Annexe 6

Formulaire de levée de réserves après soutenance

Année universitaire : **2025-2026.**

Université Abou Bekr Belkaid Tlemcen

Faculté des Sciences de la Nature et de la Vie et des Sciences de la Terre et de l'Univers

Département de **Biologie**

Données d'identification du doctorat :

Nom et prénom de la doctorante : **BELKHADEM Sarra**

Intitulé de la thèse « **Caractérisation morphométrique et moléculaire des races caprines (*capra hircus*) locales dans l'ouest Algérien ».**

Données d'identification du membre de jury :

	Nom prénom	Affiliation
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Directrice	Pr. TABET AOUL Nacera	Univ. Oran 1
Examinateurs	Dr. MAHAMI Fatima Zahra Pr. GAOUAR Suheil Semir Bechir Dr. TEFIEL Hakim Pr. BOUBLENZA Lamia	Ecole Supérieur en Sciences Biologiques d'Oran (ESSBO) Univ. Tlemcen Univ. Tissemsilt Univ. Tlemcen

Vu le procès-verbal de soutenance de la thèse sus citée comportant les réserves suivantes :

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Et après constations des modifications et corrections suivantes :

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Le ....23/10/2025....

Présidente de jury de soutenance (Nom/Prénom et signature)

Nassima Soulimane

République Algérienne Démocratique et Populaire

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TLEMCEN
FACULTE DES SCIENCES DE LA NATURE ET DE LA VIE
ET SCIENCES DE LA TERRE ET DE L'UNIVERS

جامعة أبي بكر بلقايد
تلمسان
كلية علوم الطبيعة و الحياة
وعلوم الأرض والكون

PROCES-VERBAL DE SOUTENANCE DE DOCTORAT

Département : Biologie

M^me BELKHADEM Sarra, Né (e) le : 02/06/1990 à Mecheria

A soutenu publiquement sa thèse de Doctorat intitulée : « **Caractérisation morphométrique et moléculaire des races caprines (*capra hircus*) locales dans l'ouest Algérien** ».

En vue de l'obtention du diplôme de doctorat, Filière : Sciences biologiques, Option : Génétique appliquée.

Le jury, formé par discision rectorale du 130 date 10/07/2025 est constitué de :

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Après délibération, le jury a pris la décision suivante :

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La Doyenne

People's Democratic Republic of Algeria
Ministry of Higher Education and Scientific Research

Abou Bekr Belkaid University – Tlemcen
Faculty of Natural and Life Sciences, and Earth and Universe Sciences
Department of Biology

Thesis

For the Degree of Doctorat

Specialization: Applied Genetics

Presented by

Mrs. BELKHADEM Sarra

Title:

Morphometric and Molecular Characterization of Local Goat Breeds (*Capra hircus*) in Western Algeria

Defended on: 23/10/2025

Approved by :

Nassima Mokhtari Soulimane	Professor	University of Tlemcen	**President**
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Academic Year*: 2024/2025*

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Dedication

To my parents, from the depths of my heart.

To my beloved husband, for your love, patience, and strength.

To my precious child, the joy of my life.

And to all my family, friends, to Amina Sari,

To all who loves me,

with love and gratitude

Sarra

Summary

This doctoral research investigates the genetic and morphological diversity of local goat populations in western Algeria, focusing on the MSTN and PRL genes and their association with body traits. The study combines morphometric analysis, molecular genotyping, and statistical tools to characterize 119 adult goats (Arabia breed) sampled from four regions: Oran, Ain Temouchent, Tlemcen, and Naama (Mecheria). Morphometric data were collected using standardized measurements and analyzed using Principal Component Analysis (PCA), Hierarchical Ascending Classification (HAC), and Shannon-Weaver diversity indices. The PCA revealed that most variation was related to overall body size and shape, while diversity indices indicated Oran had the highest morphological variability. Molecular analyses focused on detecting polymorphisms in the MSTN (related to muscle growth) and PRL (associated with lactation) genes using PCR-RFLP. Results showed that almost all individuals were homozygous for the A allele of MSTN, with only one heterozygote, and all individuals were homozygous for the B allele of PRL. The study concludes that while phenotypic diversity exists among local populations, genetic variation at MSTN and PRL loci is limited. The integration of morphometric and molecular data offers valuable insights for genetic conservation and breeding strategies aimed at enhancing meat and milk production in Algerian goats. Expanding molecular analyses using highly polymorphic markers, GWAS, and whole-genome sequencing will improve the assessment of genetic diversity and support targeted breeding programs integrating phenotypic and genetic data. Additionally, raising farmers' awareness of local breed conservation will contribute to a national strategy for the sustainable management of goat populations in Algeria.

Keywords: Phenotypic, genotypic, variability, MSTN, PRL, goat, Algeria

Résumé

Cette recherche doctorale explore la diversité génétique et morphologique des populations locales de chèvres dans l'ouest de l'Algérie, en mettant l'accent sur les gènes MSTN (myostatine) et PRL (prolactine) et leur association avec les caractéristiques corporelles. L'étude repose sur une approche combinée d'analyses morphométriques, de génotypage moléculaire et d'outils statistiques. Un total de 119 chèvres adultes (Race Arabia) a été prélevé dans quatre régions : Oran, Aïn Témouchent, Tlemcen et Naâma (Mécheria). Les données morphométriques ont été recueillies selon des mesures standardisées, puis analysées à l'aide de l'Analyse en Composantes Principales (ACP), de la Classification Ascendante Hiérarchique (CAH) et de l'indice de diversité de Shannon-Weaver. L'ACP a montré que la majorité de la variation est liée à la taille et à la conformation corporelle globale, tandis que l'indice de diversité indique que la région d'Oran présente la plus grande variabilité morphologique. L'analyse moléculaire a porté sur la détection des polymorphismes des gènes MSTN (croissance musculaire) et PRL (lactation) par la méthode PCR-RFLP. Les résultats ont révélé que presque tous les individus étaient homozygotes pour l'allèle A du gène MSTN, à l'exception d'un seul hétérozygote, et tous étaient homozygotes pour l'allèle B du gène PRL. L'étude conclut que, malgré une diversité phénotypique notable entre les populations locales, la variation génétique aux loci MSTN et PRL reste faible. L'intégration des données morphologiques et génétiques fournit des informations utiles pour la conservation génétique et la mise en place de stratégies de sélection visant à améliorer la production de viande et de lait chez les chèvres algériennes. L'élargissement des analyses moléculaires à l'aide de marqueurs hautement polymorphes, du GWAS et du séquençage complet du génome permettra d'améliorer l'évaluation de la diversité génétique et de soutenir des programmes de sélection ciblés intégrant les données phénotypiques et génétiques. Par ailleurs, la sensibilisation des éleveurs à la conservation des races locales contribuera à une stratégie nationale pour la gestion durable des populations caprines en Algérie.

Mots-clés : Variabilité phénotypique, génotypique, MSTN, PRL, caprin, Algérie

ملخص

تتناول هذه الأطروحة دراسة التنوع الجيني والمورفولوجي لدى سلالات الماعز المحلية في غرب الجزائر، مع التركيز على الجينين) MSTN الميوستاتين) و) PRLالبرولاكتين) وعلاقتهما بالصفات الجسمانية. اعتمدت الدراسة على منهج يجمع بين التحليل المورفومتري، والتوصيف الجزيئي، والتحليل الإحصائي. تم جمع عينات من 119 رأسًا من الماعز السلالة العربية، البالغة من أربع ولايات: وهران، عين تموشنت، تلمسان والنعامة (مشريّة). تم قياس الصفات الجسمانية باستخدام أدوات دقيقة، ثم تحليلها باستخدام تحليل المكونات الرئيسية (PCA) والتصنيف التصاعدي الهرمي(HAC) ، بالإضافة إلى مؤشر التنوع لشانون وويفر. أظهر تحليل PCA أن معظم الاختلافات تتعلق بالحجم العام وشكل الجسم، فيما بيّن مؤشر شانون أن ولاية وهران سجلت أعلى تنوع مورفولوجي.

على المستوى الجزيئي، استخدمت تقنية PCR-RFLP للكشف عن الطفرات في جيني MSTN و .PRLأظهرت النتائج أن جميع الأفراد تقريبًا كانوا متماثلي الزيجوت للأليل A في الجين MSTN ، مع وجود فرد واحد فقط غير متماثل، كما أن جميع الأفراد كانوا متماثلي الزيجوت للأليل B في الجين .PRL توصلت الدراسة إلى أن هناك تنوعًا ظاهريًا ملحوظًا بين الماعز المحلية، إلا أن التنوع الجيني عند موضعي MSTN و PRLكان محدودًا. تعزز هذه النتائج أهمية الجمع بين البيانات الظاهرية والجينية في وضع استراتيجيات تحسين وراثي تهدف إلى تعزيز إنتاج اللحم والحليب والحفاظ على الموارد الوراثية للماعز المحلي في الجزائر .إن توسيع التحليلات الجزيئية باستخدام الواسمات عالية التعدد الشكلي، ودراسات الارتباط على مستوى الجينوم(GWAS) ، وتسلسل الجينوم الكامل سيسهم في تحسين تقييم التنوع الجيني ودعم برامج الانتخاب الموجهة التي تدمج البيانات المظهرية والجينية. بالإضافة إلى ذلك، فإن توعية المربين بأهمية الحفاظ على السلالات المحلية ستساهم في وضع استراتيجية وطنية للإدارة المستدامة لمجموعات الماعز في الجزائر.

الكلمات المفتاحية: التباين الظاهري والجيني، MSTN، PRL، الماعز، الجزائر

List of Abbreviations

A. Morphometric characters

Abbreviation	Meaning
BL	Body Length
EL	Ear Length
TL	Tail Length
PL	Pelvic Length
NL	Neck Length
HL	Head Length
CS	Chest Size
AC	Abdominal Circumference
PW	Pelvic Width
CW	Chest Width
HW	Height at Withers
BH	Back Height
SH	Sacrum Height
CD	Chest Depth
FD	Flank Depth

B. Statistical Analysis

Abbreviation	Meaning
PCA	Principal Component Analysis
HAC	Hierarchical Ascending Classification
ANOVA	Analysis of Variance
H'	Shannon-Weaver Diversity Index
E	Evenness Index
PI	Precision Index

C. Molecular Biology & Genetics

Abbreviation	Meaning
DNA	Deoxyribonucleic Acid
PCR	Polymerase Chain Reaction
RFLP	Restriction Fragment Length Polymorphism
PCR-RFLP	PCR followed by restriction digestion
HWE	Hardy-Weinberg Equilibrium
MSTN	Myostatin Gene
PRL	Prolactin Gene
PRLR	Prolactin Receptor Gene
dNTPs	Deoxynucleotide Triphosphates
TBE	Tris-Borate-EDTA (electrophoresis buffer)
EDTA	EthylenediaminetetraaceticAcid (anticoagulant)

D. Laboratory Units and Terms

Abbreviation	Meaning
µL / ul	Microliter
mL	Milliliter
ng	Nanogram
bp	Base Pairs
°C	Degrees Celsius
V	Volt
S / s	Second
min	Minute
cm	Centimeter
UV	Ultraviolet

E. Institutional Names

Abbreviation	Meaning
LGMC	Laboratory of Molecular and Cellular Genetics
GenApAgiE	Laboratory of Applied Genetics in Agronomy, Ecology and Public Health
USTO-MB	University of Science and Technology of Oran - Mohamed Boudiaf

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Introduction

I. Introduction

Improved breeding and nutrition have boosted the efficiency of growth in different livestock production sectors. However, performance often depends on the use of top-tier feed, which may be a limiting factor. 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 an important source of meat and milk for producing 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 adapted to their habitats (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 sparked 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; 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 and lactation (Abdel-Aziem et al., 2018). Numerous studies have documented 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 (McPherron & Lee, 1997; Grobet et al., 1998). Several studies have found an association between myostatin and prolactin with body traits in goats (Bi et al., 2020; Liu et al., 2020).

1. Objectives of this thesis

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 analyze 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 programs for better meat production and growth.

This thesis is organized into several sections. The first presents a literature review covering general information on goat, animal genetic resources, and their characterization, with a particular focus on the morphometric characteristics of the goat population studied and the molecular analysis. The second section is dedicated to the materials and methods, detailing the various techniques used to study the polymorphism of the MSTN and PLP genes in a selected sample. The third section presents the results, followed by a discussion. Finally, the last part offers a conclusion along with perspectives for future research.

Bibliographic review

II. Bibliographic review

1. Caprine species

Goats are mammals classified under the Bovidae family and the Artiodactyla order. As herbivorous ruminants, they possess a complex digestive system that allows them to efficiently process plant-based diets. Researchers have identified and described various subfamilies within this group, highlighting their diverse characteristics and adaptations (Fournie, 2006). Across different regions of the world, goats hold significant economic and nutritional value. They serve as a primary source of milk, meat, and hides, particularly in rural and developing areas where livestock farming is a major component of subsistence agriculture. Their ability to thrive in harsh environments, including arid and mountainous regions, makes them a vital resource for communities facing food insecurity (Gourine, 1989) In a more general classification, caprines (*Capra*) can be categorized as follows:

Kingdom: *Animalia* (Animals)

Phylum: *Chordata* (Vertebrates)

Class: *Mammalia* (Mammals)

Infraclass: *Placentalia*

Order: *Cetartiodactyla* (Artiodactyls)

Suborder: *Ruminantia* (Ruminants)

Family: *Bovidae* (Bovids)

Subfamily: *Caprinae* (Caprines)

Genus: *Capra*

Species: *Capra hircus* (Domestic Goat)

Corbet (1978), Corbet and Hill (1980), and Denis (2000) recognized six distinct species within the genus *Capra*, namely: *Capra aegagrus*, *Capra ibex*, *Capra caucasica*, *Capra cylindricornis*, *Capra pyrenaica*, and *Capra falconeri*.

-Capra aegagrus: Bezoar ibex or wild goat, considered the wild ancestor of the domestic goat (*Capra hircus*)

- ***Capra ibex***: Alpine ibex, native to the European Alps

- ***Capra caucasica***: West Caucasian goat, inhabits the western Caucasus Mountains.

- ***Capra cylindricornis***: East Caucasian goat, found in the eastern Caucasus region.

- ***Capra pyrenaica***: Iberian ibex, endemic to the Iberian Peninsula.

- ***Capra palconeri***: Characterized by its twisted horns; native to Central Asia.

2. Origin and geographic distribution

Goats (*Capra hircus*), domesticated from the wild bezoar (*Capra aegagrus*) around 10,000 years ago in the Fertile Crescent (Figure 01), were among the earliest livestock to be tamed by humans. This domestication involved various wild populations (Amills et al., 2017; Naderi et al., 2008), laying the foundation for the rich genetic diversity observed in modern goats. Following domestication, goats quickly dispersed across Europe, Africa, and Asia due to their remarkable adaptability, reaching the Iberian Peninsula and Southern Africa by 7,000 and 2,000 years ago, respectively (Daly et al., 2018). Genetic studies indicate that this spread followed multiple migration routes, shaped by geographical barriers and human activity, which produced distinct gene pools in regions such as Europe, Africa, and West Asia. Over time, these migratory patterns, combined with geographical and reproductive isolation as well as further introductions, led to significant regional diversification, especially evident in Central and Northern Europe (Amills et al., 2017).

