Phenotypic and molecular characterization of goat populations in western Algeria

Sarra Belkhadem[1,2]* Ikram Mkedder[1,3]
Semir Bechir Suheil Gaouar[1] Nacera Tabet Aoul[2,4]

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Summary

Background: Goat farming is vital in arid regions. In Algeria, local goats make an important contribution to meat and milk production. Yet, despite their economic importance, goats are not used to their full potential. This is largely due to the limited breeding programmes and the lack of genetic studies. Phenotypic and genetic analyses can be used to determine livestock adaptability and productivity. Morphometric traits provide insights into body structure and growth, while molecular studies identify key genes like MSTN coding for myostatin, which regulates muscle growth and development, and PRL coding for prolactin, which is important in milk production and the development of mammary glands. ***Aim***: This study investigates the phenotypic and molecular genetic traits of local goat populations in western Algeria. ***Methods***: Morphometric data and blood samples were collected from 119 adult goats across four regions (Oran, Ain-Temouchent, Tlemcen and Mecheria). The traits measured included body, ear and tail length, as well as heights at different points of the body. ***Results***: Descriptive analysis showed that body length (BL), chest size (CS) and abdominal circumference (AC) had the highest mean values, while chest depth (CD) was the most stable trait with minimal variation. Principal Component Analysis (PCA) revealed a strong correlation between traits, such as the height at the withers, back and sacrum height. Using PCR-RFLP technology, genotypic frequencies for the MSTN and PRL loci were found after DNA extraction for all blood samples. The PCA of morphometric traits and genotypes of the two genes, MSTN and PRL, revealed that the MSTN gene demonstrates a moderate positive correlation with the neck length and pelvis width traits. On the other hand, the population showed low genetic diversity by studied regions, with higher variability in Oran compared to Tlemcen. ***Conclusions***: The study underscores the critical need to develop and improve breeding strategies to increase overall meat and milk production. Furthermore, it highlights the largely untapped potential of goat farming in Algeria, a sector which could contribute significantly to the national agricultural production and rural economy.

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■ INTRODUCTION

Improved breeding and nutrition has boosted the efficiency of growth in different livestock production sectors. However, performance often depends on the use of high quality feed, which may be a limiting factor. New approaches are being devised, involving the use of alternative feed to improve ruminant development, sustain efficiency and safeguard the quality of animal products (Brameld & Parr, 2016). Goats are important source of meat and milk. Scientists are studying how genetic differences in goats may affect important traits, such as reproduction. These differences are valuable when it comes to breeding more productive goats. They also reveal how different breeds are related (Sodhi *et al*., 2007). In Algeria, goat farming is a significant agricultural activity, particularly in harsh environments, such as mountains, steppes and the Sahara. The diverse local breeds are well

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1. Laboratory of Applied Genetics in Agronomy, Ecology and Public Health (GenApAgiE). Biology Department, University Abou Bekr Belkaid, Tlemcen, Algeria

2. Laboratory of Molecular and Cellular Genetics, Department of Applied Molecular Genetics, Faculty of Natural and Life Sciences, University of Science and Technology of Oran Mohamed Boudiaf, Oran, Algeria

3. Research Unit on Science Mediation, Center for Scientific and Technical Information Research, Tlemcen, Algeria

4. Department of Biotechnology, Faculty SNV, University Oran1 Ahmed Benbella, Oran, Algeria

* Corresponding Author:
Phone: +213 699120261; Email: sara02belkhadem@gmail.com

adapted to their environments (Fantazi *et al*., 2017; Belkhadem *et al*., 2019). With the increasing demand for goat meat, improving certain growth traits in local breeds is a top priority (Bi *et al*., 2020). This issue has generated interest in studies on the phenotypic and genetic characterization and selection within the Algerian goat population. In Algeria, four local breeds have been identified using microsatellites: Arbia, Mekatia, M'zabite and Naine of Kabyle (Fantazi *et al*., 2017). In recent years, studies conducted by various authors have yielded interesting results, revealing that the four native Algerian goat breeds are distinct and have a good level of genetic diversity (Manallah & Dekhili, 2011; Dekhili *et al*. 2013; were investigated for eight qualitative morphological traits and 17 body measurements. Sampling included three environmental areas: Northern, Central and Southern area. Coefficients of variation ranged from 10.9 percent to 34.7 percent, showing high heterogeneity. Canonical analyses showed that differences in body measurements between the three area-populations were large and significant in all traits ($P < 0.001$ Belantar *et al*. 2018; Benyoub *et al*. 2018; Belkhadem *et al*. 2019; Laouadi *et al*. 2020; Sahraoui *et al*. 2020).

The myostatin (MSTN) gene is a growth and differentiation factor. It plays a key role in growth and muscle development. It is essential for muscle growth (Abbas *et al*. 2023) and regulates muscle development by inhibiting excessive growth. It is highly conserved across different tissues and species, highlighting its essential biological role. While primarily expressed in skeletal muscle, it is also present at lower levels in other tissues, including the cardiac muscle and mammary gland, where it may influence growth and metabolism (Ji *et al*., 1998). Therefore, the MSTN gene and its variants are increasingly the focus of studies to investigate the association between growth and meat traits in animal breeding and reproduction (Liu *et al*., 2020). The prolactin (PRL) gene plays an important role in growth, variation of growth muscle and lactation (Abdel-Aziem *et al*., 2018). Numerous studies have reported associations between PRL polymorphisms and wool or cashmere traits in goats and sheep (Shamsalddini *et al*., 2016; El-Shorbagy *et al*., 2022; Nowier *et al*., 2023). Mutations in the MSTN and PRL genes significantly influence zootechnical traits in goats, enhancing growth and feed conversion efficiency for meat production (MSTN) or improving milk yield and lactation for dairy production (PRL). Targeted breeding strategies could harness the potential of these mutations (Grobet *et al*., 1998; McPherron & Lee, 1997). Several studies have found an association between myostatin and prolactin with body traits in goats (Bi *et al*., 2020; Liu *et al*., 2020).

