficient gene flow, and potential inbreeding. A population has a genotype frequency deviation when the HWE assumptions are devastated. A few possible explanations exist for the variations noticed in some population markers, including selection against heterozygous individuals, non-amplification (null alleles), inbreeding, and group defective alleles. The HWE was examined for each population; the findings are displayed in Table 4. The genetic equilibrium assessment for each examined breed showed highly significant differences ($p < 0.001$) for all loci (Wright's statistics, according to [14]). Some studies have reported similar situations [9,10,39]. Observed null allele frequencies for all microsatellites below the critical value (20%) indicated that these studied markers could confidently identify genetic diversity in these native sheep breeds. The mean value of Nei's gene diversity (H_T), between-breed diversity value (D_{ST}), and coefficient of gene differentiation (G_{ST}) were determined as 0.938, 0.102, and 0.109, respectively. With an average of 2.01 across all populations, the gene flow (Nm, or number of migrants per generation) estimated for this study was high (Table 4). The Nm value obtained was lower than those reported in studies conducted on various goat breeds [4,9,40,49]. This value, along with the F_{ST} (0.118), suggests a moderate level of genetic differentiation between the populations, indicating that some gene flow still occurs. Table 5 summarizes the genetic diversity results according to the studied population.

The mean number of alleles (MNA) in the breeds varied from 8.00 in the Red Sokoto breed to 16.41 in the Arbia breed. Values between 6.5 and 12.94 have been reported for the MNA across different breeds [1,5,6,9,10,35,39,44]. The observed heterozygosity ranged from 0.65 (Red Sokoto and West African Dwarf breeds) to 0.87 (Naine of Kabylie breed) and is higher than the results published by Missohou *et al.* [30]. Algerian native goat breeds exhibited heterozygosity values ranging from 0.82 to 0.89, as reported by Tefiel *et al.* [9]. In contrast, the heterozygosity observed in Algerian and Turkish goat breeds was between 0.77 and 0.88, according to Tefiel *et al.* [10]. In the present study, the lowest He value was obtained in Red Sokoto at 0.70, while the highest values were observed in Arbia and Naine of Kabylie at 0.90 (Table 5). The values obtained for the He parameter were higher than those reported for native goat breeds from Egypt and Syria [47] and some Italian breeds [5]. While the He values ranged from 0.67 to 0.74 in Southern Italian breeds [1], values between 0.88 and 0.99 were reported in Algerian breeds [9].

In most populations, the He values were higher than the Ho values. This discrepancy indicates a deficiency in heterozygosity, as previously reported by Missohou *et al.* [30]. Although 124 unique alleles were detected in the stud-