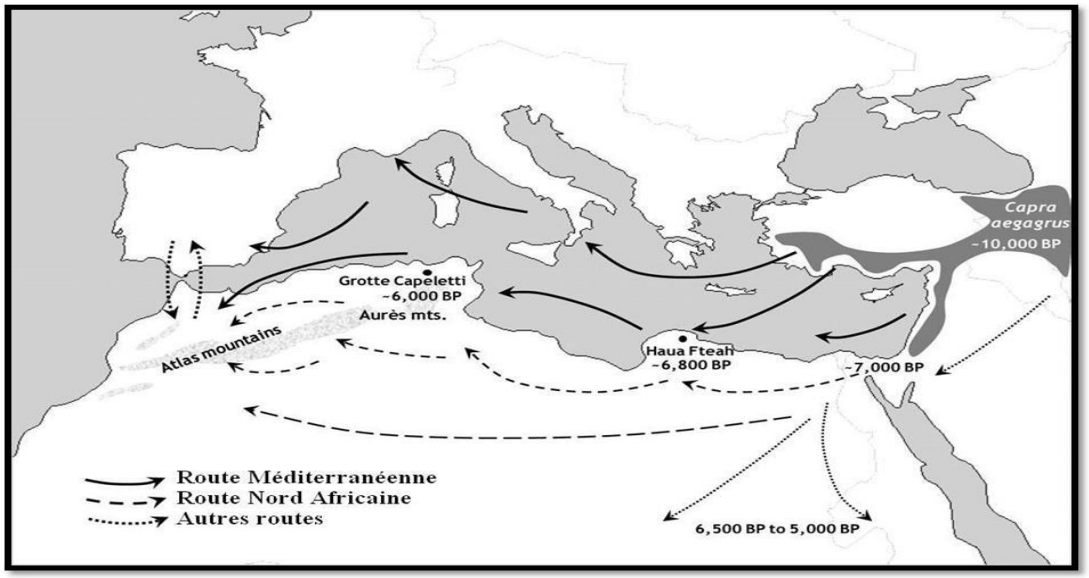

Figure 01: The spread of goat pastoralism in North Africa (**Pereira et al., 2009)**

The arrows indicate the two hypothesized routes for the dispersal of domestic goats from their domestication areas (dark gray zone) to the North African continent. The location of some archaeological sites where caprine (sheep/goat) remains have been identified is also shown. Adapted from Newman (1995), Fernandez et al. (2006) and Zeder (2008).

3. Description of the species

Goats are characterized by a robust, compact, and hairy body, adapted to diverse and often harsh environments. They possess short, sturdy limbs and a solid neck, while the head is relatively small and shows considerable variability in shape and profile depending on the breed. The facial features typically include a narrow forehead, a pointed snout, and often a small beard. The horns, present in both sexes, vary in size, curvature, and orientation, and are generally larger and more developed in males. The tail is triangular, hairless on its ventral side, and usually carried straight, contributing to the animal's balance on uneven terrain. The eyes are large, bright, and expressive, with horizontal (transverse) pupils and an iris ranging from yellow to light brown, features that enhance peripheral vision and are particularly useful for detecting predators. Unlike sheep, goats lack lacrimal fossae (tear pits). Their ears are highly mobile, allowing precise sound localization; their shape and carriage vary by breed from long and pendulous to short and erect or medium and horizontal. The hooves are hard and compact, with a strong cannon bone, giving goats exceptional agility and sure-footedness on rocky or mountainous terrain. This anatomical structure reflects their ecological adaptation and behavioral versatility, enabling them to exploit marginal pastures and survive in environments unsuitable for other domestic ruminants (Marmet, 1971; Fournier, 2006; Bendaoud, 2009).

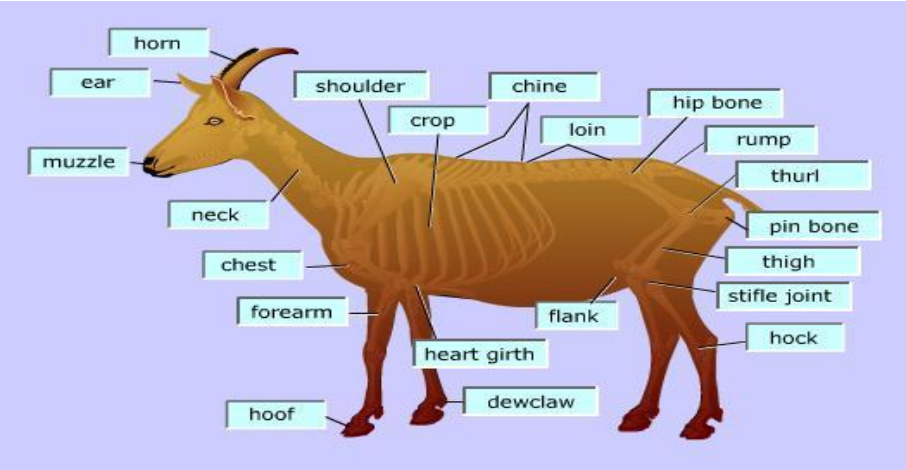

Figure 02: Anatomic of goat (https://www.goatbiology.com/animations/bones.html)

4. Genetic Resources of Goats in the world

4.1. European Goat

4.1.1. Alpine breed

The Alpine goat is a robust dairy breed native to the Alpine massif of France and Switzerland. It is medium-sized, and all colors of Coat: Black and white are common in this breed. Among the most common are burnt bread" or "chamoisée," featuring black legs and a dorsal stripe, along with multicolored white spots on a black or brown coat. The head, whether or not with horns, and with or without hair, is of medium length. medium with broad forehead and muffle. Its profile is concave; the ears are worn erect. In a fairly closed cornet, the udder is voluminous and well attached front and back. retracting well after milking, with thin and supple skin (Quittet, 1977; Charron, 1986; Benalia, 1996; Babo, 2000; Gilbert, 2002).

4.1.2. Saanen breed

Native to the Saanen Valley in Switzerland, it is a strong development, deep, thick, possessing a good bone structure, coat and hair are uniformly white, the hair is short, the head, with or without horns, with or without ears, pals, with or without beard, has a broad and flat forehead. The ears are worn at least horizontally, the chest deep, wide and long, the udder is globose, very wide at its top which gives it a stronger development in width that in depth. Saanen is a better producer of milk in the world, and gives Especially excellent, highly meaty kids (Holmes-pegler, 1966; Quittet, 1977; Benalia, 1996; Babo, 2000; Gilbert, 2002).

4.1.3. Poitevine breed

The Poitevine goat is a medium-sized animal with a long, sleek appearance; its coat has hair of a more or less dark brown up to black. The white occupies the belly, the inner side of the limbs, the underside of the tail, and the head. generally, without horns, is triangular, and carries two small white spots going sometimes up to the very marked white stripes on each side of the chamfer, theChignons are quite straight. The Poitevine goat is a strong dairy producer Quittet (1977).

4.1.4. Maltese Breed

The Maltese goat is a good milk producer. It is found in the coastal regions of Europe and is characterized by a convex (ram-like) nose, more or less drooping ears, a long head with a straight profile, and a long, well-horizontal back. Its coat is white with long hair (Holmespegler, 1966; Quittet, 1977; Benalia, 1996; Babo, 2000; Gilbert, 2002).

- **Murcian Breed**

Originating from the Murcia province, this breed is characterized by a fine head horizontally carried ears, rare horns, and a long neck. The body is long and rounded with short hair. The coat color ranges from chestnut to dark brown, sometimes black. While rustic in nature, this breed has well-developed dairy qualities (Dekkiche, 1987).

4.1.5. Rogue Breed

Originally found among large sheep flocks in Provence that migrated to the Alps during summer, the Rove goat served multiple purposes: guiding sheep as lead animals (menons), nursing twin or orphaned lambs, and providing shepherds with goat milk and meat for sustenance. The Rove goat is a compact, muscular breed, characterized by thick, sturdy limbs and large hooves that support its well-distributed muscle mass traits deliberately selected for meat production, unlike other French breeds primarily improved for dairy (Capgenes, 2007).

4.1.6. Toggenburg Breed

Originating from the Toggenburg province of Switzerland, this breed is regaining popularity due to its excellent dairy capabilities, with animals frequently exported to Germany and England. Toggenburg goats are characterized by their light brown coats featuring distinctive grayish stripes on the cheeks, gray muzzle, and gray hair on the legs up to the knees and ear edges. On average, males stand 75-83 cm at the withers, while females measure 70-80 cm. Adult males typically weigh 63 kg, compared to 45 kg for females. Although Toggenburg goats are proficient milk producers, their yield is somewhat lower than that of the Saanen breed (French, 1971).

4.2. Asian breeds

4.2.1. Angora Goat Breed

Originating from the Himalayan region, the Angora goat is a hardy breed that was domesticated in Asia Minor and subsequently developed in the Ankara region of Turkey. Characterized by its small stature, compact head, and pendulous ears, this breed produces a distinctive white, curly, or wavy fleece that yields high-quality mohair fiber. While renowned for its fiber production, the Angora goat offers relatively low outputs in terms of meat and milk production (Holmes-Pegler, 1966; Charlet & Le Jaouen, 1977; Quittet, 1977; Babo, 2000; Gilbert, 2002; Corsy, 1991).

4.2.2. Cashmere Goat Breed

The Cashmere goat is a hardy, small-framed breed renowned for its exceptional cold climate adaptability and the superior quality of its fleece. Indigenous to the Kashmir region between India and Tibet, this breed produces the fine, luxurious cashmere fiber that is unique to its kind. While valued primarily for its wool, the cashmere goat also demonstrates remarkable resilience in harsh environments (Holmes-Pegler, 1966; Quittet, 1977; Fantazi, 2004).

4.3. African Goat Population

The African goat population is predominantly represented by the Nubian breed, characterized by its medium stature (60-70 cm at the withers), narrow head, and distinctive long, broad, pendulous ears. This breed features a short-haired coat that ranges from light to dark reddish-brown in color. As the most widely recognized African goat variety, the Nubian breed has become particularly notable for its adaptation to various African climates and production systems (Fantazi, 2004).

5. Algerian Genetic Resources

5.1. Goat Populations in Algeria

The species *Capra hircus* in Algeria comprises highly diverse populations, all belonging to traditional genetic lines. In addition to these local populations primarily of Nubian ancestry there are animals with mixed bloodlines from standardized breeds (including the Arbia, Mekatia, M'zabite, and Kabyle dwarf varieties). Algeria's goat population can be classified into four major types (Bey and Laloui, 2005). The Arbia breed is primarily found in the Laghouat

region, while the Naine de Kabyle breed inhabits the Kabylie and Aurès mountains. The Mekatiabreed is located in the high plateaus and certain northern areas, and finally, the M'Zabitebreed is situated in the northern part of the Sahara. The husbandry of these well-adapted breeds is geared toward mixed production (meat and milk) (Hellal, 1986; Dekkiche, 1987; Sebaa, 1992; Takoucht, 1998).

5.1.1. Arbia Breed

According to Dekkiche (1987) and Madani et al. (2003), the Arbia is the most dominant population, belonging to the Nubian breed. It is primarily found in the high plateaus, steppic, and semi-steppic zones. This breed is characterized by a small stature (50-70 cm), a hornless head, and long, broad, drooping ears. Its coat is multicolored (black, gray, and brown) with long hair (12-15 cm). The Arbia goat has an average milk production of 1.5 liters per day (Figure 03).

Figure 03: Arbia Breed (Laouadi et al., 2020)

5.1.2. Mekatia Breed

According to Guelmaoui and Abderehmani (1995), the Mekatia breed originates from Ouled Nail (Djelfa) and is primarily found in the Laghouat region. It is likely the product of crossbreeding with Mediterranean breeds (Tedjani, 2010). The Mekatia goat (Figure 04) exhibits an elongated body with a straight topline and a slightly convex profile in some individuals. Its coat varies in color (gray, beige, white, and brown) and consists of short, fine hair measuring 3-5 cm in length. Males possess a robust head, while females have backward-curving horns, a goatee, and occasionally two wattles (less common), along with long, pendulous ears that may reach up to 16 cm. Average body weight is 60 kg for males and 40 kg for females, with wither heights of 72 cm and 63 cm, respectively. The udder is well-balanced,

square-shaped, and firmly attached, with two-thirds of females having large teats. Milk production ranges from 1 to 2 liters per day (Hellal, 1986).

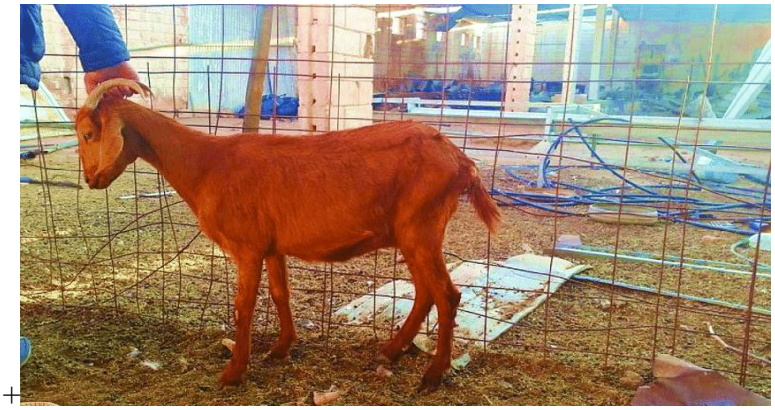

Figure 04: Female of Mekatia breed (Laouadi et al., 2020)

5.1.3. M'zabite Breed

Also known as "the red goat of the oases" (Figure 05), this breed originates from Metlili or Berriane (Ghardaïa). It is characterized by an elongated, straight, and rectilinear body, with males measuring 68 cm at the withers and females 65 cm, weighing 50 kg and 35 kg, respectively. The coat exhibits three primary colors: dominant fawn, brown, and black, with most individuals having short hair (3-7 cm). The head is fine, often bearing backward-curving horns when present, with a convex profile and long, pendulous ears (15 cm). The M'zabite breed is particularly noteworthy for its milk production capacity (2.56 kg/day) (Hellal, 1986).

Figure 05: M'zabite (ITELV. Department of Conservation of Goat Species in Algeria)

5.1.4. Kabyle Dwarf Goat

The Kabylie breed, commonly known as the "Dwarf Kabylie," is considered a descendant of the Pamel goat (Capra promaza) (Guelmaoui and Abderehmani, 1995). According to Pedro (1952) and Hellal (1986), this indigenous breed populates the mountainous regions of Kabylie and the Aurès. Characterized by its robust and stocky build, the breed exhibits small stature (66 cm for males and 62 cm for females), which justifies its "dwarf" designation, with a body length ranging from 65 to 80 cm and respective weights of 60 kg and 47 kg. The breed features an elongated body with a straight topline, a fine head bearing backward-curving horns, and variable coat coloration dominated by beige, russet, white, red pied, black pied, and black. Ear morphology varies with coat color, presenting small and pointed ears in white-coated individuals versus moderately long ears in beige-coated specimens. Hair length distribution shows 46% of individuals with long hair (3-9 cm) and 54% with short hair (not exceeding 3 cm). Primarily raised for meat production of appreciable quality, the breed demonstrates poor dairy performance (Figure 06).

Figure 06: The Kabyle breed (ITELV. Department of Conservation of Goat Species in Algeria)

6. Improved Breeds in Algeria

The improved goat breeds in Algeria include the Maltese, Murciana, Toggenburg, and more recently, the Alpine and Saanen varieties, which were introduced during the colonial period as part of a genetic improvement strategy for the national goat herd (Manallah, 2012). According to Kerkhouche (1979), the Maltese and Murcian goats were initially established in Oran and coastal regions during colonial times, with subsequent introduction efforts of high-performance animals occurring post-independence in Mitidja, Tizi-Ouzou, Sétif, and the Upper Chlef region. Early 20th-century sources (Geoffroy, 1919; Huart du Plessis, 1919; Diffloth, 1926) document the widespread presence of Maltese goats along the Algerian coastline, highlighting their

historical significance in the country's livestock development programs. These exotic breeds were primarily introduced to enhance milk production capabilities, though their adaptation to local conditions and long-term impact on indigenous populations warrant further investigation.

According to Decaen and Turpault (1969), the Maltese breed is predominantly found in coastal regions including Annaba, Skikda, and Algiers, as well as in oasis areas. In efforts to enhance adaptation and improve zootechnical performance (particularly milk and meat production) of local goat populations, Algeria has introduced several high-performance breeds such as Saanen, Alpine, and Maltese (Bey and Laloui, 2005).

7. Crossbred Populations in Algerian Goat Husbandry

The crossbred populations consist of animals resulting from uncontrolled breeding between local goat populations and introduced breeds. Although these crossbreeding attempts remain limited in scope, the offspring exhibit several advantageous characteristics: significant body size, well-developed musculature, frequent twin pregnancies, and appreciable milk production, typically with short hair coats (Khelifi, 1997). These crossbred animals are primarily found in state-run agricultural operations (Chellig, 1978).