This study aims to improve our understanding of local Algerian goat breeds by focusing on a few key areas. First, it will identify the morphological variations between individual goats, by applying discriminant analysis to the morphometric characteristics of the goat population studied. Second, the study seeks to analyse the MSTN and PRL genes using a molecular approach. Lastly, it explores how these genes might be linked to body traits. The findings could help improve breeding programmes to improve growth and meat production.

■ MATERIAL AND METHODS

Study regions

This study used a purposive sampling method. Goats were selected according to their geographic distribution and herd size across four states in western Algeria: Oran (42 individuals) and Ain-Temouchent (23 individuals), representing the coastal region; Tlemcen (21 individuals) and Mecheria (33 individuals), representing the steppe region (Figure 1). These states were chosen because the local breeders' cooperation meant we had access to a variety of goat populations. It also provided a guarantee that the samples collected were representative of the genetic and phenotypic diversity found in the different geographical areas. The sampling was conducted in February, May and June 2023 in relation to different criteria, such as goat reproductive cycles and seasonal fluctuations that impact herd size and composition. Thus, we were able to determine the genetic diversity of the local goat populations in the four states selected.

Phenotypic data collection

The study to investigate various morpho-biometric traits of local goats was conducted in four different states and involved 119 adult goats. The traits measured were selected from morphological studies (Manallah & Dekhili, 2011). They included body length (BL), ear length (EL), tail length (TL), pelvis length (PL), neck length (NL), head length (HL), chest size (CS), abdominal circumference (AC), pelvis width (PW), chest width (CW), height at the withers (HW), back height (BH), sacrum height (SH), chest depth (CD), and flank depth (FD). Blood samples were also collected from each goat to provide additional data for genetic analysis.

Molecular study

DNA Extraction

Genomic DNA was extracted from whole blood samples using the salting out technique, according to the NaCl protocol (Miller *et al*., 1988).

Polymerase Chain Reaction (PCR)

We diluted all DNA samples to a standard of 1/10 of their concentrated DNA. Two pairs of primers were used for amplifying each of the MSTN and PRL loci. In the case of MSTN, the primers were F: CCGGAGAGACTTTGGGCTTGA and R: TCATGAGCACCCACAGCG GTC. For PRL, the primers were F: ATTCCTGGAGCCAAAGAG and R: TGTGGGCTTAGCAGTTGT (Abdel-Aziem *et al*., 2018). The amplification reaction was carried out in a 20 μl volume containing 2 μl genomic DNA, 4 μl of PCR mixture (Solidebiodyne), 0.5 μl of each primer and 13 μl ultrapure water. PCR amplification was carried out on a thermal cycler (Biometra T personal) with the

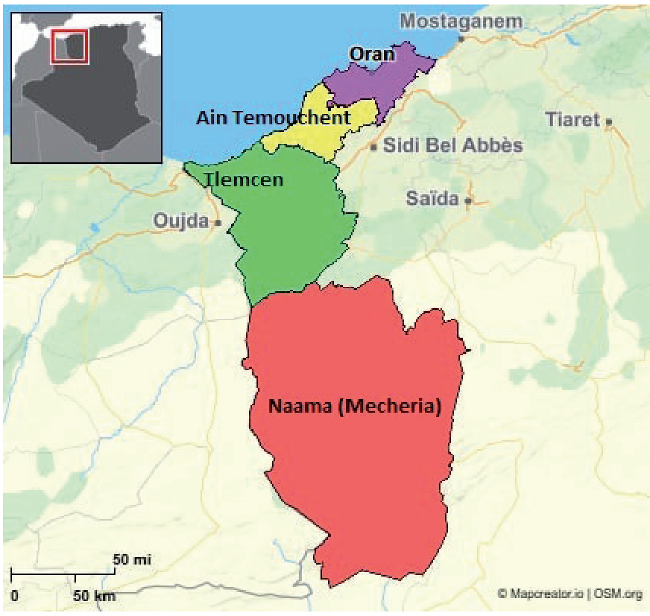

Figure 1: *Geographical distribution of sampling in four states in western Algeria /// Répartition géographique des échantillons dans quatre régions de l'ouest de l'Algérie*

following conditions for MSTN: primary denaturation in the first cycle at 94°C for 4 min, denaturation at 94°C for 60 s, annealing at 55.5°C for 35 s, elongation at 72°C for 2 min, with a number of cycles of 35, and a final extension at 72°C for 4 min. The PCR amplification conditions for PRL were: primary denaturation in the first cycle at 95°C for 5 min, denaturation at 94°C for 30 s, annealing at 56°C/35 s, elongation at 72°C/30 s, with a number of cycles of 35 and a final extension at 72°C for 10 min. All PCR products were resolved on 1% agarose gel electrophoresis at 100 V. The gels were treated with ethidium bromide and visualized under ultraviolet (UV) light.

Restriction Fragment Length Polymorphism

The procedure was conducted with 30 μl of reaction mixture per sample, comprising 10 μl of PCR product, 3 μl of 10× buffer and 2 μl of restriction enzyme digest (Eco24I and HaeIII) specific to each gene and made up with ultrapure water. The reaction mixtures were incubated overnight at 37°C. The digestion products were then separated by electrophoresis on a 2.5% agarose gel and stained with ethidium bromide. The bands were visualized under UV light.

Statistical analysis

All statistical analyses were conducted using SPSS 21 software. We used discriminant analysis to classify the quantitative data collected from the four states. Before the statistical tests began, a normality test was performed on the various character values. A principal component analysis (PCA) was carried out to group similar individuals and to differentiate goats in relation to specific criteria. Here, the aim was to create a classification system to clearly identify the populations studied. Ascending Hierarchical Classification (AHC) was utilized to determine the optimal number of groups within our sample. The hierarchical clustering was performed using a dendrogram to group individuals on the basis of their similarities. The clustering process was conducted by applying an agglomerative approach, whereby individuals with the highest similarity were merged iteratively.