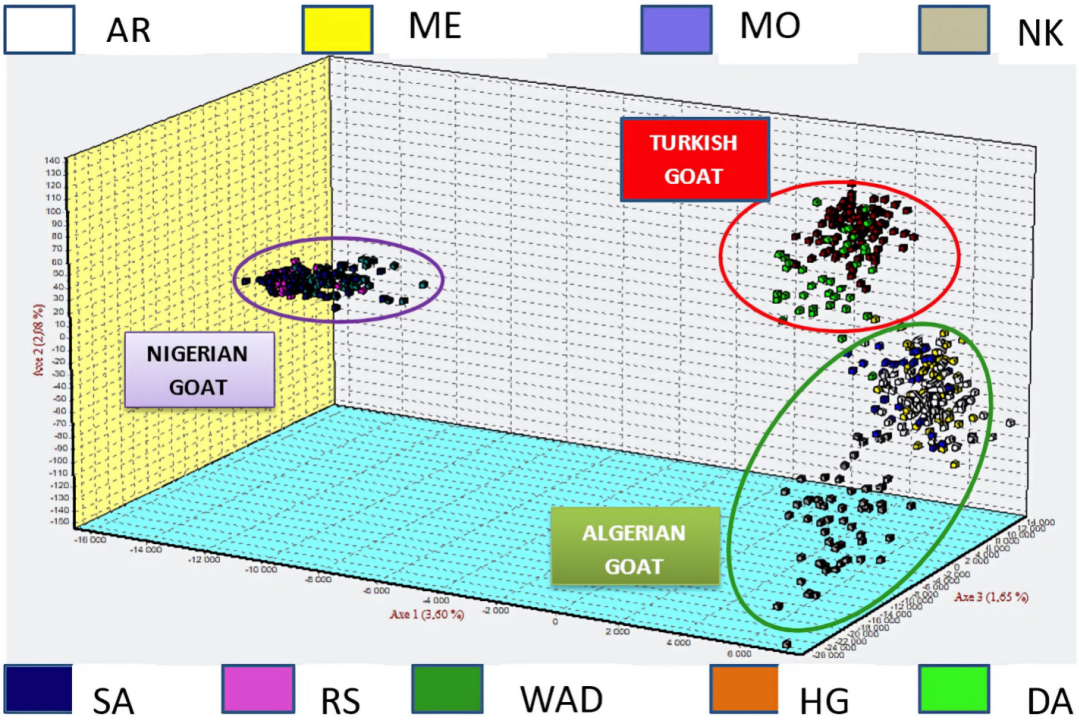

Fig. 1. The factorial correspondence analysis (FCA) results show the relationship between nine goat populations. AR, Arbia; ME, Mekatia; NK, Naine of Kabylie; MO, M'zabite; HG, Hair Goat; DA, Damascus; RS, Red Sokoto; WAD, West African Dwarf; SA, Sahel.

Table 6. Nei's genetic identity (above diagonal) and genetic distance (below diagonal) matrix are unbiased.

Breeds	ME	MO	AR	NK	RS	WAD	SA	HG	DA
ME	0	0.344	0.384	0.358	0.071	0.106	0.070	0.386	0.392
MO	1.067	0	0.525	0.423	0.122	0.168	0.108	0.391	0.312
AR	0.957	0.644	0	0.426	0.127	0.163	0.121	0.328	0.371
NK	1.026	0.861	0.853	0	0.109	0.104	0.110	0.271	0.317
RS	2.648	2.106	2.065	2.219	0	0.867	0.984	0.124	0.160
WAD	2.242	1.781	1.815	2.264	0.867	0	0.846	0.134	0.192
SA	2.660	2.224	2.109	2.205	0.984	0.846	0	0.123	0.173
HG	0.951	0.938	1.114	1.304	0.124	0.134	0.123	0	0.568
DA	0.937	1.164	0.993	1.149	0.160	0.192	0.173	0.568	0

AR, Arbia; ME, Mekatia; NK, Naine of Kabylie; MO, M'zabite; HG, Hair Goat; DA, Damascus; RS, Red Sokoto; WAD, West African Dwarf; SA, Sahel.

ied populations, only 54 had a frequency greater than 5%. Conversely, the highest number of private alleles with a frequency exceeding 5% was observed in the Damascus breed. Of the total private alleles observed in the studied populations, 43.5% had a frequency greater than 5%. It has been reported that unique alleles observed at frequencies exceeding 20% within a population can be considered a positive indicator for conserving genetic diversity [42].

Table 6 shows that the breeds with the lowest and highest genetic identities are the Red Sokoto and Sahel breeds (0.984) and the Mekatia and Sahel breeds (0.070), respectively.

According to these findings, the genetic distance between the Red Sokoto and Sahel breeds is greater than between Mekatia and Sahel breeds. In the present study, the genetic similarity values obtained between the breeds, based on Nei's similarity and distance matrix, ranged from 0.123 to 0.984. In contrast, the genetic distance values varied from 0.123 to 2.660. Considering the genetic distance and similarity matrix, the lowest genetic identity value was observed between the Mekatia and Sahel breeds (0.070). In contrast, the highest genetic identity value was obtained between the Red Sokoto and Sahel breeds. The Nigerian, Algerian, and Turkish goat breeds are categorized separately from other breeds based on the FCA test axes; however, the