8. Species Reserves Worldwide

The global goat population reserve is estimated at 1.01125 billion head (Figure 07), highlighting its significant role in agriculture and biodiversity. However, the financial value of this specific reserve has declined steadily from 1.14 billion (2019) to 1.05 billion (2023), signaling potential challenges such as reduced funding, market pressures, or operational inefficiencies.

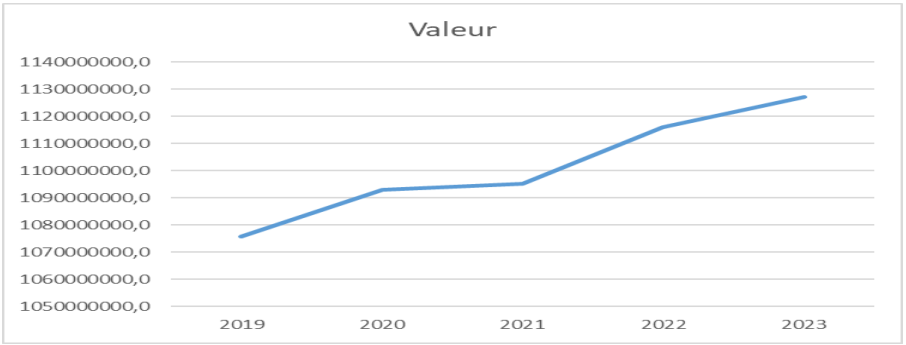

Figure 07: Global Goat Stock/Reserves of head by year (FAO, 2023)

This contrast between stable global reserves and localized financial downturns underscores the need for targeted strategies such as improved resource allocation, diversification of revenue streams, or policy support to safeguard both economic and ecological sustainability in goat-related initiatives.

9. Species Stock in Algeria

In recent years, there has been a steady increase in the global goat population in Algeria, reflecting broader trends in livestock production and agricultural practices (Figure 08).

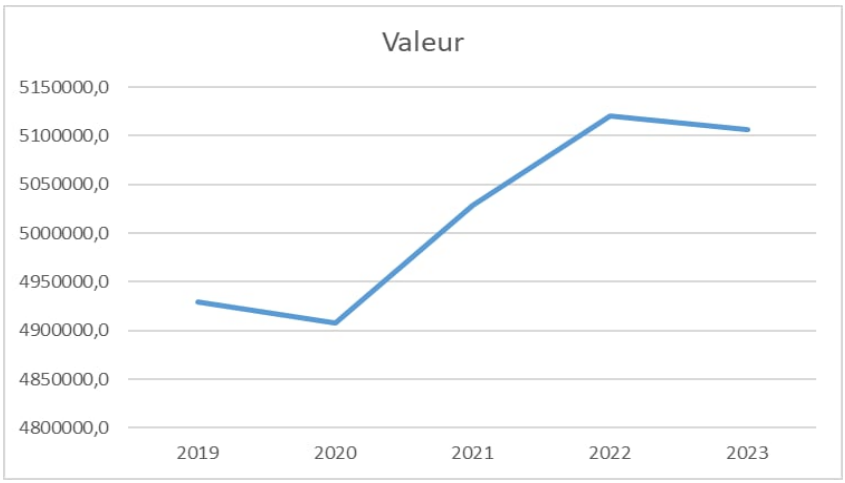

Figure 08: Goat Stock/Reserves of head by year, in Algeria (FAO, 2023)

This growth may be linked to goats' adaptability to harsh climates, rising demand for goat products (milk, meat, etc.), sustainable farming initiatives, or efforts to boost food security. However, deeper analysis of regional policies, market trends, and environmental factors would provide clearer insights into the causes of this trend.

10. Species Reproduction

10.1. Puberty

Puberty can be defined as the age and weight at which animals become capable of reproduction. In males, this occurs when they are able to successfully impregnate a female after mating (male puberty), while in females, it is when they can conceive during estrus and carry a pregnancy to term (female puberty). In both sexes, puberty is generally preceded by a period of several weeks known as the pre-pubertal phase, during which external stimulation can trigger the onset of puberty (Benaissa, 2008). According to Vanwarbeck (2008), sexual behavior in

young male kids begins very early, starting at 4 to 5 months of age. However, it is recommended not to breed them before 7 months of age. Female kids also reach puberty early, and it is advised to separate them from young males by 3.5 months at the latest. They can only be successfully bred at around 6 months of age, once they reach a minimum weight of 30 to 35 kg. Mediterranean breeds exhibit a short seasonal anestrus, particularly when social factors (such as the male effect) or nutritional conditions are properly managed (Lindsay, 1996; Zarazaga et al., 2009).

10.2.Estrous Cycle

The estrus period in dairy goats lasts 24 to 48 hours and is characterized by significant behavioral changes. Goats display more obvious signs of estrus than sheep: they become restless, mount other goats and allow themselves to be mounted, bleat frequently, wag their tails rapidly, and exhibit reduced appetite and lower milk production. The vulva appears pink, congested, often moist, sometimes dilated, and may discharge fluid that becomes viscous and clearer toward the end of estrus. Ovulation occurs approximately 36 hours after the onset of estrus (Renou, 2012).

The average cycle length is 21 days. At the beginning of the breeding season, three types of cycles can be observed:

- **Short cycles**: 5 to 7 days (10% of cases)
- **Normal cycles**: 15 to 25 days (80% of cases)
- **Long cycles**: 26 to 35 days (10% of cases)

10.3.Puberty in Male Goats (Bucks)

Buck puberty is marked by increased testosterone secretion, the onset of spermatogenesis, and the development of sexual behavior. Viable sperm production and successful copulation can occur as early as 4 to 6 months of age. At this stage, the buck's weight typically reaches 40–60% of its adult live weight (Zarrouk et al., 2001).

Like females, bucks exhibit seasonal sexual activity, with peak reproductive behavior coinciding with elevated plasma testosterone levels in autumn (Janudeen et al., 2000). Notably, this testosterone surge also alters the buck's odor during the breeding season, a phenomenon linked to pheromonal signaling (Chemineau et al., 1994).

Mediterranean goat breeds exhibit shorter seasonal anestrus compared to temperate breeds, especially when social factors (e.g., the *male effect*) and nutritional conditions are properly managed (Lindsay, 1996; Zarazaga et al., 2009).

In Algeria, Yahia (2006) demonstrated the existence of seasonal variations in the sexual activity of local goats in the Kabylie region by evaluating estrous activity through meticulous heat detection via direct observation of the animals twice a day (morning and evening) for a duration of half an hour each time. The same author added that he observed no complete absence of estrus manifestations in any month of the study period. However, the period of intense estrus manifestations occurs in autumn and continues into winter, with percentages of 42% and 32.5%, respectively. Then, there is a decline in this intensity during spring and early summer. Subsequently, estrous activity begins to increase again in late summer. This leads us to conclude that local goats in Kabylie reproduce throughout the year but with reduced sexual activity during the spring and summer seasons. The Draâ goat, like the D'man sheep breed, exhibits year-round cyclicity with a slight decline in February (Olguin, 2009).

According to Tefiel (2015), imported Saanen goats were found to be capable of reproducing year-round, and their sexual activity could be continuous, with no complete cessation recorded at any point. However, this activity varied from high to low throughout the year, as indicated by the number of matings recorded during different months. The sexual activity of Saanen goats was high during the period from August to February but declined from March to July. Thus, the reproduction of Saanen goats could be described as weakly seasonal. In contrast, in Algeria, these same goats exhibited high sexual activity starting in August and continuing until the end of February. For the rest of the year, the activity persisted but at a lower intensity.

11. Common Goat Diseases and Health Issues

11.1. High Death Rate in Baby Goats

High kid mortality rates remain a major challenge in goat production, particularly in tropical and subtropical regions. According to Benaissa (2008), this significant loss of young animals is often accepted as normal by farmers, though it severely limits productivity. While specific diseases sometimes contribute, the primary cause is inadequate nutrition for mother goats, resulting in insufficient milk production, stunted kid growth, and heightened vulnerability to diseases (Bhattacharyya, 1988). This underscores how proper feeding of breeding does is critical for kid survival and overall herd health

11.2. Priority Diseases (OIE Lists A & B, and Other Diseases)

Goats are vulnerable to a range of diseases that compromise their productivity and cause significant economic losses, particularly in Algeria, where goat farming is an economic pillar. Priority diseases, as classified by the World Organisation for Animal Health (OIE), include:

- **List A** (rapid spread, major economic impact – e.g., foot-and-mouth disease)
- **List B** (endemic, moderate impact – e.g., brucellosis)

Among the most common conditions identified in the literature:

- **Mastitis**

Mastitis, an inflammation of the udder, is primarily caused by pathogens such as *Staphylococcus aureus*, *Streptococcus* species, and various environmental bacteria, including coliforms. This condition has significant consequences for dairy production, as it leads to reduced milk yield, compromised milk quality, and diminished suitability for cheese-making. These impacts collectively result in substantial economic losses for the dairy industry (Baudry et al., 1997; Bergonier et al., 2002).

- **Paratuberculosis (Johne's Disease)**

Paratuberculosis, also known as Johne's disease, is a chronic intestinal infection caused by *Mycobacterium avium* subsp. *paratuberculosis*. This pathogen progressively damages the intestinal lining, leading to clinical symptoms such as persistent diarrhea and significant weight loss. The disease is of particular concern in Algeria, where a high prevalence has been reported, especially in intensive livestock farming systems (Casamitjana, 1996).

- **Enterotoxemia (Pulpy Kidney Disease)**

Enterotoxemia, primarily caused by *Clostridium perfringens* type D, is a serious condition frequently associated with sudden dietary changes, particularly in intensive production systems. These abrupt nutritional shifts promote rapid bacterial proliferation and toxin production, leading to severe clinical signs that are often fatal. The disease poses a significant threat to herd health and productivity (Jamet, 1995; Chartier &Broqua, 1995).

- **Pregnancy Toxemia (Ketosis)**

Pregnancy toxemia is a metabolic disorder that typically occurs in the final stages of gestation and results from an inadequate energy supply to meet the demands of fetal development. The condition is particularly prevalent in goats carrying multiple fetuses, as their energy requirements are significantly higher. Without proper nutritional management, affected animals may experience severe clinical symptoms, posing risks to both maternal and fetal health (Chartier & Broqua, 1995; Bezille, 1995).

- **Respiratory Diseases**

Pasteurellosis, a respiratory disease primarily caused by *Mannheimiahaemolytica* serotype A2, is a significant concern in small ruminants. Outbreaks are often triggered or exacerbated by environmental stressors such as sudden weather changes, overcrowding, or transport, which weaken the animals' immune defenses and facilitate the development of pneumonia. This condition can lead to considerable morbidity and mortality, particularly in intensive or poorly managed systems (Casamitjana, 1997; Chartier et al., 1995).

- **External Parasites**

Common infestations in goats include lice (*Damaliniacaprae*, *Linognathusstenopsis*) and mange mites (*Chorioptescaprae*, *Psoroptes cuniculi*). These ectoparasites can significantly impact goat health by causing skin irritation, leading to reduced milk production and a weakened immune response, which makes animals more susceptible to other infections. Effective management of these infestations is crucial for maintaining herd health and productivity (Casamitjana, 1997).

These diseases, combined with factors such as malnutrition, inadequate veterinary care, and poor farming practices, significantly limit the productive and reproductive potential of Algerian goat breeds. In many regions, extensive management systems, characterized by low-quality feed resources, irregular health monitoring, and limited access to modern breeding programs, exacerbate these challenges. As a result, the genetic potential of local breeds remains underexploited, hindering both productivity and sustainability of goat farming in Algeria.

12. Genetics of the Species

The goat species (*Capra aegagrus hircus*) is characterized by a diploid chromosome number of 2n = 60 (Figures 09, 10). With the exception of the Y heterochromosome, which is a very small metacentric chromosome, all other chromosomes are acrocentric. The 29 pairs of autosomes show a regularly decreasing size (Françoise Hulot, 1969).

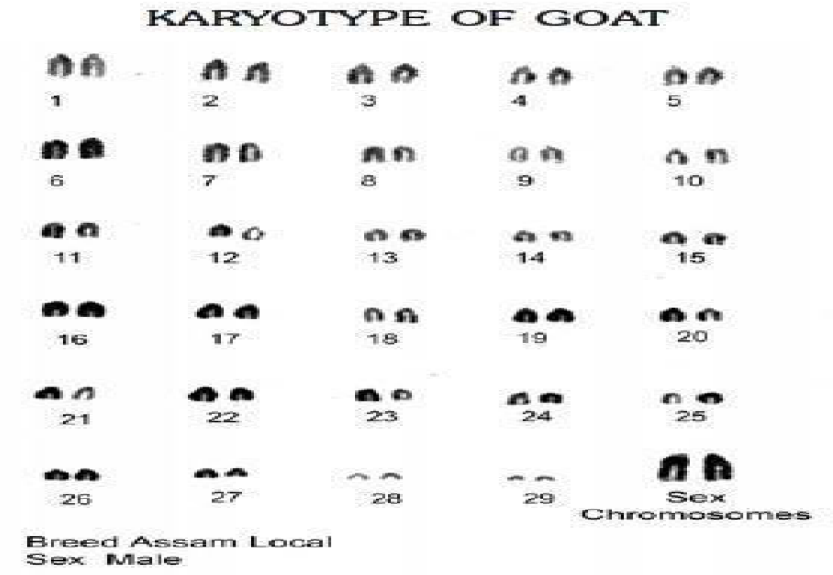

Figure 09: Karyotype of a female goat (Bula & Dharmeswar, 2011)

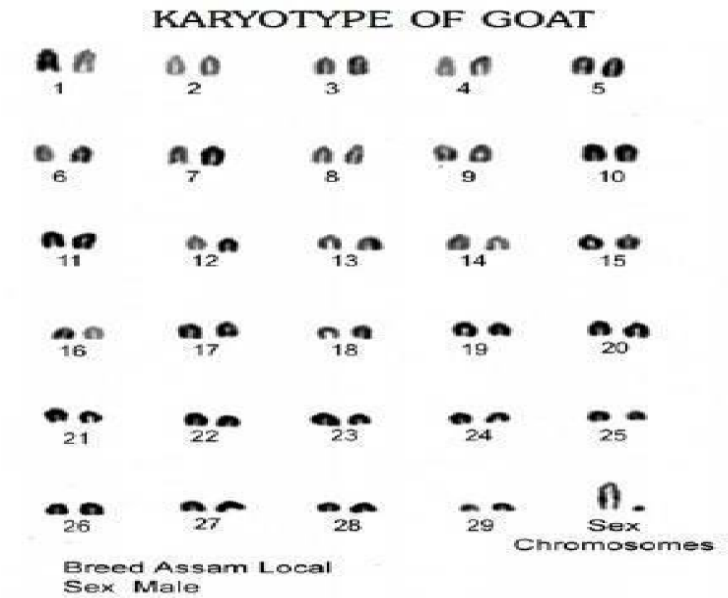

Figure 10: Karyotype of a male goat (Buck) (Bula & Dharmeswar, 2011)

12.1. Different methods for characterization and selection of animal populations

12.1.1.Morpho-biometric characterization

Morpho-biometric methods involve measuring quantifiable physical traits such as wither height, body length, weight, conformation, and coat color to differentiate breeds and assess their productive potential. In Algeria, these methods have been extensively used to characterize local goat breeds. For instance, the Mekatia breed is distinguished by its elongated body (averaging 60 kg for males and 40 kg for females) with a wither height of 72 cm (males) and 63 cm (females), while the Kabyle Dwarf exhibits a more compact build (66 cm for males and 62 cm for females) with a meat-production orientation (Hellal, 1986; Laouadi et al., 2020). Morphometric discriminant analysis, employing statistical techniques like Principal Component Analysis (PCA), enables the differentiation of individuals and breeds based on morphological characteristics. Studies have shown, for example, that the M'zabite breed can be distinguished from the Arbia by its straighter body and longer drooping ears (15 cm compared to 12-15 cm) (Fantazi, 2018). These methods are particularly relevant for doctoral research in Algeria as they are accessible, cost-effective, and allow for field data collection to complement genetic analyses.