The Shannon-Weaver Diversity Index was recalculated using Excel for Windows (Version 2021) with the formula:

$$H'=-\sum i=1spi\cdot \ln(pi) \qquad \text{(equation 1)}$$

Here, pi represents the proportion of the total samples attributed to species i, which is determined by dividing the number of individuals from species i by the total number of samples. The letter s denotes the total number of species and Hmax=ln(S) indicates the maximum possible diversity. Regularity E is calculated as H'/Hmax. The Shannon-Weaver diversity index is a statistical measure used to quantify diversity within a population. It considers both the richness and evenness of observed categories.

The genotypic and allelic frequencies, as well as the observed and expected heterozygosity, were calculated by direct counting. Additionally, we performed a chi-square test (χ^2) for the Hardy-Weinberg equilibrium (HWE). Thus, using a two-allele model and a significance threshold of $p < 0.05$ and ddl = 1, we were able to determine whether the population is in Hardy-Weinberg equilibrium.

■ RESULTS

Descriptive analysis of quantitative characteristics

The different body measurements of goats are reported in Table I.

The characteristic traits CS, AC, HW, BH and SH have the highest average values. AC has the largest spread, ranging from 69 to 106 cm. CD shows low variability, which may indicate structural homogeneity. EL and PW have the lowest average values, with EL showing notable variation. Several characters, like TL and HL, show tight groupings around their mean with low variability.

Table II highlights regional differences in goat body traits across Mecheria, Tlemcen, Ain-Temouchent and Oran. Tlemcen goats exhibit the largest body sizes, with the highest averages for BL (73.9 cm) and AC (93.2 cm), which suggests superior growth. In Mecheria and Ain-Temouchent, goats display similar averages for skeletal traits, such as PL and BH, indicating consistency across these regions. We observed lower values for certain traits in Oran, for example EL and TL, and a relatively high HW, suggesting a balanced structure. In terms of variability, the Oran and Ain-Temouchent goats show more diversity in traits like PW and CW compared to Mecheria, where there is greater uniformity across traits. The ranges indicate that Tlemcen goats have the longest BL (up to 83 cm), whereas the Mecheria goats have the shortest (56 cm). These regional differences may reflect environmental influences or specific breeding practices tailored to local conditions.

All the measurements of studied variables were presented in Principal Component Analysis (PCA) (Figure 2).

In Figure 2, the PCA illustrates the relationships between various morphometric measurements in goats. The first three principal components explain 66.29% of the total variance. PC1 (39.25%) reflects overall size and includes measurements of length, such as BL, EL, TL, PL, HL, CS, AC, HW, BH, SH and CD. These constitute the most significant variables in the dataset. PC2 (19.50%) highlights shape differences and group variables of width, such as NL, PW, CW and FD, which change in similar directions. PC3 accounts for 7.54% of the total variance and captures finer distinct traits, which are not reflected in the overall size (PC1) or the primary shape differences (PC2). The characteristics of PC1 and PC2 often include subtle

Table I: Descriptive analysis of body measurements in the surveyed population /// *Analyse descriptive des mensurations corporelles de la population enquêtée*

	BL	EL	TL	PL	NL	HL	CS	AC	PW	CW	HW	BH	SH	CD	FD
Mean	68.63	18.91	12.51	17.29	29.90	21.00	80.30	86.03	27.52	39.35	71.30	69.79	71.85	31.23	30.70
Median	69.00	18.00	12.00	17.00	30.00	21.00	80.00	85.00	28.00	39.00	71.00	69.00	71.00	31.00	30.00
SD	6.22	5.14	1.97	2.52	4.00	1.92	5.95	7.91	4.95	6.02	5.28	4.92	4.65	1.16	4.40
Minimum	53.00	6.00	8.00	14.00	21.00	16.00	68.00	69.00	17.00	25.00	61.00	60.00	63.00	24.00	23.00
Maximum	90.00	35.00	18.00	32.00	41.00	29.00	99.00	106.00	49.00	58.00	91.00	88.00	88.00	41.00	42.00

Body length (BL), Ear Length (EL), Tail Length (TL), Pelvis Length (PL), Neck Length (NL), Head Length (HL), Chest Size (CS), Abdominal Circumference (AC), Pelvis Width (PW), Chest Width (CW), Height at the Withers (HW), Back Height (BH), Sacrum Height (SH), Chest Depth (CD), Flank Depth (FD). Standard Deviation (SD) /// *Longueur du corps (BL), longueur des oreilles (EL), longueur de la queue (TL), longueur du bassin (PL), longueur du cou (NL), longueur de la tête (HL), tour de poitrine (CS), circonférence abdominale (AC), largeur du bassin (PW), largeur de la poitrine (CW), hauteur au garrot (HW), hauteur du dos (BH), hauteur du sacrum (SH), profondeur de la poitrine (CD), profondeur des flancs (FD). Écart-type (SD)*

Table II: *Regional differences in goat body traits in Mecheria, Tlemcen, Ain-Temouchent and Oran, Algeria /// Différences régionales dans les caractéristiques corporelles des chèvres à Mecheria, Tlemcen, Ain-Temouchent et Oran, Algérie*