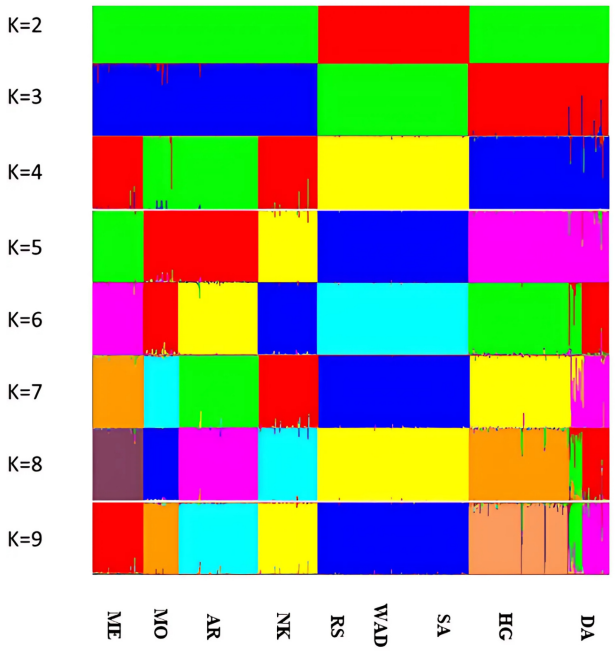

Fig. 2. Population structure results obtained by STRUCTURE analyses for the K (2 to 9) values of the nine breeds. AR, Arbia; ME, Mekatia; NK, Naine of Kabylie; MO, M'zabite; HG, Hair Goat; DA, Damascus; RS, Red Sokoto; WAD, West African Dwarf; SA, Sahel.

FCA graph indicates that the Algerian and Turkish breeds exhibit a degree of admixture (Fig. 1).

Fig. 2 illustrates the structure analysis results, revealing various genetic clustering scenarios (K = 2–10) within the studied populations. This visual narrative reveals the complex patterns of population stratification and provides a detailed understanding of genomic subdivisions within the analyzed dataset.

Table 7 presents estimates, including posterior probabilities ([Ln Pr(X|K)]) for various clustering numbers (K) and highlighting ΔK values.

ΔK values were obtained from various clustering scenarios according to Evanno *et al*. [26]. The genetic distance dendrogram and the FCA graph both reveal a triple genetic landscape. The ΔK values indicate three distinct genetic profiles in the studied breeds.

4. Conclusion

This study used twelve microsatellite markers to explore the genetic makeup of goat populations in Algeria, Türkiye, and Nigeria. The results reveal a rich genetic landscape with high diversity and distinctiveness among the breeds. This study highlights the importance of genetic variation, particularly in heterozygote deficiency, which requires careful breeding strategies and population management. Population structure analyses, such as the factorial correspondence analysis and structure analysis, reveal clear genetic clusters and the impact of historical influences, trade networks, and environmental adaptations on the genetic makeup of these goat populations. The historical role of the Mediterranean Sea as a transportation route has significantly impacted the genetic diversity observed today. These findings have practical implications for conservation and breeding efforts, guiding targeted breeding strategies to preserve and enhance desirable traits within each breed. The heterozygote deficiency in some breeds requires careful management to mitigate potential impacts on genetic diversity. This study also contributes valuable knowledge for the sustainable management of these vital livestock genetic resources, particularly in the face of climate change and market dynamics. Moreover, this study enhances our understanding of goat genetics and provides a foundation for informed decision-making in conserving and utilizing these diverse and resilient livestock breeds.

Table 7. Estimated posterior probabilities [Ln Pr(X|K)] for different numbers of inferred clusters (K) and ΔK statistic.

K	[Ln Pr(X|K)]	ΔK
2	–32.735,38	—
3*	**–30.57528**	**306.169536**
4	–29.58423	2.307277
5	–28.79582	0.241814
6	–27.97583	1.746374
7	–27.37508	191.003279
8	–27.56440	0.406924
9	–27.98596	0.292837
10	–28.07864	—

*The optimal number of groups is marked in bold, [Ln Pr(X|K)]: posterior probabilities ΔK: used to estimate the most probable number of populations.

Availability of Data and Materials

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Author Contributions

HT, MC, KF, KSA and BK collected data, performed blood sampling. HT, OY, IC and SBSG performed the molecular analyses. HT, MC interpreted the data, wrote the first draft of the manuscript. HT, MC performed statistical analysis. HT, OY, IC and SBSG Interpreted data and supervised laboratory analyses. HT, MC, OY, IC and SBSG conceived, designed, and supervised the research, wrote, critically reviewed and edited the manuscript. All authors contributed to editorial changes in the manuscript. All authors read and approved the final manuscript. All authors have participated sufficiently in the work and agreed to be accountable for all aspects of the work.

Ethics Approval and Consent to Participate

The protocol was approved by the Ethics Committee of the university of Abou Bekr Belkaid, Tlemcen (approval number: 32/2022), number of type approval 16/10/2022 EDCTU. The study is reported in accordance with ARRIVE guidelines of experimental animals.

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Conflict of Interest

The authors declare no conflict of interest.