12.1.2. Immunogenetic characterization

Immunogenetic methods analyze biochemical markers, such as blood groups, serum proteins (albumin, transferrin, hemoglobin), and milk caseins (CSN1S1, CSN2, CSN3), to assess genetic diversity and relationships between populations.

Although less common today due to the rise of molecular techniques, these approaches have played a historical role in characterizing goat populations. In Algeria, caseins are studied for their impact on milk quality, particularly in the M’zabite breed, known for its high milk yield (2.56 kg/day) (Fantazi, 2018). Blood group polymorphisms, such as those in the MNS system, have been used to identify genetic variations linked to environmental adaptation—for example, between steppe breeds (Arbia) and mountain breeds (Naine de Kabylie) (Fantazi, 2018).

While these methods are less precise than DNA analyses, they remain useful for preliminary studies or in contexts where resources for molecular analyses are limited.

12.1.3.Cytogenetic characterization

Cytogenetic characterization examines the karyotype of goats, which have a diploid number of 60 chromosomes (2n=60), including 29 pairs of acrocentric autosomes and a metacentric Y chromosome (Hulot, 1969). This method helps detect chromosomal abnormalities, such as translocations or deletions, and confirms the species classification of populations as *Capra hircus*.

In Algeria, cytogenetic studies have validated the genetic homogeneity of local breeds while identifying minor variations in crossbred populations resulting from hybridization with introduced breeds, such as Saanen or Maltese (Fantazi, 2018). For example, analyses have shown that crossbred populations occasionally exhibit minor chromosomal abnormalities, potentially linked to genetic incompatibilities.

Although less common than molecular approaches, cytogenetics remains a complementary tool for doctoral research, as it allows the study of population genetic stability and the assessment of crossbreeding effects on genetic diversity.

12.1.4.Genetic characterization

Molecular methods, particularly those centered on DNA analysis, have become the cornerstone of genetic characterization in goat populations due to their high accuracy, reproducibility, and depth of information. These techniques have significantly advanced our ability to assess genetic diversity, determine population structure, and identify loci associated with traits of economic interest.

Among the most widely used molecular markers are microsatellites, or short tandem repeats (STRs), which are dispersed throughout the eukaryotic genome and estimated to number between 30,000 and 100,000 loci (Stallings et al., 1991). Single nucleotide polymorphisms (SNPs) represent another prevalent marker type, occurring with high frequency, approximately one every 300 to 1,000 base pairs-making them highly suitable for high-throughput genotyping (Kaplan & Delpech, 1993; NHGRI, 2020).

The adoption of these markers has catalyzed the implementation of marker-assisted selection (MAS**)**, a method that allows breeders to select animals carrying desirable alleles based on their genotype rather than solely on phenotypic traits or pedigree records. MAS is particularly advantageous for improving traits with low heritability, complex genetic architecture, or late

expression, as it enables early and precise selection decisions that accelerate genetic gain (Dekkers & Hospital, 2002).

A variety of DNA-based techniques support these advances, including polymerase chain reaction (PCR), restriction fragment length polymorphism (RFLP), simple sequence repeat (SSR) analysis, and high-throughput SNP genotyping platforms. These tools facilitate the identification of breed-specific or trait-linked markers, enabling targeted selection strategies to enhance key production traits such as growth performance, fertility, disease resistance, milk yield, and resilience to environmental stressors (Notter, 1999; Tosser-Klopp et al., 2014).

The emergence of genomic selection and next-generation sequencing (NGS) has further transformed breeding programs by providing access to comprehensive genome-wide data. These technologies enable both common and rare variants to be captured, feeding into genome-wide association studies (GWAS) and whole-genome sequencing (WGS) to uncover statistically robust genotype–phenotype relationships (Meuwissen et al., 2001; VanRaden, 2008; Brito et al., 2017). Such insights support the calculation of genomic estimated breeding values (GEBVs), dramatically improving the accuracy and predictive power of selection.

In addition to production-focused applications, molecular methods play a critical role in conservation genetics. They are instrumental in monitoring genetic diversity, assessing inbreeding levels, and guiding the sustainable management of endangered or locally adapted goat breeds (FAO, 2011; Taberlet et al., 2008), many of which are key to maintaining genetic resources and cultural heritage.

As molecular technologies continue to become more cost-effective and accessible, their integration into routine breeding practices is increasingly viable—even for smallholder systems in developing regions. This shift marks a new era of precision breeding, where genomic tools are not only enhancing productivity but also contributing to the sustainability and adaptability of global goat farming systems.

Microsatellite markers provide a powerful framework for evaluating genetic variation both within and among goat populations. In Algeria, the use of these markers has been pivotal in distinguishing the genetic identity of indigenous breeds such as Arbia, Mekatia, M’zabite, and Naine de Kabylie. Multiple studies have consistently highlighted the high genetic diversity present within these populations, an essential indicator of their adaptive potential and overall genetic health (Fantazi et al., 2017; Belkhadem et al., 2019). Among these, the M’zabite breed

has shown particularly high allelic richness and heterozygosity compared to the Arbia breed differences that likely reflect its evolutionary adaptation to the arid and challenging conditions of southern Algeria. These insights underscore the critical role of molecular tools in the conservation of local genetic resources and in guiding sustainable breeding programs tailored to specific environmental conditions.

13. Economically Important Genes in Goats

Goats (*Capra hircus*) are among the most economically and ecologically significant livestock species worldwide, providing vital resources such as milk, meat, and fiber, particularly in marginal environments. Recent advancements in genomics have profoundly enhanced our understanding of the genetic architecture underlying these traits, thereby revolutionizing modern breeding programs. Whole-genome scans conducted by Wan et al. (2023) identified 312 genes under selection, including *CSN1S1* and *DGAT1*, which are associated with milk yield and composition; *KRTAP* gene families involved in fiber structure and quality; and *EPAS1*, a gene implicated in physiological adaptation to high-altitude hypoxia. These discoveries facilitate the implementation of marker-assisted selection (MAS), allowing breeders to target economically important traits with greater precision (Brzáková et al., 2021). Furthermore, genes such as *CAPN1* have been linked to improved meat tenderness (Amills et al., 2017), while *TRPM8* is associated with thermoregulation, offering genetic pathways for enhancing resilience to climate stressors (Wan et al., 2023). In addition to production traits, immune-related loci such as those within the major histocompatibility complex (MHC) class II region have emerged as valuable markers for improving disease resistance (Bertolini et al., 2018). As reviewed by Siddiki et al. (2020), these genomic innovations complement conventional selection methods and contribute to the conservation of genetic diversity (Stella et al., 2018), underscoring their transformative potential for sustainable and resilient goat farming systems.

Genetic research in goats increasingly focuses on identifying genes associated with economically significant traits such as muscle development and lactation performance. Among the most extensively studied are the myostatin (MSTN) and prolactin (PRL) genes, which play pivotal roles in meat and milk production, respectively.

The MSTN gene, located on chromosome 2 (NC_030813.1: g.62532872–62540950), encodes a protein that functions as a negative regulator of skeletal muscle growth.

Polymorphisms within this gene, particularly a 5.8-kb deletion in the 3′ untranslated region (3′ UTR), have been shown to significantly enhance muscle hypertrophy and growth rates, especially in meat-producing breeds such as the Boer goat (Zhang et al., 2020; Pan et al., 2021). This deletion is thought to reduce the expression or alter the post-transcriptional regulation of MSTN, thereby attenuating its inhibitory effect on muscle cell proliferation and differentiation. Consequently, individuals carrying such mutations exhibit increased muscle mass, making this locus a valuable molecular marker for marker-assisted selection in meat-oriented breeding programs.

Conversely, the PRL gene, located on chromosome 20 (NC_030831.1: g.31805445–31810422), plays a critical role in the initiation and maintenance of lactation. Its receptor gene, PRLR, is also involved in the hormonal signaling pathway that regulates mammary gland function. Specific variants, such as the g.31807321C>T polymorphism in the promoter region of PRL, have been linked to variation in milk yield and composition, including fat and protein content, in high-performing dairy breeds like Saanen (Boulanger et al., 2014; Costa et al., 2016; Lan et al., 2007). This mutation may influence the binding affinity of transcription factors to the promoter region, thereby modulating gene expression levels and impacting lactation efficiency.

The genetic diversity observed at these loci offers promising functional markers for selective breeding. Favorable MSTN alleles can be harnessed to improve growth traits and carcass yield, while beneficial PRL variants can be selected to enhance milk productivity and quality. Moreover, these polymorphisms contribute to explaining phenotypic variation among goat breeds, reflecting their adaptation to specific production systems and environments.

Importantly, these locus-specific insights are increasingly integrated into genome-wide association studies (GWAS) and whole-genome sequencing (WGS) efforts. Recent studies (e.g., Wan et al., 2023) highlight the transformative potential of combining candidate gene analyses with high-resolution genomic data. Such integrative approaches are reshaping goat breeding strategies by establishing robust genotype–phenotype correlations, ultimately enabling more precise, efficient, and sustainable genetic improvement programs tailored to specific production goals.

Material and Methods

III.Material and Methods

1. General Overview of the Study Regions

This section provides a geographical and ecological characterization of the research areas, focusing on key environmental features, demographic factors, and agricultural practices relevant to goat farming. The study encompasses distinct agro-ecological zones of Algeria, each representing diverse climatic and environmental conditions that influence goat morphology and adaptation. These zones range from the humid and sub-humid coastal areas of Oran and Ain Temouchent, characterized by relatively mild temperatures and richer pastures, to the semi-arid and arid regions of Tlemcen and Naama (Mecheria), where goats are exposed to harsher conditions, limited vegetation, and greater thermal stress.

The objective of this study is to perform a morphometric characterization of local goat populations across these regions, in order to evaluate their phenotypic diversity, adaptive traits, and potential for sustainable breeding and conservation programs in Algeria (Figure 11).

Figure 11: Geographical distribution of sampling in four states in western Algeria

Data were collected through field visits and a structured survey administered to local breeders across several communes. The survey included questions related to herd composition, management practices, breeding strategies, housing conditions, feeding systems, and production objectives. In addition to interviews, direct on-farm observations were performed to assess practical aspects of goat husbandry and to document the socio-economic context of small ruminant farming.

2. Experimental Material

2.1. Animal Material

The study was conducted on a total of 119 local goats, all characterized as adult and unrelated individuals

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 09). 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.

2.2. Measurement equipment

The following materials were used for morphometric data collection:

- **Measuring tape** (graduated in centimeters) for linear body measurements (e.g., height at withers, body length, chest girth).
- **Digital camera** to photograph animals for phenotypic documentation and conformation analysis.
- **Notebook** for recording measurements and observations in the field.

2.3. Datacollection

2.3.1. External measurements (Quantitative Traits)

Measurements were taken using a graduated measuring tape (cm precision). A total of 15 morphometric measurements were recorded. The traits measured were selected from morphological studies (FAO, 2023). They included (Figure 12):

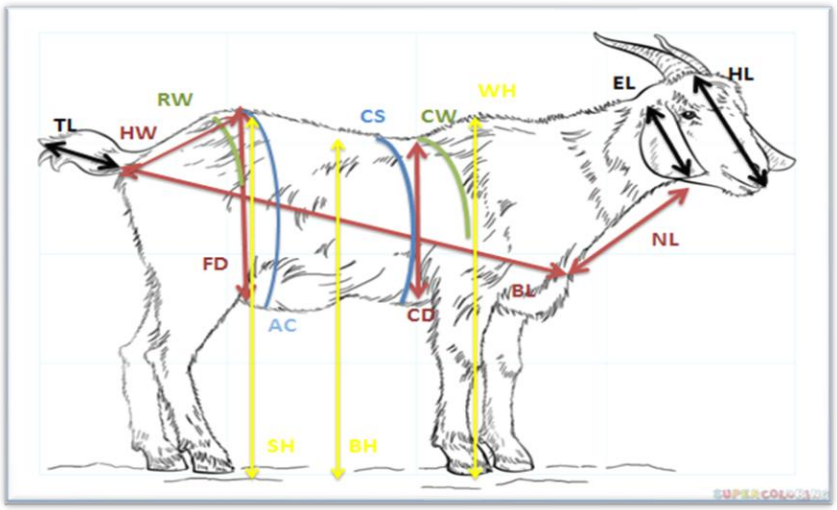

Figure 12: External measurements used in the study

- **Head Length (HL)**: Distance from occiput to nose tip
- **Ear Length (EL)**: Base to distal extremity
- **Neck Length (NL)**: Throat to shoulder angle
- **Body Length (BL)**: Shoulder point to pin bone
- **Pelvic Length (PL)**: Hip bone to pin bone distance
- **Hip Width (HW)**: Distance between hip prominences
- **Rump Width (RW)**: Distance between pin bones
- **Chest size (CS)**: Circumference behind withers at girth
- **Chest Width (CW)**: Transverse measurement behind withers
- **Chest Depth (CD)**: Sternum to dorsal line at girth
- **Wither Height (WH)**: Ground to withers summit *(Most cited size parameter - Laoun, 2007)
- **Back Height (BH)**: Mid-dorsal line to ground
- **Sacrum Height (SH)**: Croup to ground
- **Flank Depth (FD)**: Hip point to stifle joint
- **Tail Length (TL)**: Tail attachment to distal end
- **Abdominal circumference (AC):** Measurement taken vertically behind the sacrum at the level of the udder.

2.3.2. Qualitative traits

- **Phenotypic Characterization Methodology**

This study employed systematic qualitative trait analysis to document morphological variation across the study population. All phenotypic observations were recorded using standardized numerical coding systems to ensure precision and analytical consistency.

Morphological Traits Assessed*:*

- **Pigmentation patterns**

For pigmentation pattern we have five phenotypes: black, white, mixed, brown, grey. These colors were applied to: coat, head, and foot coloration.

- **Horn patterns**

For horns we have used for horn morphology (presence/absence)

The standardized approach facilitates both intra-study consistency and future comparative analyses, while the combination of gross morphological and detailed pigmentation descriptors provides a comprehensive framework for understanding phenotypic diversity in relation to genetic variation. Such rigorous phenotypic characterization is particularly valuable for association studies seeking to link observable traits with underlying genetic markers.

3. Statistical Analyses

3.1. Descriptive Statistics

Multivariate analysis enables a higher-level examination by comparing different distributions. This approach allows for precise evaluation of interactions between selected variables, identification of systematic variable combinations, and extraction of the key components structuring the studied populations.

The analysis of all traits is based on the principles of multidimensional statistical analysis (Jivotovski, 1985). Before the statistical tests began, a normality test (correction by Bonferroni test) was performed on the various character values. All statistical analyses were conducted using SPSS21 software (v.19).

- **Principal Component Analysis (PCA)**

Principal Component Analysis (PCA) is a multivariate statistical technique used to reduce dimensionality and synthesize information from datasets containing individuals and quantitative variables. By transforming the original variables into uncorrelated principal components, PCA identifies patterns of similarity between individuals, reveals homogeneous groups, and establishes typologies. Simultaneously, it analyzes correlations between variables, creating synthetic variables that capture the most significant variance in the data. This dual approach allows researchers to examine relationships between individual typologies and variable patterns (Kouani et al., 2007), making PCA particularly valuable for exploring complex morphological datasets in animal characterization studies.

- **Hierarchical Ascending Classification (HAC)**

As part of multivariate data analysis methods, Hierarchical Ascending Classification (HAC) aims to provide a simplified schematic representation of rectangular data tables where columns represent descriptors and rows represent observations. The primary objective of classification is to partition the sample into homogeneous groups of observations, with each group clearly distinct from others. However, the goal is often more refined, seeking to identify sections within main groups, then progressively smaller subdivisions within these sections, ultimately establishing a hierarchical structure of nested partitions with increasing granularity across the initial observation set (Maurice Roux, 2006).