Area		BL	EL	TL	PL	NL	HL	CS	AC	PW	CW	HW	BH	SH	CD	FD
Mecheria	Mean	68	22.19	12.22	17.93	32.74	21.74	80.58	85.58	30.12	45.51	73.90	72.45	73.77	30.70	28.90
	Median	69.00	22.00	12.00	17.00	32.00	22.00	80.00	85.00	30.00	46.00	73.00	72.00	72.00	30.00	29.00
	SD	5.84	4.91	2.14	3.24	3.473	1.48	6.19	7.79	4.90	5.29	4.49	5.03	5.60	3.01	3.08
	Minimum	56.00	11.00	8.00	14.00	26.00	19.00	69.00	70.00	20.00	33.00	66.00	65.00	66.00	26.00	23.00
	Maximum	77.00	30.00	18.00	32.00	41.00	27.00	99.00	105.00	49.00	58.00	84.00	86.00	88.00	39.00	36.00
Tlemcen	Mean	73.90	20.47	13.71	19.00	24.09	20.66	83.52	93.28	23.19	35.76	69.47	68.90	71.85	34.00	36.85
	Median	74.00	19.00	14.00	18.00	24.00	20.00	84.00	94.00	23.00	36.00	70.00	69.00	71.00	34.00	37.00
	SD	4.98	6.27	2.14	2.66	2.16	2.08	5.40	6.98	2.44	2.98	5.51	4.26	3.88	2.00	2.28
	Minimum	62.00	9.00	10.00	16.00	21.00	18.00	72.00	81.00	18.00	31.00	61.00	62.00	66.00	31.00	32.00
	Maximum	83.00	35.00	17.00	26.00	28.00	25.00	97.00	106.00	29.00	46.00	80.00	80.00	82.00	38.00	41.00
Ain-Temouchent	Mean	66.82	17.65	12.52	16.65	30.86	21.60	78.56	84.65	28.21	35.30	68.95	68.04	70.91	29.78	29.95
	Median	67.00	18.00	12.00	16.00	30.00	21.00	79.00	83.00	28.00	35.00	69.00	68.00	70.00	30.00	30.00
	SD	5.72	2.83	1.90	1.74	3.16	2.42	5.72	8.84	2.99	3.87	4.39	4.52	3.52	2.72	2.89
	Minimum	53.00	9.00	10.00	15.00	26.00	18.00	70.00	69.00	23.00	28.00	61.00	60.00	65.00	25.00	25.00
	Maximum	76.00	24.00	16.00	21.00	37.00	29.00	92.00	104.00	36.00	44.00	78.00	76.00	80.00	34.00	37.00
Oran	Mean	67.45	16.40	12.11	16.33	30.26	20.50	79.45	83.50	27.40	38.83	71.66	69.23	70.95	31.02	29.38
	Median	67.00	16.00	12.00	16.00	31.00	21.00	79.00	82.00	28.00	40.00	71.00	69.00	70.00	31.00	29.00
	SD	6.08	4.11	1.59	1.43	4.108	1.641	5.71	5.67	5.392	5.00	5.38	4.74	4.47	3.22	4.102
	Minimum	57.00	6.00	10.00	14.00	23.00	16.00	68.00	73.00	17.00	25.00	63.00	63.00	63.00	25.00	23.00
	Maximum	90.00	30.00	15.00	21.00	38.00	25.00	97.00	95.00	43.00	51.00	91.00	88.00	87.00	41.00	42.00

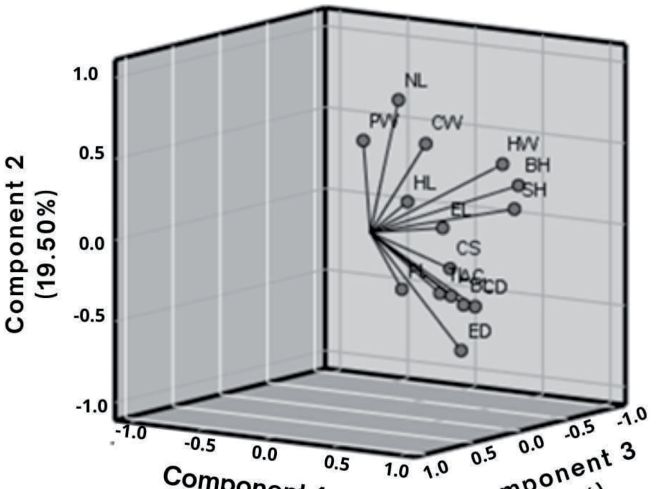

Figure 2: Presentation of body measurements by PCA in goat populations in western Algeria /// *Présentation des mensurations corporelles selon l'ACP dans les populations caprines de l'ouest de l'Algérie*

morphological features, such as specific aspects of head shape, ear size or other measurements that reflect individual variation between goats. While PC3 represents a smaller portion of total variability, it highlights additional dimensions of phenotypic diversity. The positive correlation between variables with similar directions (e.g., NL, CW, PW) suggests that common aspects of body conformation are shared. Animals with longer necks may also tend to have broader chests and wider pelvises. The correlated traits may indicate overall structural robustness, which is often linked to growth potential, physical strength and productivity in terms of meat or milk yield.

In the PCA, the variables ED, BL, CD and CS form separate clusters. This indicates that they capture specific morphological features, which are influenced by factors that differ from those affecting overall size or shape. Unlike the traits in the main size cluster, which tend to increase or decrease together due to common growth factors, these particular measurements probably reflect unique features, for example ear size, body length or chest width, which are shaped by distinct genetic, environmental or developmental factors. These traits are in separate groups, suggesting that they respond independently to selective pressures, such as targeted breeding, nutritional variations or local adaptations. This observation highlights the additional layers of phenotypic diversity.

The analysis of classification of the goat population in western Algeria is presented in Figure 3.

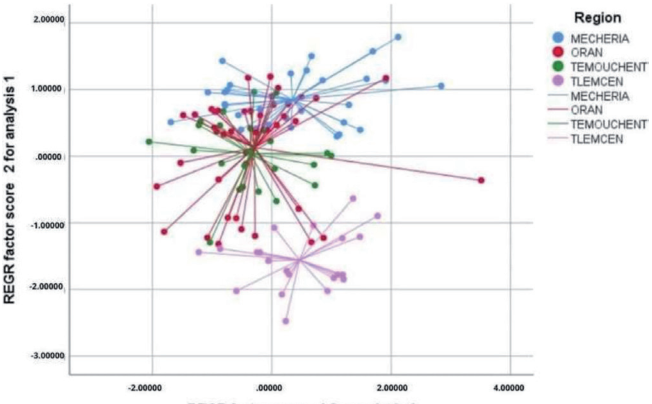

Figure 3: Barycentric distribution of individuals, by region /// *Répartition barycentrique des individus par région*

According to Figure 3, there are four groups, which indicate a measure of dispersion or distance from a central tendency. This scatter plot represents the distribution of factor scores from a PCA multivariate analysis in four states: Mecheria, Oran, Ain-Temouchent and Tlemcen. Each color represents a different region. The dots mark individual observations and the lines connect them to the center, which could indicate the mean or central tendency of each group. Mecheria and Oran show a wider spread of points, suggesting greater variability within the goat population in these states. In contrast, the points pertaining to individual goats in Tlemcen are closely grouped in the lower half of the plot, indicating that they have more similar characteristics. Ain-Temouchent displays a moderate spread, highlighting potential differences in the traits captured by this analysis. Mecheria and Oran appear to have more diverse samples, while Tlemcen exhibits greater homogeneity. The hierarchical clustering was performed using a dendrogram (Figure 4).