References

[1] Criscione A, Bordonaro S, Moltisanti V, Marletta D. Differentiation of South Italian goat breeds in the focus of biodiversity conservation. Small Ruminant Research. 2016; 145: 12–19. https://doi.org/10.1016/j.smallrumres.2016.09.011.

[2] Cañón J, García D, García-Atance MA, Obexer-Ruff G, Lenstra JA, Ajmone-Marsan P, *et al*. Geographical partitioning of goat diversity in Europe and the Middle East. Animal genetics. 2006; 37: 327–334. https://doi.org/10.1111/j.1365-2052.2006.01461.x.

[3] Martin BG. Arab Migrations to East Africa in Medieval Times. the International Journal of African Historical Studies. 1974; 7: 367. https://doi.org/10.2307/217250.

[4] Ligda C, Altarayrah J, Georgoudis A. Genetic analysis of Greek sheep breeds using microsatellite markers for setting conservation priorities. Small Ruminant Research. 2009; 83: 42–48. https://doi.org/10.1016/j.smallrumres.2009.04.002.

[5] Iamartino D, Bruzzone A, Lanza A, Blasi M, Pilla F. Genetic diversity of Southern Italian goat populations assessed by microsatellite markers. Small Ruminant Research. 2005; 57: 249–255. https://doi.org/10.1016/j.smallrumres.2004.08.003.

[6] Agaoglu OK, Ertuğrul O. Assessment of genetic diversity, genetic relationship and bottleneck using microsatellites in some native Turkish goat breeds. Small Ruminant Research. 2012; 105: 53–60. https://doi.org/10.1016/j.smallrumres.2011.12.005.

[7] Gurler S, Bozkaya F. Genetic Diversity of Three Native Goat Populations Raised in the South-Eastern Region of Turkey. Kafkas Universitesi Veteriner Fakultesi Dergisi. 2013; 19: 207–213. https://doi.org/10.9775/kvfd.2012.7475.

[8] Keskin M, Yilmaz O, Gündüz Z, Ata N, Gül S, Cemal İ, *et al*. Microsatellite panels for parentage testing of Kilis goats reared in Turkey. Turkish Journal of Veterinary & Animal Sciences. 2019; 43: 94–101. https://doi.org/10.3906/vet-1809-21.

[9] Tefiel H, Ata N, Chahbar M, Benyarou M, Fantazi K, Yilmaz O, *et al*. Genetic characterization of four Algerian goat breeds assessed by microsatellite markers. Small Ruminant Research. 2018; 160: 65–71. https://doi.org/10.1016/j.smallrumres.2018.01.021.

[10] Tefiel H, Ata N, Fantazi K, Yilmaz O, Cemal I, Karaca O, *et al*. Microsatellite based genetic diversity in indigenous goat breeds reared in algeria and Turkey. The Journal of Animal & Plant Sciences. 2020; 30: 1115–1122. https://doi.org/10.36899/JAPS.2020.5.0127.

[11] Whannou HRV, Spanoghe M, Dayo GK, Demblon D, Lanterbecq D, Dossa LH. Genetic diversity assessment of the indigenous goat population of Benin using microsatellite markers. Frontiers in Genetics. 2023; 14: 1079048. https://doi.org/10.3389/fgene.2023.1079048.

[12] FAO, 2011. FAO Animal Production and Health Guidelines (pp. 100). In Division APaH (ed.) Food and Agricultural Organization of the United Nations: Rome, Italy. 2011.

[13] Peakall R, Smouse PE. GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research—an update. Bioinformatics (Oxford, England). 2012; 28: 2537–2539. https://doi.org/10.1093/bioinformatics/bts460.

[14] Yeh FC, Yang RC, Boyle TBJ, Ye ZH, Mao JX. POPGENE: The User-Friendly Shareware for Population Genetic Analysis. Edmonton, AB, Canada: University of Alberta 1997.

[15] Marshall TC. Cervus, 3.0, Cervus is a computer program for assignment of parents to their offspring using genetic markers. Cervus, a Windows package for parentage analysis using likelihood approach. 2006. Available at: http://www.fieldgenetics.com (Accessed: 2 July 2008).

[16] Kalinowski ST, Taper ML, Marshall TC. Revising how the computer program CERVUS accommodates genotyping error increases success in paternity assignment. Molecular ecology. 2007; 16: 1099–1106. https://doi.org/10.1111/j.1365-294X.2007.03089.x

[17] Wright S. Evolution in Mendelian Populations. Genetics. 1931; 16: 97–159. https://doi.org/10.1093/genetics/16.2.97.