3.2. Analysis of Variance (ANOVA)

Analysis of variance (ANOVA) and factorial analysis are statistical techniques used to determine whether one or more dependent variables (response variables) are associated with one or more independent variables (explanatory factors). For all quantitative variables, we assessed whether significant differences existed between individuals based on their location (localities), population types, and breeds present in the region - effectively evaluating the influence of environment, population, and breed on these quantitative measurements (Ramousse, 1996). Body measurements were analyzed using SPSS software (v.19), with the effects of region compared through Student-Newman-Keuls multiple comparison tests.

- **Independent Student's test**

This parametric test compares means between groups and is specifically used for two independent or paired samples (with distinct versions for each case), requiring quantitative data

measured on an interval or ratio scale; when more than two samples are involved, an appropriate ANOVA should be employed instead.

- **Shannon-Weaver Diversity Index**

The Shannon-Wiener diversity index (H') measures the amount of information provided by a sample about the community structure from which the sample is derived, as well as how individuals are distributed among different species. This index reflects both species richness and evenness, offering insight into the ecological diversity of a given habitat.

H' = - Σ Pi ln Pi

H': Shannon biodiversity index.

i: A species in the study environment.

Pi: Proportion of species *i* relative to the total number of species.

- **Evenness (Equitability)**

Evenness (or equitability) measures the distribution of individuals among species within a community

This index allows for the comparison of community structures. The value of **H'** equals zero if the community contains only one species, and reaches **$Log_2(S)$** if all species have the same number of individuals. These two values define the range within which **H'** varies (Barbault, 1995).

Evenness represents a second fundamental dimension of diversity (Ramade, 1984). According to Dajoz (1995), it reflects how individuals are distributed across different species. It is calculated as the ratio between the observed diversity (**H'**) and the maximum possible diversity (**Hmax**), expressed as:

E = H' / Hmax

where **$Hmax = Log_2(S)$**

(*S* = total number of species in the community.)

This index helps assess whether a community is dominated by a few species or if individuals are evenly distributed among all species.

The evenness index (E), which ranges from 0 to 1, serves as a measure of how evenly individuals are distributed among species within a community. When E approaches, it indicates that nearly all individuals belong to a single dominant species, whereas a value of 1 reflects perfect evenness where all species are equally abundant. This index essentially quantifies the proximity of the observed Shannon diversity (H') to the theoretical maximum diversity (Hmax). Beyond ecological applications, this method has been successfully adapted for assessing intra-

population diversity in genetic studies. In this context, species richness is replaced by phenotypic class richness, and species frequency is substituted by phenotypic class frequency within populations. This modified approach proves particularly valuable in population genetics, as it provides crucial insights into both within-population and between-population genetic diversity patterns (Chentoufi, 2014). The versatility of this index makes it a powerful tool for comparing diversity across different biological organizational levels, from ecological communities to genetic populations

4. Molecular Analysis

The blood samples, approximately 5 ml each, were collected aseptically through jugular vein puncture. The blood was drawn into EDTA (ethylenediaminetetraacetic acid) anticoagulant tubes. All samples were transported under controlled low temperature conditions to the LGMC laboratory at USTO-MB, where they were subsequently frozen for DNA extraction

5. DNA Extraction

Genomic DNA was extracted from whole blood using the conventional NaCl-based method (Miller et al., 1988). The extraction was performed in LGMC laboratory at USTO-MB (University of Science and Technology of Oran - Mohamed Boudiaf). The extracted DNA samples were then stored at -20°C for subsequent use.

6. Principles of Genotyping Techniques

6.1. Principle of Conventional PCR

The polymerase chain reaction, commonly known as PCR (Polymerase Chain Reaction), is a DNA amplification method developed in 1985 by American biochemist Kary Mullis. This revolutionary technique enables exponential in vitro replication of a double-stranded DNA fragment through the enzymatic activity of a heat-resistant DNA polymerase (Taq polymerase) derived from the thermophilic bacterium *Thermus aquaticus*.

The technique is based on the use of short nucleotide sequences called primers, typically composed of 20 to 25 nucleotides, which are complementary to the 3' ends of both strands of the target DNA fragment. These primers specifically flank the sequence to be amplified. The reaction alternates between three-step cycles:

1. Denaturation of double-stranded DNA to obtain single strands.
2. Primer annealing to the template strands.
3. Primer extension by DNA polymerase to synthesize the complementary strand.

The repetition of these cycles results in exponential amplification of the target sequence (Mullis K et al., 1986).

6.2. Principle of PCR-RFLP

PCR-RFLP (Polymerase Chain Reaction - Restriction Fragment Length Polymorphism) is a widely used molecular biology technique for detecting specific genetic variations. This method combines DNA amplification by PCR with restriction enzyme digestion to analyze variations in DNA cutting patterns.

The PCR-RFLP technique relies on the principle that genetic mutations can either introduce or eliminate restriction enzyme recognition sites, thereby altering DNA fragmentation patterns. When a mutation creates a new restriction site, the enzyme will cleave the amplified DNA at this additional location, producing smaller fragments. Conversely, if a mutation abolishes an existing restriction site, the DNA remains uncut at that position, resulting in larger fragments. These digestion products are then separated by gel electrophoresis, where differences in fragment sizes become visible as distinct banding patterns. By comparing these patterns to reference samples, researchers can identify specific genetic variations, including single nucleotide polymorphisms (SNPs) or other sequence alterations. This approach is particularly valuable for genotyping known mutations that affect restriction sites, enabling applications in medical diagnostics, population genetics, and microbial typing. However, its utility is limited to polymorphisms that modify enzyme recognition sequences, and it requires prior knowledge of both the target DNA sequence and its restriction map for accurate interpretation. The method's strength lies in its cost-effectiveness and reliability for detecting well-characterized genetic

variants, though more comprehensive techniques like sequencing are necessary for discovering novel mutations.

7. Standardization and Amplification of Target Genes

All genomic DNA samples were normalized to a working concentration of 1:10 dilution to ensure consistent template quantity across PCR reactions. Gene-specific amplification was performed for two key loci: the myostatin (MSTN) gene, involved in muscle growth regulation, and the prolactin (PRL) gene, associated with reproductive functions. The MSTN locus was amplified using the primer pair F: CCGGAGAGACTTTGGGCTTGA and R: TCATGAGCACCCAGAGCGGTC, while the PRL gene was targeted with primers F: ATTCCTGGAGCCAAAGAG and R: TGTGGGCTTAGCAGTTGT, as previously

established by Abdel-Aziem et al. (2018). All the primers were provided from GenApAgiE **(**Laboratory of Applied Genetics in Agronomy, Ecology and Public Health).

PCR reactions were optimized using a total volume of 20 µL per reaction. Each reaction mixture contained 2 µL of diluted genomic DNA as the template, 4 µL of Solidebiodyne PCR master mix, which includes Taq polymerase, deoxynucleotide triphosphates (dNTPs), and reaction buffer, 0.5 µL each of forward and reverse primers at a concentration of 10 µM, and 13 µL of molecular-grade water to bring the total volume to 20 µL. This optimized setup ensured efficient amplification of the target DNA under consistent reaction conditions.

Thermocycling conditions were carefully optimized for the amplification of each target gene. For MSTN amplification, the protocol began with an initial denaturation at 94°C for 4 minutes, followed by 35 cycles consisting of denaturation at 94°C for 60 seconds, annealing at 55.5°C for 35 seconds, and extension at 72°C for 2 minutes. A final extension step at 72°C for 4 minutes was included to complete the reaction. In contrast, the amplification of the PRL gene followed a slightly different protocol, starting with an initial denaturation at 95°C for 5 minutes, followed by 35 cycles of denaturation at 94°C for 30 seconds, annealing at 56°C for 35 seconds, and extension at 72°C for 30 seconds. This reaction concluded with a final extension at 72°C for 10 minutes. These optimized conditions ensured specific and efficient amplification of the target gene fragments.

Post-amplification, PCR products were quality-checked by electrophoresis on 1% agarose gels prepared in 1× TBE buffer. Electrophoresis was conducted at 100V for approximately 30-45 minutes, followed by ethidium bromide staining (0.5 µg/mL) for 15 minutes. DNA bands were visualized under UV transillumination using a gel documentation system, confirming successful amplification of the expected fragment sizes before proceeding to subsequent RFLP analysis. This standardized protocol ensured reproducible amplification of both target loci across all experimental samples.

8. Restriction Fragment Length Polymorphism (RFLP) Analysis

For RFLP genotyping, a 30 µL digestion reaction was prepared for each sample to ensure effective restriction enzyme activity and accurate genotype determination. Each reaction consisted of 10 µL of purified PCR product (approximately 50–100 ng), 3 µL of 10× restriction enzyme buffer to provide optimal reaction conditions, and 2 µL of a gene-specific restriction enzyme—Eco24I for MSTN gene analysis or HaeIII for PRL gene analysis. The volume was brought to 30 µL with 15 µL of nuclease-free water. This setup enabled precise cleavage at

specific recognition sites within the amplified DNA fragments, facilitating the detection of genetic polymorphisms through downstream analysis.

The digestion protocol involved overnight incubation at 37°C (14-16 hours) in a dry bath incubator to ensure complete enzymatic cleavage of all target sequences. Following digestion, the restriction fragments were resolved by electrophoresis on 2.5% high-resolution agarose gels prepared in 1× TBE buffer. The higher agarose concentration was selected to optimize separation of smaller DNA fragments expected from the restriction analysis.

Electrophoresis was performed at 80V for 90 minutes, after which gels were stained with ethidium bromide (0.5 μg/mL) for 20 minutes. DNA banding patterns were visualized using a UV transillumination system and documented with a gel imaging workstation. Fragment sizes were determined by comparison with a 50-1000 bp DNA ladder run alongside the digested samples.

This RFLP protocol allowed for clear discrimination of different genotypes based on the characteristic restriction patterns for each gene:

- For MSTN: Eco24I recognition sites produced distinct fragment profiles
- For PRL: HaeIII cleavage patterns revealed polymorphic variations

The extended digestion time and optimized electrophoresis conditions ensured reproducible and reliable detection of restriction site polymorphisms between samples.

9. Hardy-Weinberg Equilibrium (HWE)

The Hardy-Weinberg Equilibrium (HWE) is a fundamental principle in population genetics that describes the expected genotype frequencies in a stable population over multiple generations, assuming the absence of evolutionary forces such as natural selection, migration, mutation, or genetic drift.

9.1. Assumptions of the Hardy-Weinberg Model

The Hardy-Weinberg principle serves as a fundamental model in population genetics, providing a framework to understand how allele and genotype frequencies behave in an idealized population. To apply this principle, several key assumptions must be met

- Infinite Population Size: The population is assumed to be very large to minimize random genetic drift.
- No Gene Flow (Migration): There is no introduction or loss of alleles due to migration.

- No Mutation: Allele frequencies remain unchanged as no new mutations occur.
- Random Mating: Individuals mate without preference for specific genotypes (no assortative mating).
- No Natural Selection: All genotypes have equal fitness, with no selective advantage.

Under these conditions, the Hardy-Weinberg principle predicts that allele and genotype frequencies will remain constant across generations.

9.2. Mathematical formulation for a locus with two alleles

For a locus with two alleles A and a, **p** represents the frequency of allele **A** and **q** the frequency of allele **a** in a population.

Under Hardy-Weinberg equilibrium, the expected genotype frequencies can be calculated as follows: the frequency of the homozygous dominant genotype (**AA**) is $\mathbf{p^2}$, the heterozygous genotype (**Aa**) is **2pq**, and the homozygous recessive genotype (**aa**) is $\mathbf{q^2}$. These genotype frequencies must satisfy the fundamental Hardy-Weinberg equation: $\mathbf{p^2 + 2pq + q^2 = 1}$.

9.3. Applications in Population Genetics:

By comparing observed genotype frequencies with expected HWE frequencies, researchers can determine whether a population is in genetic equilibrium or if evolutionary forces (e.g., selection, inbreeding, or genetic drift) are influencing allele distribution.

9.3.1. Wilson Score

The Wilson score is a statistical method for estimating confidence intervals, particularly suited for small sample sizes or when dealing with proportions bounded between 0 and 1such as allele frequencies, where:

- 0 indicates the complete absence of an allele
- 1 means the entire population carries the allele

Unlike traditional methods (e.g., normal approximation-based confidence intervals), the Wilson score provides reliable intervals even for extreme proportions (near 0 or 1) and performs well with limited data.

The Wilson score interval is calculated as:

$$\hat{p} \pm \frac{Z\alpha 2}{\sqrt{N}} \sqrt{\frac{\hat{p}1-\hat{p}}{n} \frac{z_{\alpha}^{2}2}{4n^{2}}}$$

Where:

$\widehat{\boldsymbol{P}}$: The observed proportion, i.e., the estimated proportion based on the sample (e.g., the number of successes divided by the sample size).

$\boldsymbol{Z\alpha 2}$: The critical value from the standard normal distribution for a given confidence level. For example, for a 95% confidence interval, $\boldsymbol{Z\alpha 2}$ = 1.96.

n: The sample size, i.e., the total number of observations in the sample.

$\widehat{\boldsymbol{p}}\boldsymbol{1-}\widehat{\boldsymbol{p}}$: The variance of the observed proportion, which measures the variability of $\widehat{\boldsymbol{P}}$.

$\frac{\boldsymbol{z_{\alpha}^{2}2}}{\boldsymbol{4n^{2}}}$: A correction term added in the Wilson formula to adjust the confidence interval, particularly useful for small samples or proportions near 0 or 1.

The complete formula combines these elements to provide a more accurate confidence interval than a simple normal approximation, accounting for adjustments needed for small sample sizes.

This formula incorporates a continuity correction term that addresses the limitations of traditional methods. Specifically, it dynamically adjusts the confidence interval based on:

- Sample size (performing well even with small)
- Distribution characteristics (accounting for extreme proportions near 0 or 1)

In population genetics, this method provides a more accurate estimation of allele frequencies, particularly when analyzing rare variants or working with limited sample sizes

9.4. Precision Index

The precision index is a statistical measure that evaluates the reliability of frequency estimates. A high precision index indicates a more accurate estimate, while a low value reflects greater uncertainty. This metric is particularly useful for:

- Comparing estimate reliability across different populations

- Assessing the impact of sample size variation on measurement confidence

The precision index (PI) quantifies the reliability of frequency estimates by comparing the 95% confidence interval (CI) width to the estimated frequency value. The CI width is calculated as the difference between the upper and lower bounds of the confidence interval.

$$\text{The precision index } = \frac{1}{the\ width\ of\ CI}$$

Results

IV. Results

1. Field Survey Results

The field survey and on-farm observations revealed that goat farming in the study area is generally a secondary activity, practiced alongside sheep breeding. Most breeders prioritize sheep production, allocating more resources, better housing, and improved feeding practices to sheep herds. In contrast, goat management remains traditional and largely informal, with limited application of zootechnical principles in breeding, feeding, and housing.

The majority of herds were found to be composed of a single local breed, with little or no evidence of crossbreeding, indicating a stable but genetically narrow population structure. Goats are primarily kept for subsistence purposes, such as household consumption or pasture management (guiding sheep), rather than for commercial production. Consequently, the economic potential of goat milk and meat remains underexploited.

Breeders expressed limited awareness of improved breeding techniques or nutritional management, and few had access to veterinary or extension services. These findings highlight the low level of intensification in goat farming systems and suggest that improving husbandry practices could significantly enhance productivity and profitability.

2. Descriptive analysis of quantitative characteristics

Statistical analyses were performed to characterize the goat populations reared in Oran, Ain Temouchent, Tlemcen, and Naama (Mecheria) regions and to assess potential differentiation among individuals.

1.1. Body Measurements

1.1.1. Descriptive analysis for quantitative traits

The different body measurements of goats are reported in Table 01.

Table 1 : Descriptive analysis of body measurements (cm) in the surveyed population

	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)

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 02).

Table 02: Regional differences in goat body traits (cm) in Mecheria, Tlemcen, Ain-Temouchent and Oran, Algeria

Area		BL	EL	TL	PL	NL	HL	CS	AC	PW	CW	HW	BH	SH	CD	FD
Mecheria	Mean	68.00	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

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)

Table 02 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.