Figure 4 shows a hierarchical classification based on all available morphological and genetic characteristics and data. This classification scheme revealed five distinct clusters. Cluster 1 comprises 11 individuals from the Arbia breed. Cluster 2 was subdivided into two sub-classes. The first sub-class was further divided into two sub-classes of 19 individuals, including 3 mixed-breed individuals. The second sub-class contains 5 individuals of the Arbia breed. Cluster 3 consists of two individuals from the Arbia breed and one mixed-breed. Cluster 4 also has three individuals, two from the Arbia breed and one mixed-breed. Cluster 5 is made up of the remaining population, which is divided into three large sub-classes.

Shannon-Weaver Diversity Index

The diversity of morphological traits shown by the Shannon-Weaver index in each studied region is presented in Table III.

The results shown in Table III reveal the low level of diversity in the studied population. The trait with a higher average diversity is BL, with the highest value observed in Oran and the lowest in Tlemcen. The traits HW, BH, SH and HL also demonstrate a low level of diversity, with a higher average value in all populations. In general, the population in Oran presents more diversity for the studied traits than the populations in the other three regions. The lowest diversity was found in the Tlemcen region.

Molecular analysis

The PCR-RFLP technique was applied to detect the MSTN and PRL genotype in the DNA of 119 individual goats from local herds in four states in western Algeria. The MSTN-PCR produced a 337 bp DNA fragment. When digested with the HaeIII restriction enzyme, the 337 bp DNA fragment shows distinct patterns based on the genotype. Individuals homozygous for the *a* allele (-/-) show a single cut, resulting in two fragments. This was not observed in any individuals in our study. Heterozygous individuals (*Aa*, +/-) exhibit both cut and uncut fragments, as found in one individual in our study. Individuals homozygous for the *A* allele (+/+) show no cutting and the original fragment remains intact, as was observed in 118 individuals.

The PRL-PCR yielded a 655 bp DNA fragment, which produced patterns based on the genotype when digested with the Eco24I restriction

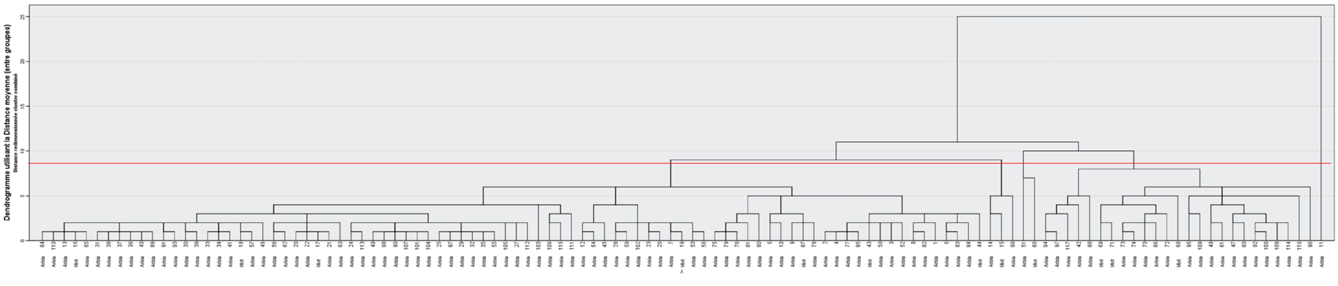

Figure 4: Dendrogram of hierarchical clustering on morphological and genetic characteristics /// *Dendrogramme de classification hiérarchique des caractéristiques morphologiques et génétiques*

Table III: Shannon-Weaver Diversity Index of studied goat population in western Algeria /// *Indice de diversité de Shannon de la population caprine étudiée dans l'ouest de l'Algérie*

		BL	EL	TL	PL	NL	HL	CS	AC	PW	CW	HW	BH	SH	CD	FD
Mechria	H	0.69	0.46	0.68	0.68	0.61	0.61	0.64	0.70	0.61	0.53	0.66	0.66	0.68	0.67	0.67
	H/Hmax	0.50	0.33	0.49	0.49	0.44	0.44	0.46	0.51	0.44	0.38	0.47	0.47	0.49	0.48	0.48
Tlemcen	H	0.46	0.51	0.49	0.44	0.40	0.53	0.49	0.45	0.45	0.47	0.53	0.52	0.54	0.37	0.36
	H/Hmax	0.33	0.36	0.35	0.32	0.29	0.38	0.35	0.32	0.32	0.34	0.38	0.37	0.39	0.26	0.26
Ain Temouchent	H	0.57	0.70	0.56	0.58	0.52	0.65	0.57	0.57	0.55	0.54	0.57	0.57	0.58	0.58	0.54
	H/Hmax	0.41	0.50	0.40	0.41	0.38	0.47	0.41	0.41	0.39	0.39	0.41	0.41	0.42	0.41	0.39
Oran	H	0.83	0.81	0.82	0.84	0.84	0.85	0.83	0.82	0.84	0.86	0.83	0.84	0.85	0.83	0.84
	H/Hmax	0.60	0.58	0.59	0.61	0.60	0.61	0.59	0.59	0.60	0.62	0.60	0.60	0.61	0.60	0.61
Mean		0.46	0.44	0.45	0.45	0.42	0.47	0.45	0.45	0.43	0.43	0.46	0.46	0.46	0.43	0.43