[18] Weir BS, Cockerham CC. Estimating F-Statistics for the Analysis of Population Structure. Evolution; international journal of organic evolution. 1984; 38: 1358–1370. https://doi.org/10.1111/j.1558-5646.1984.tb05657.x.

[19] Nei M. Genetic distance between populations. The American Naturalist. 1972; 106: 283–292.

[20] Goudet J. FSTAT, A Program to Estimate and Test Gene Diversities and Fixation Indices (Version 2.9.3.). University of Lausanne: Lausanne, Switzerland. 2001. https://api.semanticscholar.org/CorpusID:90348083.

[21] Belkhir K, Borsa P, Goudet J, Chikhi L, Bonhomme F. GENETIX: logiciel sous WindowsTM pour la génétique des populations. Laboratoire Génome et Populations, CNRS UPR 9060, Université Montpellier II, France. 2001.

[22] Pritchard JK, Stephens M, Donnelly P. Inference of Population Structure Using Multilocus Genotype Data. Genetics. 2000; 155: 945–959. https://doi.org/10.1093/genetics/155.2.945.

[23] Falush D, Stephens M, Pritchard JK. Inference of Population Structure Using Multilocus Genotype Data: Linked Loci and Correlated Allele Frequencies. Genetics. 2003; 164: 1567–1587. https://doi.org/10.1093/genetics/164.4.1567.

[24] Falush D, Stephens M, Pritchard JK. Inference of population structure using multilocus genotype data: dominant markers and null alleles. Molecular Ecology Notes. 2007; 7: 574–578. https://doi.org/10.1111/j.1471-8286.2007.01758.x.

[25] Hubisz MJ, Falush D, Stephens M, Pritchard JK. Inferring weak population structure with the assistance of sample group information. Molecular Ecology Resources. 2009; 9: 1322–1332. https://doi.org/10.1111/j.1755-0998.2009.02591.x.

[26] Evanno G, Regnaut S, Goudet J. Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. Molecular ecology. 2005; 14: 2611–2620. https://doi.org/10.1111/j.1365-294X.2005.02553.x.

[27] Earl DA, vonHoldt BM. STRUCTURE HARVESTER: a website and program for visualizing STRUCTURE output and implementing the Evanno method. Conservation Genet-