1.1.2. Principal Component Analysis (PCA)

All the measurements of studied variables were presented in Principal Component Analysis (PCA) (Figure 13).

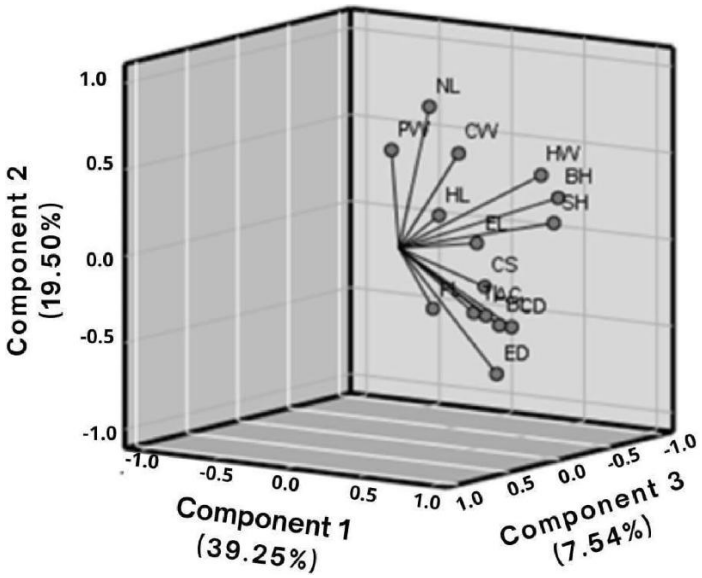

Figure 13: Presentation of body measurements by PCA in goat populations in western Algeria

In Figure 13, 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 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.

1.1.3. Analysis of classification

The analysis of classification of the goat population in western Algeria is presented in Figure 14.

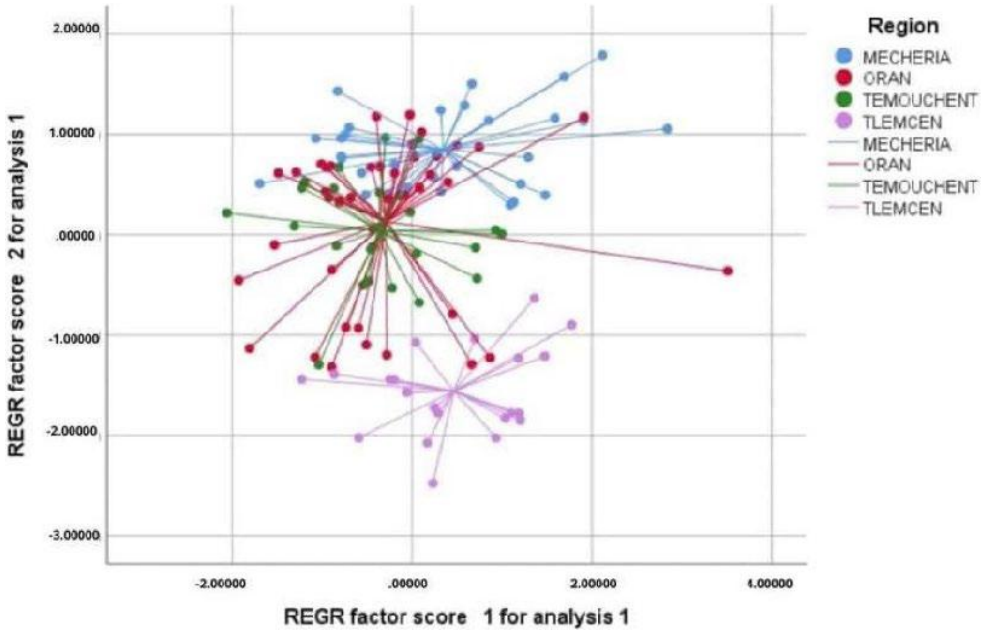

Figure 14: Barycentric distribution of individuals, by region

According to Figure 14, 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 hierarchicalclustering was performed using a dendrogram (Figure 15).

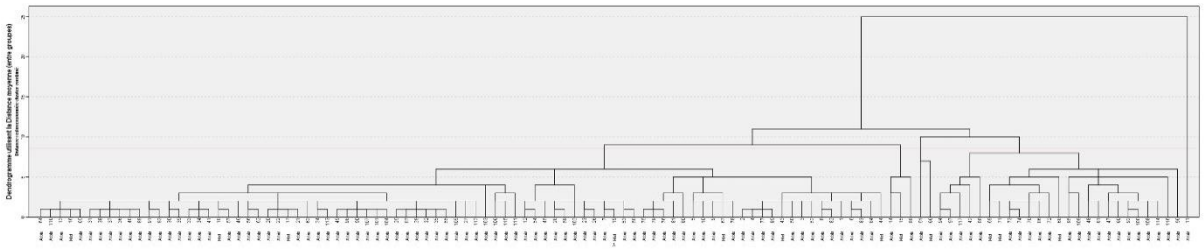

Figure 15: Dendrogram of hierarchical clustering on morphological and genetic characteristics

Figure 15 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 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.

1.1.4. 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 03 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.

Table 03: Shannon-Weaver Diversity Index of studied goat population in western Algeria

		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 n Width (PW), Chest Width (CW), Height at the Withers (HW), Back Height (BH), Sacrum Height (SH), Chest Depth (CD), Flank Depth (FD)

1.2. Descriptive Analysis for qualitative traits

The data represents the distribution of head colors observed in a goat population. Each percentage corresponds to the prevalence of a specific head color (Figure16).

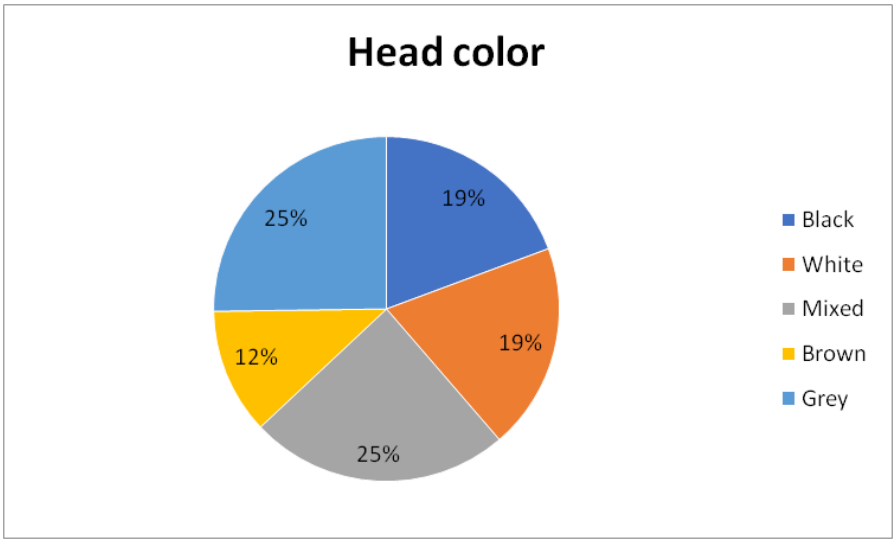

Figure 16: distribution of head colors observed in the goat population

The head color distribution in the goat population shows that Black and Mixed (both at 25%) are the most common, followed closely by Brown and Grey (19% each), while White is the rarest (12%). This balanced distribution, totaling 100%, suggests genetic diversity within the herd, potentially influenced by natural selection, breeding practices, or environmental adaptation

For the distribution of coat color observed in a goat population, each percentage corresponds to the prevalence of a specific coat color (Figure 17).

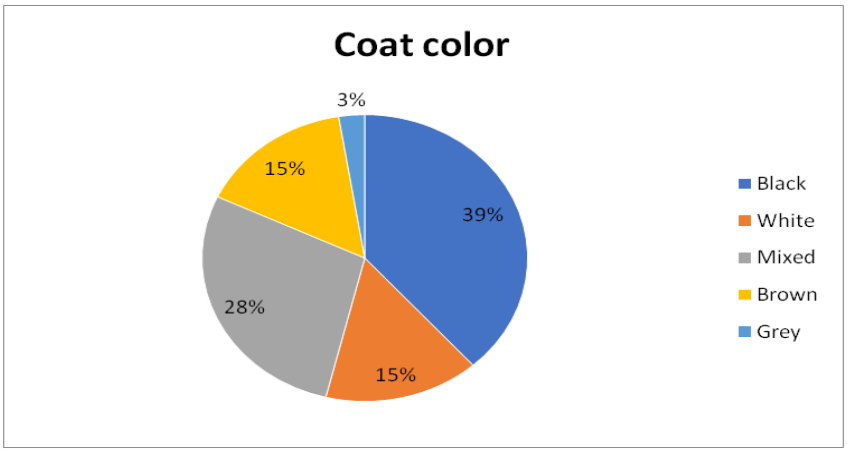

Figure 17: distribution of coat colors observed in the goat population

The coat color distribution for this goat population appears inconsistent, there are five color categories (Black, White, Mixed, Brown, Grey) Mixed (31%) and Grey (29%) dominate, likely due to genetic dominance or selective breeding favoring these traits. Black (21%) and White (17%) are moderately common, while Brown (2%) is exceptionally rare, suggesting it may be a recessive trait or less preferred in breeding programs

For the distribution of feet color observed in a goat population, percentage corresponds to the prevalence of a specific feet color (Figure 18).

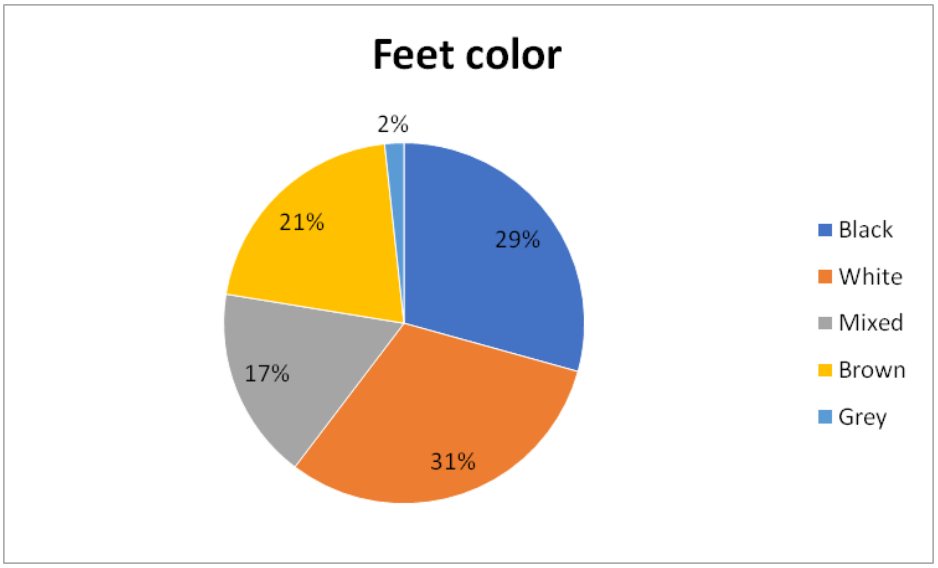

Figure 18: distribution of feet color observed in the goat population

The Feet color data lists five categories (Black, White, Mixed, Brown, Grey). Mixed (31%) and Grey (29%) are the most prevalent foot colors, followed by Black (21%) and White (17%), while Brown is exceptionally rare (2%). This skewed distribution may reflect genetic dominance (e.g., Mixed/Grey), selective breeding preferences, or environmental adaptation.

For the distribution of horn observed in a goat population, each percentage corresponds to the horn presence or absence (Figure 19).

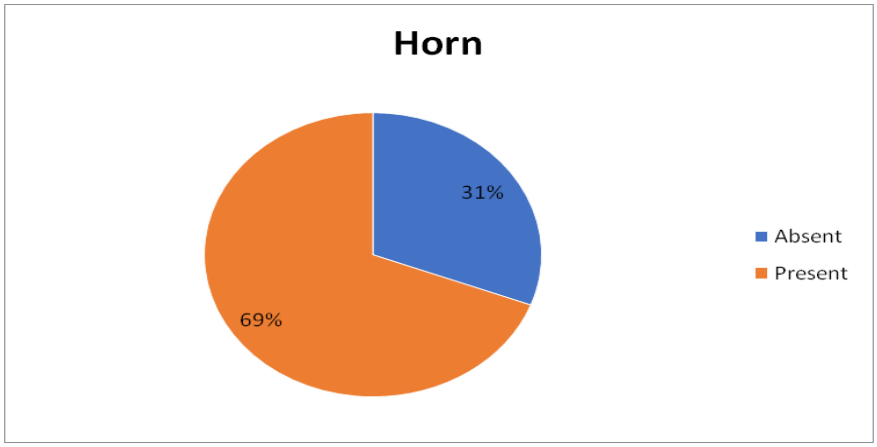

Figure 19: the presence of horns in a population

The data categorizes the presence of horns in a population (likely goats), with 31% of individuals having absent horns and 69% having present horns. This indicates horns are a predominant trait, possibly due to genetic dominance, selective breeding favoring horned individuals, or limited dehorning practices. The high prevalence of horns (69%) could reflect breed-specific characteristics, environmental advantages (e.g., defense, social hierarchy), or natural genetic expression. The absence in 31% might suggest recessive genes, intentional dehorning for safety, or breeding against horns.

3. 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. The digestion patterns depended on the presence or absence of the HaeIII recognition site within the amplified region.

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 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 $\chi 2$ were calculated and are presented in Table 04.

Table 04: Allele frequency, observed heterozygosity (Ho), estimated heterozygosity (He) and v2 values of PRL-Eco24I/PCR-RFLP and MSTN-HaeIII/PCR-RFLP ($P < 0.05$)

Gene	Allele Frequency		Observed Het(H_o)		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

2.1. Correlation between MSTN and PRL genes

The associations between variations in the MSTN and PRL genes and specific body traits in goats in western Algeria are presented in Figure 20.

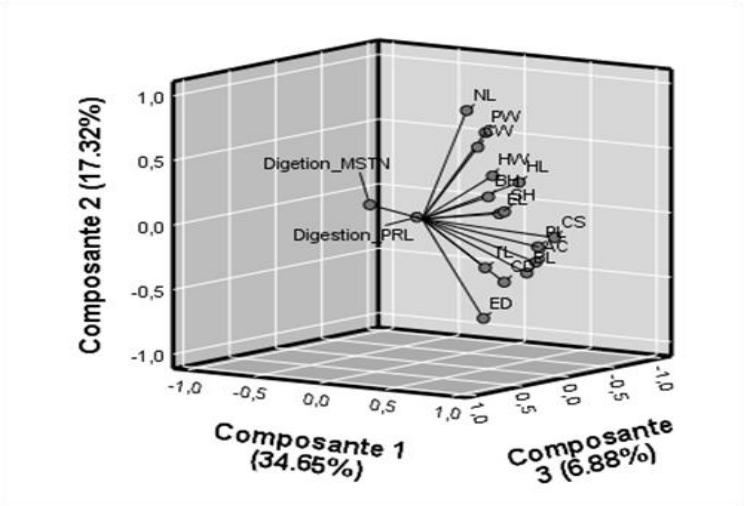

Figure 20: Principal Component Analysis of MSTN and PRL Gene Effects on Goat Body Traits

Figure 20 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.

Discussion

V. 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.

The analysis of coat color, feet color, horn presence, and data validation in the goat population reveals critical insights into genetic diversity, human influence, and methodological rigor. Coat color distribution (25% Black, 25% Mixed, 19% Brown, 19% Grey, 12% White) demonstrates balanced genetic variability, with Black and Mixed coats likely reflecting heterozygous dominance or polygenic inheritance (Griffiths et al., 2020), while the rarity of White coats may align with selective avoidance due to increased predation risk in certain environments (Smith et al., 2018) or recessive alleles (e.g., the *ASIP* gene influencing pigmentation; Fontanesi et al., 2010).