Body length (BL), Ear Length (EL), Tail Length (TL), Pelvis Length (PL), Neck Length (NL), Head Length (HL), Chest Size (CS), Abdominal Circumference (AC), Pelvis Width (PW), Chest Width (CW), Height at the Withers (HW), Back Height (BH), Sacrum Height (SH), Chest Depth (CD), Flank Depth (FD) /// *Longueur du corps (BL), longueur des oreilles (EL), longueur de la queue (TL), longueur du bassin (PL), longueur du cou (NL), longueur de la tête (HL), tour de poitrine (CS), circonférence abdominale (AC), largeur du bassin (PW), largeur de la poitrine (CW), hauteur au garrot (HW), hauteur du dos (BH), hauteur du sacrum (SH), profondeur de la poitrine (CD), profondeur des flancs (FD).*

enzyme. Individuals that are homozygous for the *b* allele (-/-) show a single cut, resulting in two fragments. This was not observed in any of the individuals in our study. Heterozygous individuals (*Bb*, +/-) exhibited both cut and uncut fragments for two individuals in our study. In contrast, individuals that are homozygous for the *B* allele (+/+) show no cutting and the original fragment is retained. This was observed in 117 individuals in the study. The allele frequencies for the two genes and the observed heterozygosity (Ho), estimated heterozygosity (He) and χ2 were calculated and are presented in Table IV.

Correlation between MSTN and PRL genes and specific body traits

The associations between variations in the MSTN and PRL genes and specific body traits in goats in western Algeria are presented in Figure 5.

Figure 5 clearly shows that the 3D PCA demonstrates the relationship between body characteristics and the MSTN and PRL genes. PC1 (34.65%), PC2 (17.32%), and PC3 (6.88%) account for 58.85% of the data variation. Traits such as NL, PW, CW, HW and HL are closely linked, which means they change together. In contrast, ED, BL and CS are inversely related, with a negative correlation. The positioning of Digestion_MSTN and Digestion_PRL suggests that they have separate effects on body features. Our results reveal that the MSTN gene is associated with muscle growth and the PRL gene is associated with metabolism or body development. Our investigation sheds light on how these genes affect different body traits in goats.

Table IV: Allele frequency, observed heterozygosity (Ho), estimated heterozygosity (He) and v2 values of PRL-Eco24I/PCR-RFLP and MSTN-HaeIII/PCR-RFLP ($P < 0.05$) /// *Fréquence allélique, hétérozygotie observée (Ho), hétérozygotie estimée (He) et valeurs v2 de PRL-Eco24I/PCR-RFLP et de MSTN-HaeIII/PCR-RFLP ($P < 0,05$)*

Gene	Allele Frequency		Observed Het (H')		Expected Het (He)		x^2
	+/+	+/-	+/+	+/-	+/+	+/-	
PRL	0.991	0.0084	0.983	0.016	0.982	0.000	0.000001
MSTN	0.0995	0.008	0.991	0.008	0.990	0.000	0.000001

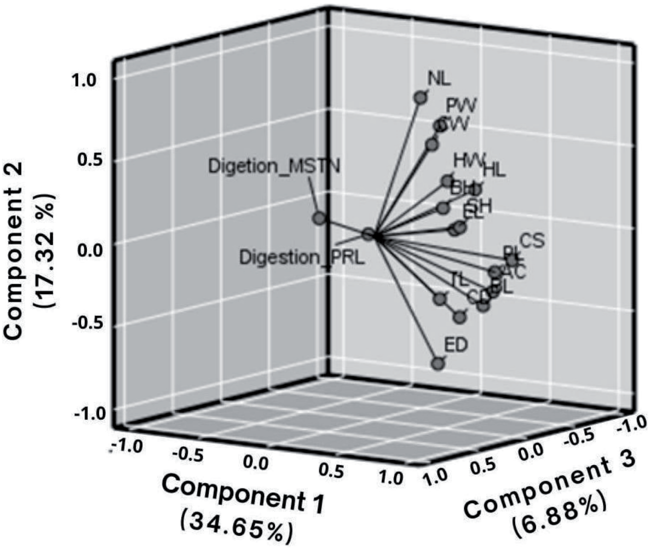

Figure 5: Principal Component Analysis of MSTN and PRL gene effects on goat body traits /// *Analyse en composantes principales des effets des gènes MSTN et PRL sur les caractéristiques corporelles des chèvres étudiées*

■ DISCUSSION

The limited availability of information on goat resources in Algeria have significantly hindered the phenotypic and molecular genetic characterization of the various local goat breeds. As a result, we know little about the diversity, adaptability and productivity of these breeds. A comprehensive understanding of the phenotypic and molecular genetic identification of goat populations in Algeria is crucial. It would contribute to the development of effective breeding strategies in order to optimize the economic potential of local goat breeds and conserve genetic diversity.

In this study, Table I provides a detailed overview of various traits, focusing on their mean values, variability and range. Several traits, such as BL, CS, AC and HW exhibit higher mean values. Traits like EL and PW, on the other hand, have much lower averages. CS and AC show significant variability across the sample, whereas traits like HL, TL and CD are stable and more consistent with lower standard deviations. CD stands out as the most stable trait, while AC has the widest range, highlighting the diversity within the dataset. This combination of highly stable and variable traits reflects a diverse pattern across the data. When comparing our findings with results from previous studies, several observations emerge. For instance, average BL in our study is 68.63 cm, which is moderate compared to 73.80 cm (Benyoub, 2018) and 76.87 cm (Laouadi *et al*., 2020), and higher than 60.60 cm (Akounda *et al*., 2023) and 65.00 cm (Belantar *et al*, 2018). Similarly, EL in this study is 18.90 cm, which is comparable to 18.80 cm (Belantar *et al*., 2018), but higher than 14.95 cm (Fantazi *et al*., 2017), 17.87 cm (Laouadi *et al*., 2020), and 13.55 cm (Akounda *et al*., 2023). In our study, HW is 71.30 cm, which is similar to 71.79 cm (Laouadi *et al*., 2020), but higher than 66.76 cm (Fantazi *et al*., 2017) and 70.82 cm (Benyoub, 2018). TL in this study is 12.51 cm, which matches (Belantar *et al*., 2018) and slightly exceeds 11.56 cm (Laouadi *et al*., 2020) and 11.97 cm (Akounda *et al*., 2023). Lastly, HL at 21.00 cm aligns closely with 21.24 cm (Belantar *et al*., 2018).