ics Resources. 2012; 4: 359–361. https://doi.org/10.1007/s12686-011-9548-7.
[28] Nei M. Bibliography. In Molecular Evolutionary Genetics (pp. 433–496). New York Chichester, West Sussex: Columbia University Press. 1987. https://doi.org/10.7312/nei-92038-016.
[29] Barker JSF. A global protocol for determining genetic distances among domestic livestock breeds. In Proc. 5th World Cong. Genet Appl. Livestock Prod (pp. 501–508). Guelph: Canada. 1994.
[30] Missohou A, Poutya MR, Nenonene A, Dayo GK, Ayssiwede SB, Talaki E, *et al*. Genetic diversity and differentiation in nine West African local goat breeds assessed via microsatellite polymorphism. Small Ruminant Research. 2011; 99: 20–24. https://doi.org/10.1016/j.smallrumres.2011.04.005.
[31] Singh G, Thakur Y, Kour A, Sankhyan V, Katoch S. Genetic characterization of Gaddi goat breed of Western Himalayas using microsatellite markers. Veterinary World. 2015; 8: 527–531. https://doi.org/10.14202/vetworld.2015.527-531.
[32] Susilorini TE, Wulandari D, Furqon A, Septian WA, Saputra F, Suyadi S. Genetic diversity of various goat breeds in East Java based on DNA microsatellite markers. Tropical Animal Science Journal. 2022; 45: 247–254.
[33] Parejo JC, Padilla JA, Calero R, Martínez-Trancón M, Sansinforiano E, Rabasco A, *et al*. Population genetic structure and conservation management of Retinta Extremena goats. Small Ruminant Research. 2015; 124: 9–16. https://doi.org/10.1016/j.smallrumres.2015.01.004.
[34] Dixit SP, Verma NK, Aggarwal RAK, Vyas MK, Rana J, Sharma A, *et al*. Genetic variability and bottleneck analyses of kanniadu goat breed based on microsatellite markers. Indian Journal of Animal Sciences. 2011; 81: 43–48. https://epubs.icar.org.in/index.php/IJAnS/article/view/2972.
[35] Dixit SP, Verma NK, Aggarwal RAK, Vyas MK, Rana J, Sharma A, *et al*. Genetic diversity and relationship among southern Indian goat breeds based on microsatellite markers. Small Ruminant Research. 2010; 91: 153–159. https://doi.org/10.1016/j.smallrumres.2010.02.015.
[36] Dixit SP, Verma NK, Aggarwal RAK, Vyas MK, Rana J, Sharma A. Genetic diversity and relationship among Indian goat breeds based on microsatellite markers. Small Ruminant Research. 2012; 105: 38–45. https://doi.org/10.1016/j.smallrumres.2011.11.026.
[37] Kumar S, Dixit SP, Verma NK, Singh DK, Pande A, Kumar S, *et al*. Genetic Diversity Analysis of the Gohilwari Breed of Indian Goat (Capra hircus) Using Microsatellite Markers. American Journal of Animal and Veterinary Sciences. 2009; 4: 49–57. https://doi.org/10.3844/ajavsp.2009.49.57.
[38] Botstein D, White RL, Skolnick M, Davis RW. Construction of a genetic linkage map in man using restriction fragment length polymorphisms. American journal of human genetics. 1980; 32: 314–331.
[39] Bosman L, van Marle-Köster E, Visser C. Genetic diversity of South African dairy goats for genetic management and improvement. Small Ruminant Research. 2015; 123: 224–231. https://doi.org/10.1016/j.smallrumres.2014.12.003.
[40] Radhika G, Raghavan KC, Aravindakshan TV, Thirupathy V. Genetic diversity and population structure analysis of native and crossbred goat genetic groups of Kerala, India. Small Ruminant Research. 2015; 131: 50–57. https://doi.org/10.1016/j.smallrumres.2015.08.008.
[41] Hedrick PW. Genetics of Population. Jones and Bartlett, Sudbury, Mass. 2000; 34–47.
[42] Glowatzki-Mullis M, Muntwyler J, Bäumle E, Gaillard C. Genetic diversity measures of Swiss goat breeds as decision-making support for conservation policy. Small Ruminant Research. 2008; 74: 202–211. https://doi.org/10.1016/j.smallrumres.2007.07.002.
[43] Frankham R, Ballou JD, Briscoe DA. An Introduction to Conservation Genetics. Cambridge University Press: Cambridge, UK. 2002. https://doi.org/10.1017/CBO9780511808999.
[44] Serrano M, Calvo JH, Martínez M, Marcos-Carcavilla A, Cuevas J, González C, *et al*. Microsatellite based genetic diversity and population structure of the endangered Spanish Guadarrama goat breed. BMC Genetics. 2009; 10: 61. https://doi.org/10.1186/1471-2156-10-61.
[45] Amie Marini AB, Hifzan RM, Tan SG, Panandam JM. Assessment of genetic diversity on goat breeds in Malaysia using microsatellite markers. Malaysian Journal of Animal Science. 2014; 17: 19–26.
[46] Bulut Z, Kurar E, Ozsensoy Y, Altunok V, Nizamlioglu M. Genetic diversity of eight domestic goat populations raised in Turkey. BioMed Research International. 2016; 2830394. https://doi.org/10.1155/2016/2830394.
[47] Elbeltagy AR, Aboul-Naga AM, Hassen H, Solouma GM, Rischkowsky B, Mwacharo JM. Genetic diversity and structure of goats within an early livestock dispersal area in Eastern North Africa. African Journal of Biotechnology. 2016; 15: 431–441. https://doi.org/10.5897/AJB2015.14891.
[48] Murital I, Afolayan O, Bemji MN, Dadi O, Landi V, Martinez A, *et al*. Genetic diversity and population structure of Nigerian indigenous goat using DNA microsatellite markers. Archivos de Zootecnia. 2015; 64: 93–98. https://doi.org/10.21071/az.v64i246.382.
[49] Kim KS, Yeo JS, Lee JW, Kim JW, Choi CB. Genetic Diversity of Goats from Korea and China Using Microsatellite Analysis. Asian-Australasian Journal of Animal Sciences. 2002; 15: 461–465. https://doi.org/10.5713/ajas.2002.461.