Feet color data (31% Mixed, 29% Grey, 21% Black, 17% White, 2% Brown), after correcting duplicate entries—highlights a skew toward Mixed and Grey traits, potentially linked to epistatic interactions (Alberts et al., 2022) or breeding preferences for adaptive traits (e.g., darker hooves for rugged terrain; Lu, 2019). The near-absence of Brown feet (2%) may reflect recessive alleles (e.g., *TYRP1* mutations; Gratten et al., 2007) or deliberate breeding against this trait.

Horn presence (69% Present, 31% Absent) underscores the interplay of natural selection (horns aiding in thermoregulation and social hierarchy; Shrestha & Fahmy, 2007) and human

practices (dehorning for safety; AVMA, 2020). The 31% absence could stem from the polled gene (Wiedemar & Drögemüller, 2015) or management protocols prioritizing safer herd interactions.

Finally, data validation insights (e.g., duplicate percentage corrections) emphasize the necessity of rigorous auditing to avoid misrepresentation of traits (Creswell & Creswell, 2018). Such methodological transparency is critical for ecological and agricultural studies (Gauch, 2003).

These findings illustrate how genetic architecture, environmental pressures, and anthropogenic practices shape trait distributions. To promote sustainable breeding, conserving rare alleles (e.g., White coats) and balancing horn management with genetic authenticity are essential. Future work should integrate genome-wide association studies (GWAS) to validate observed patterns (Hayes & Goddard, 2010).

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 and perspectives

VI.Conclusion and perspectives

This study provides a comprehensive analysis of the morphometric and genetic characteristics of local goat populations in western Algeria, focusing on the local breeds. By integrating phenotypic measurements, molecular techniques, and statistical analyses, the research reveals critical insights into the diversity, adaptability, and productivity of these breeds.

Key findings highlight moderate phenotypic diversity, with traits such as body length (BL), height at withers (HW), and abdominal circumference (AC) showing significant regional variation. Principal Component Analysis (PCA) underscored the influence of skeletal and muscular traits on overall conformation, while the Shannon-Weaver index indicated higher diversity in coastal regions like Oran compared to inland areas. Molecular analysis of the *MSTN* (muscle growth) and *PRL* (lactation and reproduction) genes revealed a predominance of homozygous genotypes, suggesting limited genetic variability and potential selective pressures or geographic isolation. Both loci adhered to Hardy-Weinberg equilibrium, reflecting stable allele frequencies but low heterozygosity, which may signal inbreeding or restricted gene flow.

The study also contextualizes these findings within Algeria's agricultural practices, where goat farming remains secondary to sheep production. Despite the economic potential of goat-derived products, traditional management practices and a lack of targeted breeding programs hinder productivity. The predominance of single-breed herds and underutilization of milk and meat resources further constrain commercial viability.

Future research should aim to expand molecular analyses by incorporating a wider range of highly polymorphic markers, such as microsatellites and single nucleotide polymorphisms (SNPs), to provide a more detailed and accurate assessment of genetic diversity within and between local goat populations. The application of genome-wide association studies (GWAS) and whole-genome sequencing (WGS) will further enable the identification of genetic variants linked to adaptive and productive traits, offering valuable insights for selection and conservation strategies.

A key perspective is the integration of phenotypic and genetic data to design targeted breeding programs that balance productivity improvement with the preservation of local genetic resources. Additionally, enhancing awareness among farmers about the economic and ecological importance of conserving indigenous goat breeds is essential to ensure community participation in sustainable livestock development. Finally, the outcomes of this research should contribute to the establishment of a national program for the sustainable management,

conservation, and valorization of goat genetic resources in Algeria, aligning scientific progress with rural development and biodiversity preservation.

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VII.References

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Publications

Phenotypic and molecular characterization of goat populations in western Algeria

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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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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

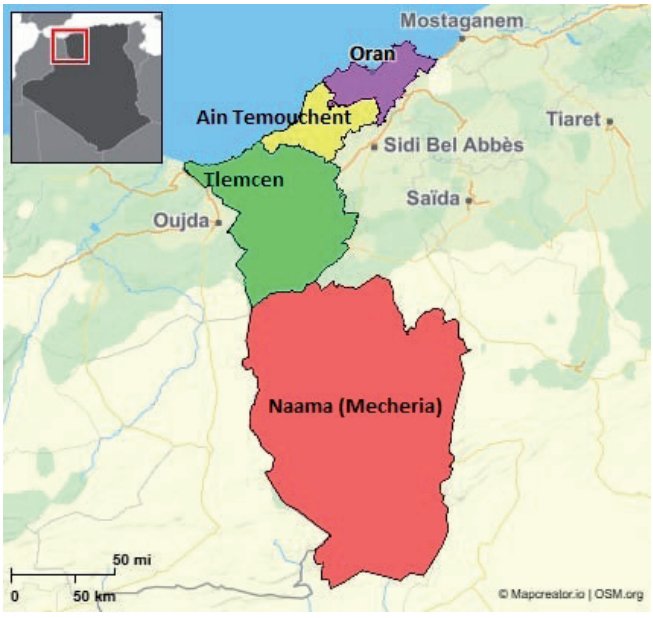

Figure 1: *Geographical distribution of sampling in four states in western Algeria /// Répartition géographique des échantillons dans quatre régions de l'ouest de l'Algérie*

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:

$$H' = -\sum_{i=1}^{s} pi \cdot \ln(pi) \qquad \text{(equation 1)}$$

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

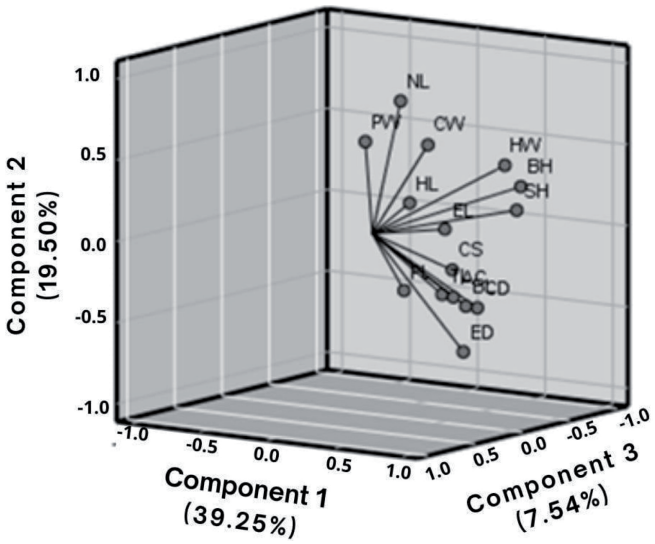

Figure 2: Presentation of body measurements by PCA in goat populations in western Algeria /// *Présentation des mensurations corporelles selon l'ACP dans les populations caprines de l'ouest de l'Algérie*

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.

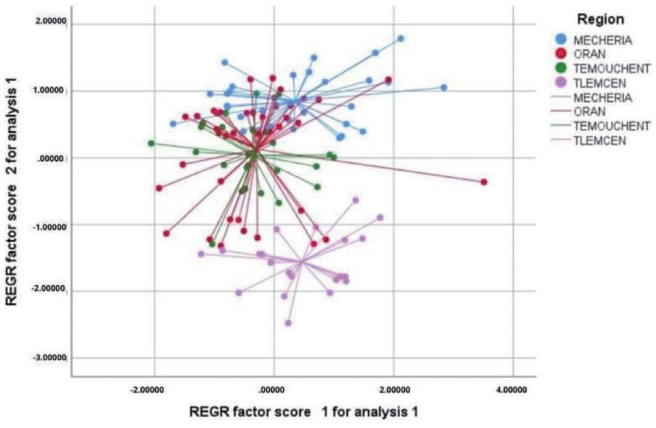

Figure 3: Barycentric distribution of individuals, by region /// *Répartition barycentrique des individus par région*

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

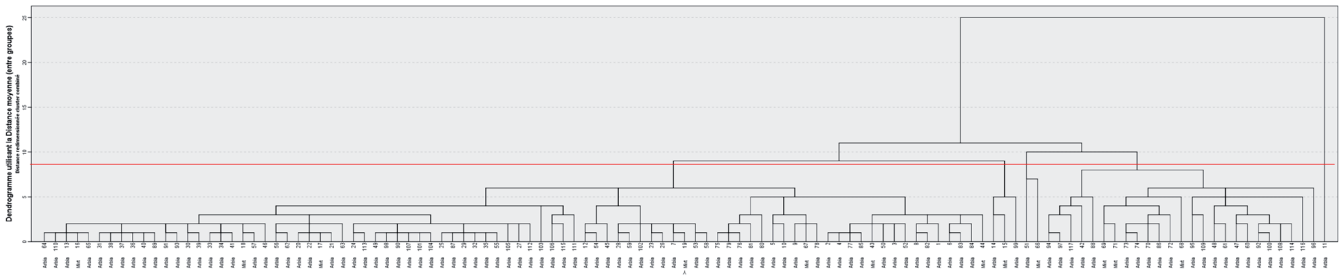

Figure 4: Dendrogram of hierarchical clustering on morphological and genetic characteristics /// *Dendrogramme de classification hiérarchique des caractéristiques morphologiques et génétiques*

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 $\chi 2$ 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

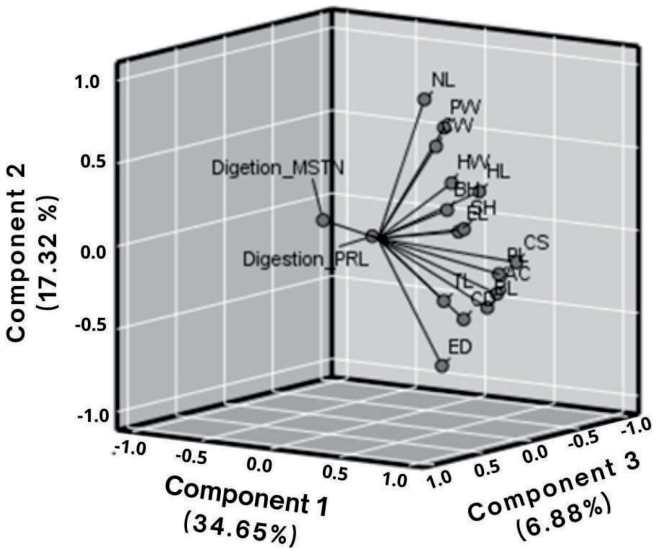

Figure 5: Principal Component Analysis of MSTN and PRL gene effects on goat body traits /// *Analyse en composantes principales des effets des gènes MSTN et PRL sur les caractéristiques corporelles des chèvres étudiées*

■ 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

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Original Research Paper

Discriminant analysis on the morphometry of local goats breed in the western of Algeria

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Abstract

The objective of this study is a morphometric characterization of local goats in western of Algeria. With the use of 19 quantitative variables, we carried out a discriminant analysis on 119 goats and 32 bucks divided into 4 Wilayas (Tlemcen, Adrar, Naama and Bechar). The discriminant analysis on males was not significant. As for the female population, the analysis of variance (ANOVA) on the region effect was highly significant p=1.32 x 10-11. A clear separation has been found between the populations, with the exception of Naama and Tlemcen, which are overlapped. Measurements belonging to chest width (LP),chest circumference (TP), chest depth (PP), rump width (LB), ischium width (LI), withers height(HG), ear length LO) and hair length (LPI).are the best variables that separate between regions in the female population, with a very high significance level (p<0.01). The area under the ROC curve (AUC) is 82.04%. This study can serve as a basis for more precise genetic characterization studies of this species.

Keywords: Goat populations; Characterization; Morphology; West of Algeria

Introduction

In some regions of the world, the goat remains the essential animal for the population's diet. It is raised mainly for its milk, meat, and hair (Hafide, 2006). In Algeria, goat farming is one of the most traditional agricultural activities associated with sheep farming, currently more than 5 million head in Algeria, but this number remains marginal in comparison with sheep farming (more than 28 million head) (FAO, 2017).

In Algeria 4 local breeds have been identified using microsatellites: Arbia, Mekatia, M'zabite and naine of Kabyle (Tefiel et al., 2018), and despite the good quality of local goat's milk in terms of fat (± 47.82g/Kg) and protein (± 33.35g/Kg), it is still intended for family consumption rather than for production (Belantar et al., 2018). This is due to the lack of information regarding the genetic and phenotypic characteristics of Algerian goats, which is essential for the development of an appropriate breeding objectives and programs for each ecosystem. Knowledge of the genetic extent variation within the breed is essential for the development of goat breeding programs (Fantazi, 2017).Several studies have been carried out on these breeds in Algeria, but few of them have focused on the difference between goats regarding their breeding area.

For a better knowledge of our goat populations, our study is based on a discriminating analysis of the morphometric characteristics of local goats in the Regionsof: Tlemcen,Adrar, Naama and Bechar, in

order to facilitate their identification and classification.

Materials and methods

The study is conducted on a number of 151 local goats (119 females and 32 males) characterized as adults and non-related, the 151 individuals are spread across four Regions; Tlemcen, Adrar, Bechar and Naama (Figure 1), 8 males and 30 females in each Wilaya with the exception of the Bechar (29 females).

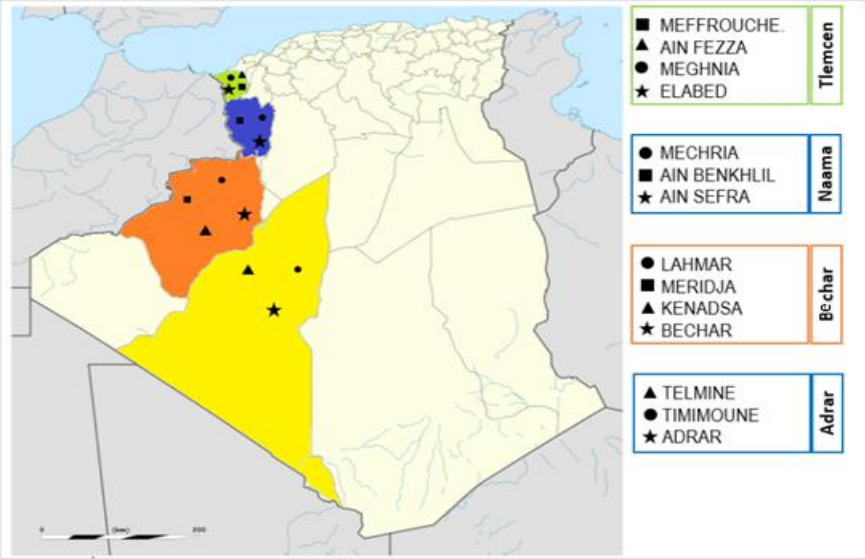

Figure 1: Map of the sampling of area.

Data collection

Measurements were taken using a tape measure. In total, 19 measurements were taken (quantitative variables) such asbody length (***LC***), head length (***LT***), neck length (***Lce***), pelvic length (***LnB***), tail length (***LQ***), rump width (***LB***), ischiumwidth ***LI***), chest width (***LP***), withers height(***HG***), back height (***HD***), sacral height (***HS***), chest circumference (***TP***), chest depth (***CD***), abdominal circumference (***TAB***), flank depth (***PF***), front cannon circumference (***TCA***), front cannon length (***LCA***), ear length (***LO***), hair length (***LPl***).

Statistical Analysis

All statistical analysis were carried out by the software R (3.5.3).The quantitative data collected on the four regions were subjected to a two-step discriminant analysis: **1/** Canonical discriminant analysis: reduction of dimensions for a better visualization of the groups and evaluating the level of significance regarding the difference between the groups (regions) through the 19 explanatory quantitative variables. **2/** Predictive discriminant analysis: proposes a classification model and verifies the accuracy of the discriminant analysis. (Marcoulides, Hershberger, 2014).Discriminant analysis requires some assumptions: the normality of distributions, the absence of multi-collinearity and the homogeneity of covariance matrices between groups (Salkind, 2010).

The two variables ***TCA*** and ***LCA*** are excluded from the analysis due to the absence of a normal distribution, the multi-collinearity between the variables was found to be very low. The variables used for the discriminant analysis were selected by the Stepwise Wilks Lambda procedure. After selecting the variables, the homogeneity of the covariance matrices is tested by the Box test, however, to reject the null hypothesis that suppose the covariance matrices are homogeneous, the test must be highly significant (Rebecca, 2008). The test box on our data matrix returned a $p\ value = 0.02$, so we accept the null hypothesis and consider that the covariance matrix in our sample is homogeneous. Before performing the discriminant analysis, the selected variables were subjected to an analysis of variance (ANOVA) towards the different regions.