Table II presents statistical data for four regions (Mecheria, Tlemcen, Ain-Timouchent and Oran) across multiple variables. The data includes mean values, standard deviation, as well as minimum and maximum values. Each variable is measured in each region, providing insights into average regional performance and variability. For instance, Mecheria shows relatively high variability in certain variables, as indicated by the standard deviations, whereas Tlemcen exhibits tighter clustering around its mean values. This summary allows us to compare regional patterns and identify similarities or significant differences across the measured factors.

The principal components identified in this study reveal a strong correlation between body traits such as HW, BH and SH. Our results align with findings from previous research (Benyoub *et al*., 2018; Belantar *et al*., 2018). Moreover, the hierarchical classification tree, which groups individuals based on their body measurements and genotype results, indicates that most animals cluster primarily according to BL and HL. The Shannon-Weaver index reflects an overall low diversity in the population. However, certain traits exhibit moderate diversity, particularly BL, for which the highest variation was observed in the Oran region. In addition to BL, other traits such as HW, BH, SH and HL also displayed higher average values, suggesting a degree of phenotypic differentiation in these specific traits across the population. In the regions under study, goats are primarily found in rural and hilly areas, where the rough terrain makes foraging difficult. Therefore, feeding requires considerable physical effort, which draws on specific body regions and muscle groups. As a result of their constant physical activity, goats have adapted their morphological and physiological characteristics in tandem with their environment over time.

Mutations in the MSTN gene are pivotal for traits related to hypertrophy, muscle mass and growth. This makes them a primary focus in studies related to growth and meat production in animal breeding. The influence of MSTN mutations is more significant compared to other gene variants, which underscores their importance in selective breeding programs to improve these traits (Bi *et al*., 2020). Conversely, the prolactin (PRL) gene plays a broader role, influencing lactation, growth, metabolism, osmoregulation, behaviour and reproduction (Chen *et al*., 2018). Given its diverse functions, prolactin is a major subject for studies related to animal productivity and reproduction.

Both the PRL-Eco24I/PCR-RFLP and MSTN-HaeIII/PCR-RFLP loci showed genotypic frequencies in the current investigation. With a chi-square value (χ^2) of 0.000001, the PRL locus showed genotypic frequencies of 0.983 for the +/+ genotype and 0.016 for the +/- genotype. Likewise, the MSTN locus displayed chi-squared values (χ^2) of 0.000001 along with genotypic frequencies of 0.991 and 0.008 for the +/+ and +/- genotypes, respectively. The population under investigation is in Hardy-Weinberg equilibrium for these two loci, as indicated by the p-values of less than 0.05 for both loci (Table IV). The predominance of the +/+ genotype for the genes may indicate a selective advantage for growth-related traits, suggesting that individuals carrying these genotypes are more likely to exhibit enhanced growth potential. This could be due to geographic isolation or intensive farming practices as suggested by Fantazi *et al*. (2017).

According to a survey of breeders and observations made during field trips for sample collection, goat farming is the second most important industry in the area, after sheep farming. Goats are, therefore, considered to be secondary. This is reflected in breeders' management practices. When it comes to goat husbandry, breeders seldom adopt appropriate zootechnical principles in crucial areas, such as breeding, housing and feeding. Goat farming is typically more casual and informal than sheep husbandry. In fact, more care and resources are allocated to sheep production. As a result, there has been limited progress regarding the optimization of goat production. The majority of goat herds are composed of a single breed, with little or no crossbreeding. This is one of the most notable patterns that emerged from our study. By relying on one local breed, a dominant and stable breed pattern has emerged in the region. This may explain the limited genetic variety in the local goat populations. Our study also found that goat milk and meat are underutilized, despite their economic potential as lucrative resources. The majority of breeders do not rear goats for commercial purposes. Instead, goats are kept to guide sheep at pasture, as a pastime or simply because of long-standing family traditions.

As a result, the economic potential of goat farming is virtually unexplored. Yet, if farmers adopted best practices in feeding, breeding and housing, the potential gains in milk and meat production would increase profitability. If goat farming is to be viewed as more than a secondary or traditional activity, a shift in breeders' attitudes is required.

■ CONCLUSION

This study provides valuable insights into the phenotypic and molecular characterization of local goat populations in western Algeria. The results reveal notable regional differences in body traits. Tlemcen goats exhibit the largest body sizes, suggesting superior growth potential, while Oran goats show greater phenotypic diversity. Regarding molecular analysis, interpretation is feasible for the MSTN gene results, whereas the PRL gene results are underrepresented on the correlation circle. The MSTN gene demonstrates a moderate positive correlation with the NL and PW traits and a strong negative correlation with the FD trait. Additionally, it exhibits an average negative correlation with TL, CD, BL, AC and PL traits in descending order. While these findings are moderately satisfactory, the negative correlations observed with certain traits, particularly BL, AC and PL, appear counterintuitive. However, it is important to emphasize that these correlations are not strong and warrant cautious interpretation. Our findings highlight the untapped potential of goat farming in Algeria. Its economic potential in terms of meat and milk production remains limited by traditional practices and the lack of optimized breeding schemes. The adoption of modern zootechnical principles, including improved feeding and better housing conditions, could significantly improve the productivity of Algerian goats. This study lays the groundwork for future research and breeding programs that focus on enhancing the performance and sustainability of local goat populations, while preserving their genetic heritage.

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Conflict of interest

The study was conducted with no conflict of interest.

Author contributions

The authors SB, SBSG and NTA were involved in defining the aim of this article. SB did the sampling, genotyping and data analysis with NTA, IM and SBSG. The manuscript was written by SB and the review was conducted by NTA and SBSG.