Results and discussion

The results of the descriptive statistics for both males and female's population are summarized in Table 1 and Table 2.

Table 1: Males descriptive statistics.

	Adrar			***Bechar***			***Naama***			***Tlemcen***		
Variables	***Mean***	***SD***	***SE***	***Mean***	***SD***	***SE***	***Mean***	***SD***	***SE***	***Mean***	***SD***	***SE***
LC	65,00	6,97	2,46	78,13	7,57	2,68	80,25	4,56	1,61	77,00	8,32	2,94
LO	16,88	3,04	1,08	17,50	3,12	1,10	20,75	2,43	0,86	16,75	3,11	1,10
LQ	12,00	1,07	0,38	12,25	2,49	0,88	13,63	1,30	0,46	11,75	1,58	0,56
LnB	21,63	1,92	0,68	22,75	2,55	0,90	24,75	1,98	0,70	23,63	3,07	1,08
Lco	22,38	2,13	0,75	26,13	4,26	1,51	26,88	1,55	0,55	27,63	5,13	1,81
LT	19,50	1,60	0,57	21,63	2,26	0,80	21,75	1,04	0,37	21,63	3,78	1,34
LCA	12,75	0,89	0,31	14,13	1,13	0,40	13,13	1,25	0,44	13,13	1,36	0,48
LPl	4,25	3,20	1,13	7,00	2,07	0,73	7,50	1,93	0,68	6,00	3,70	1,31
TP	72,50	5,68	2,01	85,50	10,21	3,61	87,75	5,87	2,08	86,50	11,05	3,91
TCA	7,75	0,89	0,31	9,25	1,16	0,41	9,38	0,74	0,26	9,25	1,04	0,37
TAB	75,63	8,99	3,18	89,38	11,13	3,94	91,50	6,65	2,35	82,25	17,38	6,15
LP	37,62	7,44	2,63	41,63	3,81	1,35	43,50	4,21	1,49	40,63	3,93	1,39
LB	20,75	1,83	0,65	25,50	3,12	1,10	27,50	2,20	0,78	28,13	5,00	1,77
LI	22,13	2,95	1,04	26,50	5,29	1,87	29,00	2,88	1,02	27,88	3,68	1,30
HG	65,25	5,20	1,84	74,25	7,25	2,56	78,38	5,85	2,07	76,25	7,21	2,55
HD	64,13	7,70	2,72	73,75	5,68	2,01	75,63	6,16	2,18	72,25	8,21	2,90
HS	67,00	6,41	2,27	72,63	8,93	3,16	75,75	4,23	1,50	75,13	8,39	2,97
PP	31,00	2,73	0,96	36,75	5,50	1,94	37,25	3,54	1,25	35,63	5,97	2,11
PF	30,63	3,11	1,10	36,88	3,36	1,19	37,38	2,26	0,80	34,63	5,26	1,86

Table 2: Females descriptive statistics

	Adrar			*Bechar*			*Naama*			*Tlemcen*		
Variables	**Mean**	**SD**	**SE**	**Mean**	**SD**	**SE**	**Mean**	**SD**	**SE**	**Mean**	**SD**	**SE**
LC	63,80	4,67	0,85	66,69	5,85	1,09	70,60	5,22	0,95	70,10	4,22	0,77
LO	15,37	2,86	0,52	17,41	2,16	0,40	18,90	3,17	0,58	16,63	3,20	0,58
LQ	11,43	1,74	0,32	11,28	1,62	0,30	11,37	1,00	0,18	11,20	1,52	0,28
LnB	20,23	1,63	0,30	20,48	1,77	0,33	20,80	1,71	0,31	20,83	1,21	0,22
Lco	23,33	2,94	0,54	24,38	2,62	0,49	24,70	2,96	0,54	25,27	3,03	0,55
LT	19,10	1,54	0,28	19,48	1,35	0,25	20,33	1,32	0,24	19,87	1,74	0,32
LCA	12,67	1,63	0,30	12,72	0,84	0,16	12,70	0,88	0,16	12,33	1,03	0,19
LPl	3,93	3,51	0,64	5,52	2,65	0,49	5,57	1,81	0,33	4,00	2,03	0,37
TP	74,37	5,46	1,00	75,76	6,59	1,22	77,57	5,20	0,95	79,30	5,63	1,03
TCA	6,93	0,58	0,11	8,00	0,71	0,13	7,90	0,71	0,13	7,90	0,71	0,13
TAB	77,60	8,22	1,50	79,97	8,86	1,65	83,17	8,15	1,49	81,10	8,45	1,54
LP	34,83	2,69	0,49	35,93	3,48	0,65	39,77	2,42	0,44	38,47	2,37	0,43
LB	20,27	2,65	0,48	21,52	2,53	0,47	24,20	1,85	0,34	24,40	2,21	0,40
LI	21,10	2,62	0,48	20,83	2,33	0,43	25,07	2,50	0,46	23,73	2,82	0,51
HG	64,13	3,85	0,70	67,76	3,01	0,56	70,43	3,98	0,73	70,07	3,11	0,57
HD	65,60	3,04	0,55	69,07	3,79	0,70	70,57	3,46	0,63	69,93	3,58	0,65
HS	67,00	3,07	0,56	70,10	4,47	0,83	70,67	3,27	0,60	70,20	3,39	0,62
PP	31,03	2,30	0,42	33,38	1,95	0,36	33,50	2,46	0,45	33,17	2,28	0,42
PF	30,87	4,40	0,80	32,14	2,52	0,47	33,90	2,25	0,41	32,30	3,10	0,57

*Standard Deviation (**SD**),Standard Error (**SE**), Body length (**LC**), Head length (**LT**), Neck length (**Lco**), Pelvic length (**LnB**), Tail length (**LQTL**),* rump *width (**LB**), Ischium width (**LI**), Chest width (**LP**), withers height(**HG**), Back height (**HD**), Sacral height (**HS**), Chest circumference (**TP**), Chest depth (**PP**), Abdominal circumference (**TAB**), Flank depth (**PF**), Front cannon circumference (**TCA**), Front cannon length (**LCA**), Ear length (**LO**), Hair length (**LPl**).*

Discriminant analysis on the female population

Variables selection

To select the variables used in the discriminant analysis, we performed the Stepwise Wilks Lambda selection. Table 03 shows only the variables that had a significant p-value compared to a risk$\alpha = 0.05$.

Table 3: Stepwise Wilks Lambda variable selection.

	Females	
Variables	Wilks Lambda	p-Value
LB	0,62659	< 0,00000
HG	0,51903	0,00008
LPl	0,44023	0,00032
LI	0,37739	0,00060
PP	0,31986	0,00035
LP	0,28965	0,01193
TP	0,26134	0,01037
LO	0,23491	0,00900

There significantly separate (< 0.01) between the four regions in (***LP, PP, TP***), and between (***LI, LB***), also between (***HG***) and (***LPl, LO***) in table 3.

Analyse of variance (ANOVA)

The analysis of variance (ANOVA) on the selected variables showed a highly significant level $(p = 1.32 \times 10^{-11})$between the four regions.

Canonical discriminant analysis

Table 3: Summary of the canonical dimensions.

Dimension	*CanRsq*	*Eigen values*	*percentage*	*Cumulative percentage*	*p-Value*
1	0.5804	1.3831	66.94	66.94	<0.00000
2	0.3140	0.4578	22.15	89.09	<0.00000
3	0.1839	0.2254	10.91	100	0.00088

***CanRsq** : squared canonical correlations.*

Table 4: Standardized canonical coefficients.

Variables	*Can1*	*Can2*	*Can3*
LB	**−0,4973**	0,2194	**0,7226**
HG	**−0,7032**	− 0,0832	0,3181
LPl	−0,3399	**−0,5000**	−0,0065
LI	−0,2434	0,4582	**−0,7788**
PP	0,4023	**−0,9449**	0,2458
LP	**−0,5388**	−0,0864	−0,3744
TP	0,2898	**0,6217**	0,4430
LO	0,2084	−0,4306	**−0,5856**

From Table 4 and Table 5, it is noted that all canonical functions have a significant separation and the first two dimensions represent 89.09%of the total separation.

The first canonical function (Can1) is characterized by a negative coefficient for the rump width (***LB***), height at the withers (***HG***) and chest width (***LP***). The second canonical function (Can2) is strongly characterized by a negative coefficient with the Chest Depth (***PP***).The third canonical function (Can3) is inversely proportional to the ischium width (***LI***) and ears length (***LO***), it has also a strong positive coefficient of the Hip Width (***LB***).

According to Figure 2, it can be seen that the Adrar group and the Bechar group are well separated from each other and from the other two groups. However, the Tlemcen and Naama groups are overlapping. We also note that the Tlemcen, Naama and Adrar groups are correlated much more with the first canonical function (Can1) while the Bechar group is correlated with the second canonical function (Can2).In summary, the population of Adrar is characterized by small goats; reduced withers height with a small width and a small chest. The Bechar population is much more characterized by their long hair, with a medium width of the animal. The populations of Naama and Tlemcen are characterized by a large size (width and height), more developed chest and relatively long hair. Other studies in Algeria have also shown the effect of geographical location on goat's morphometry, according to Dekhili *et al.*, (2013) the goats from the wilaya of Setif indicated a significant difference between the North, Centre and South of the Wilaya, with a withers height of 70.2 cm, 68.4 cm, 59.5 cm; a chest circumference of 77.2cm, 76.7cm, 67.5cm, a hip width of 17.7cm, 15.6cm, 14.2cm and a hair length of 11.7cm, 10cm, 8.8cm, respectively between the North, Centre and South. This expresses that southern goats of Setif are characterized by a small size and short hair, while northern goats are characterized by their large size and long hair. According to Fantazi *et al* (2017), the high body measurements of Arbia goats imply that they are good walkers with long hair to resist the cold in steppe agro systems, the naine of Kabylie is small in size and better adapted to the steep areas of the "Kabylian" mountains, whilethe Mekatia and M'zabite breeds have a mixed height, they have short hairs and adapt better to the high temperatures of the Sahara. This suggests that the populations of Naama and Tlemcen in our study may be of the Arbia breed due to their large size and long hair and given the

mountainous topography and cold climate of these regions. The short hair and small size of Adrar's population can be explained by the Saharan climate.

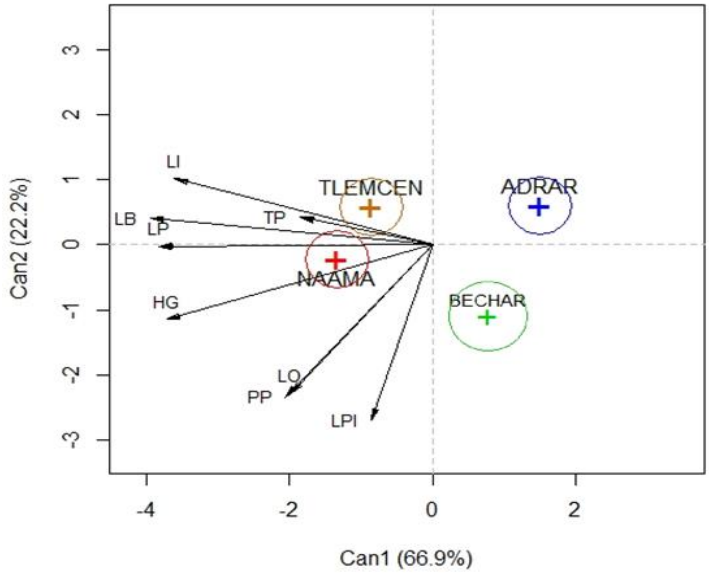

Figure 2: Distribution of group centres with 95% confidence interval according to the first two canonical functions (female population).

Predictive discriminant analysis

Table 6 represents the raw linear function that serves as a classification model for other individuals. This model is used to verify the precision of the test, using a confusing matrix and the calculation of the Area Under the ROC Curve (AUC).

Table 6: Raw linear functions

Vars	LD1	LD2	LD3
LB	0,213633	0,094234	0,310429
HG	0,207265	-0,024516	0,093767
LPl	0,142041	-0,208904	-0,002736
LI	0,095423	0,179610	-0,305301
PP	-0,187468	-0,440265	0,114522
LP	0,194473	-0,031192	-0,135117
TP	-0,052836	0,113328	0,080762
LO	-0,080253	-0,165787	-0,225453

Confusion matrix

The confusion matrix represents the ranking of our 119 individuals after using the linear model (Table 6); the new classification of our 119 individuals is called Predictions. It then cross-references the predictions with the initial classification (Table 7) in the form of a contingency table.

Table 7: The confusion matrix of the predictive discriminant analysis (Female population).

Predictions		Adrar	Bechar	Naama	Tlemcen
Initial classification	Adrar	**21**	3	1	1
	Bechar	6	**21**	3	3
	Naama	0	3	**21**	6
	Tlemcen	3	2	5	**20**

The values on the diagonal represent the individuals that remained on the same class (region) after the prediction using the linear model, they are the subjects correctly classified. According to Table 7, there are 69.75% of our individuals well classified, which indicate an error rate of 30.25%. This rate is in fact due to the low separation between the population of Naama and Tlemcen (Figure 01), if the two classes are combined into one, an error rate of 21% is obtained with an accuracy of 79%. To further explore the accuracy, the probability of the confusion matrix is estimated, this probability is calculated with the area under the ROC curve (AUC).

Area under the ROC curve (AUC)

It is an overall precision summary of the discriminant analysis; it varies from 0.5 for an accuracy of chance to 1.0 for a perfect precision. (Kelly *et al*., 2016). This is equivalent to the probability that a randomly selected member of one class has a lower probability of belonging to the other class than a randomly selected member of the other class. (David and Robert, 2001).So, a model that achieves an AUC of 0.5 is no better than a random classification. (Nick, 2015).The AUC of our discriminant analysis is 84.08%. We can conclude that the accuracy of our model is highly significant.

Males discriminate analysis

The discriminant analysis on males did not show a significant result, only two variables were significant in the selection of variables and the separation is very low. Almost all four groups are overlapped with a wide confidence interval (Figure 3).

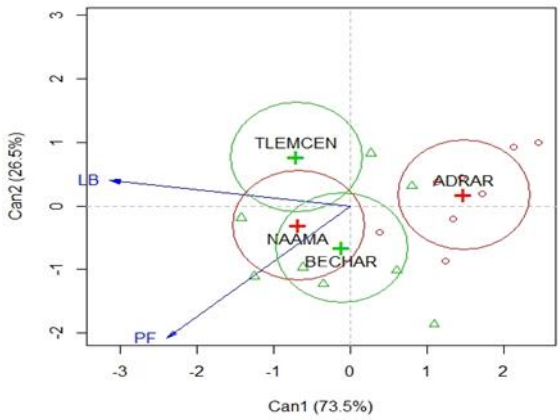

Figure 3: Males discriminant analysis

Conclusion

Our study is based on the morphometry of local Algerian goats, 119 does and 32 bucks were characterized by 19 quantitative variables, distributed in 4 western Wilayas of Algeria (Adrar, Bechar, Tlemcen and Naama).The discriminant analysis on the female population showed that there is a significant difference ($p < 10^{-10}$) between the four studied regions (Tlemcen, Adrar, Bechar and Naama). Among the 19 quantitative variables used, there are 8 variables that best separate between regions, these variables are chest width (***LP***), chest depth (***PP***), chest circumference (***TP***), ischium width (***LI***), Hip width (***LB***), height at withers (***HG***), hair length (***LPl***) and ear length (***LO***). Naama and Tlemcen group have a weak separation while the other groups are well separated from each other. The accuracy of the analysis is highly significant with an.AUC=84.04%. The discriminant analysis on males is not significant due to the small number of individuals (9 males in each region). This study can serve as a solid basis for further more precise genetic characterization studies of the goat breeds in Algeria.

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