Ethics approval

All procedures were carried out in accordance with the ethical standards of the relevant institutional and national guidelines for the care and use of animals, as stipulated by the Ministry of Agriculture and Rural Development of Algeria, under law number 88-08 concerning veterinary activities.

Data availability

The data were not deposited in an official repository. The data that support the study findings are available from the authors upon request.

Declaration of Generative AI in the writing process

The authors did not use any artificial intelligence-assisted technologies in the writing process.

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Résumé

Belkhadem S., Mkedder I., Gaouar S. B. S., Tabet Aoul N. Caractérisation phénotypique et moléculaire des populations caprines dans l'ouest de l'Algérie

Contexte : L'élevage de chèvres est vital dans les régions arides, notamment en Algérie, où les chèvres locales contribuent largement à la production de viande et de lait. Malgré leur importance économique, ces populations restent sous-utilisées en raison de l'insuffisance des programmes d'élevage et des études génétiques. Les analyses phénotypiques et génétiques permettent d'évaluer l'adaptabilité et la productivité. Les traits morphométriques donnent un aperçu de la structure corporelle et de la croissance, tandis que les études moléculaires identifient des gènes clés tels que MSTN codant pour la myostatine, qui régule la croissance et le développement des muscles, et PRL codant pour la prolactine, qui joue un rôle important dans la production de lait et le développement des glandes mammaires. ***Objectif :*** Cette étude porte sur les caractéristiques phénotypiques et génétiques moléculaires des populations locales de chèvres dans l'ouest de l'Algérie. ***Méthodes*** : Des données morphométriques et des échantillons de sang ont été collectés sur 119 chèvres adultes dans quatre régions (Oran, Ain-Temouchent, Tlemcen et Mecheria). Les caractéristiques mesurées étaient la longueur du corps, la longueur des oreilles, la longueur de la queue et les hauteurs à différents points du corps. ***Résultats :*** L'analyse descriptive a montré que la longueur du corps (BL), le tour de poitrine (CS) et la circonférence abdominale (AC) avaient les valeurs moyennes les plus élevées, tandis que la profondeur de poitrine (CD) était le caractère le plus stable avec une variation minimale. L'analyse en composantes principales (ACP) a révélé une forte corrélation entre des caractères tels que la hauteur au garrot, la hauteur du dos et la hauteur du sacrum. Les fréquences génotypiques pour les loci MSTN et PRL ont été déterminées par PCR-RFLP après l'extraction de l'ADN de tous les échantillons de sang. L'ACP des caractères morphométriques et des génotypes des deux gènes a révélé que le gène MSTN présente une corrélation positive modérée avec les caractères NL et PW. D'autre part, la population a montré une faible diversité génétique par zone, avec une variabilité plus élevée à Oran par rapport à Tlemcen. ***Conclusions*** : L'étude souligne le besoin critique de développer et d'améliorer les stratégies de sélection visant à accroître la productivité globale, en particulier dans les domaines de la production de viande et de lait. En outre, elle met en évidence le potentiel largement inexploité de l'élevage caprin en Algérie qui, s'il est correctement exploité, pourrait contribuer de manière significative au secteur agricole et aux économies rurales.

Mots-clés : Caprin, caractérisation, variabilité génétique, ressource animale, Algérie

Resumen

Belkhadem S., Mkedder I., Gaouar S. B. S., Tabet Aoul N. Caracterización fenotípica y molecular de las poblaciones caprinas del oeste de Argelia

Contexto: La ganadería caprina es vital en las regiones áridas, especialmente en Argelia, donde las cabras locales contribuyen ampliamente a la producción de carne y de leche. A pesar de su importancia económica, estas poblaciones son infrautilizadas debido a la insuficiencia de programas ganaderos y de estudios genéticos. Los análisis fenotípicos y genéticos permiten evaluar la adaptabilidad y la productividad. Los rasgos morfométricos proporcionan una imagen de la estructura corporal y del crecimiento, mientras que los estudios moleculares identifican genes clave tales como el MSTN codificador de la miostatina, que regula el crecimiento y el desarrollo de los músculos, y el PRL codificador de la prolactina, que juega un papel importante en la producción de leche y el desarrollo de las glándulas mamarias. ***Objetivo:*** Este estudio trata sobre las características fenotípicas y genéticas moleculares de las poblaciones locales de cabras en el oeste argelino. ***Métodos***: Se recogieron datos morfométricos y muestras de sangre de 119 cabras adultas en cuatro regiones (Orán, Aïn Témouchent, Tremecén y Méchria). Las características medidas fueron la longitud del cuerpo, la longitud de las orejas, la longitud de la cola y las alturas en diferentes puntos del cuerpo. ***Resultados:*** El análisis descriptivo mostró que la longitud del cuerpo (BL), el contorno del pecho (CS) y la circunferencia abdominal (AC) tenían los valores medios más elevados, mientras que la profundidad de pecho (CD) era el carácter más estable, con una variación mínima. El análisis de componentes principales (ACP) reveló una fuerte correlación entre caracteres tales como la altura en la cruz, la altura en el lomo y la altura en el sacro. Las frecuencias genotípicas para los loci MSTN y PRL se determinaron mediante PCR-RFLP después de la extracción del ADN de todas las muestras de sangre. El ACP de los caracteres morfométricos y de los genotipos de los dos genes reveló que el gen MSTN presenta una correlación positiva moderada con los caracteres NL y PW. Por otro lado, la población mostró poca diversidad genética por zona, con una variabilidad más elevada en Orán respecto a Tremecén. ***Conclusiones***: El estudio subraya la necesidad crítica de desarrollar y de mejorar las estrategias de selección con el objetivo de aumentar la productividad global, en particular en los campos de producción cárnica y de leche. Por otro lado, pone en evidencia el potencial ampliamente inexplotado de la ganadería caprina en Argelia que, si se explota correctamente, podría contribuir de manera significativa al sector agrícola y a las economías rurales.

Palabras clave: Caprino, caracterización, variación genética, recurso de la fauna, Argelia