

Systematic Review

Genetic diversity of sheep breeds in the Maghreb using Microsatellite Markers: A systematic review

Yacine OUINTEN^{1*}, Bachir MEDROUH², Imene LAFRI³, Khadidja BOUSSAID³,
Malika BRAHIMI⁴, Hamza REBHI², Gota MOROTA^{5*}

¹ Genetic and Animal Production Laboratory, Agro-Pastoralism Research Center (CRAPast), Djelfa 17000, Algeria

² Epidemiology and Animal Health Laboratory, Agro-Pastoralism Research Center (CRAPast), Djelfa 17000, Algeria

³ Biology of microbial systems and food science Laboratory, Agro-Pastoralism Research Center (CRAPast), Djelfa 17000, Algeria

⁴ Cartography and Geomantic Laboratory, Agro-Pastoralism Research Center (CRAPast), Djelfa 17000, Algeria

⁵ Laboratory of Biometry and Bioinformatics, Department of Agricultural and Environmental Biology, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Bunkyo, Tokyo 113-8657, Japan

*Corresponding Author: Phone: +213 771 717 729; E-mail: byoyacine@gmail.com gmorota@g.ecc.u-tokyo.ac.jp

Article history: Received: November 3rd 2025; Revised: December 31st 2025; Accepted: January 20th 2026

Abstract

Sheep are one of the most important domestic farm animals for agriculture and food production in North Africa, with a wide diversity of indigenous breeds threatened with extinction. According to FAO, approximately 17% of sheep breeds worldwide are at risk of extinction, including at least five native North African breeds: Rembi, Sidahou, D'men, Hamra, and Berber. To date, few large-scale genomic studies have been devoted to investigating the structure of the sheep population in this region. The objective of this study was to provide a detailed assessment of the current state of the genetic structure and admixture patterns of different sheep populations in the Maghreb, based on recent work using microsatellite markers. Following the PRISMA guidelines, four databases were searched, resulting in the inclusion of 17 eligible articles in this systematic review. Our findings indicate significant gaps in research efforts, as several breeds in several regions have received limited scientific attention, with studies per breed ranging from 1 to 12. Most of the studies investigated the four main breeds of the region. Regarding the number of microsatellites used, most studies followed the FAO guidelines. However, the sample size remained relatively small in most articles compared to the 40 animals recommended by FAO/ISAG. Greater within-population variation than between-population variation was reported, with most having a mean number of alleles greater than 10 and expected and observed-heterozygosity, and polymorphism-informative-content greater than 0.5. This study provides useful information for the future development of conservation programs for the various endangered breeds in the Maghreb.

Keywords: Genetic diversity, Indigenous breeds, Microsatellite markers, Systematic review.

المخلص

تعد الأغنام من أهم الحيوانات الزراعية المحلية للزراعة وإنتاج الغذاء في شمال إفريقيا، مع وجود تنوع واسع من السلالات المحلية المهددة بالانقراض. حتى الآن، لم يتم إجراء سوى عدد قليل من الدراسات الجينومية الشاملة للتحقيق في بنية تعداد الأغنام في هذه المنطقة. كان الهدف من هذه الدراسة هو تقديم تقييم مفصل للحالة الحالية للبنية الجينية وأنماط الاختلاط بين مختلف تجمعات الأغنام في المغرب العربي، استنادًا إلى الأعمال الحديثة التي تستخدم علامات الميكروساتلايت. وفقًا للإرشادات PRISMA، تم البحث في أربع قواعد بيانات، مما أدى إلى إدراج 17 مقالة مؤهلة في هذه المراجعة المنهجية. كشفت نتائجنا عن نقص في الدراسات حول سلالات معينة وفي مناطق فرعية معينة. بحثت معظم الدراسات في السلالات الأربع الرئيسية في المنطقة. فيما يتعلق بعدد الميكروساتلايت المستخدمة، اتبعت معظم الدراسات إرشادات منظمة الأغذية والزراعة (FAO)؛ ومع ذلك، ظل حجم العينة صغيرًا نسبيًا في معظم المقالات. تم الإبلاغ عن تباين أكبر داخل المجموعة منه بين المجموعات، حيث كان متوسط عدد الأليلات في معظم الحالات أكبر من 10، وكان التباين المتوقع والملاحظ ومحتوى معلومات التعدد الشكلي أكبر من 0.5. توفر هذه الدراسة معلومات مفيدة للتطوير المستقبلي لبرامج الحفاظ للسلالات المختلفة المهددة بالانقراض في المغرب الكبير.

الكلمات المفتاحية: التنوع الجيني، السلالات المحلية، الميكروساتلايت، مراجعة منهجية.

Introduction

Livestock play an important role in the world economy, with domesticated animals accounting for 30 to 40% of the global economic value of agriculture (FAO/WB, 2024). Livestock genetic resources are rapidly eroding, with an estimated two low-diversity breeds disappearing each week; accordingly, DAD-IS reports that nine breeds are at risk and twelve others have an unknown risk status in the Maghreb region (FAO/DAD-IS, 2025). Therefore, it is necessary to establish a conservation program to record the diversity of livestock genetic resources (Hanotte and Jianlin, 2006). To achieve this, a thorough knowledge of population structure, including sources of genetic variability within and between populations, is essential, especially in developing countries (Sheriff, Belay, and Haile 2013; Sheriff and Bireda, 2016; Mahmoudi et al., 2011).

Punctuation problem when using sources

Artificial and natural selection have contributed to the phenotypic and genetic diversity of livestock (Groeneveld et al., 2010), which is the variety of alleles and genotypes present in a population (Frankham et al., 2002). Genetic diversity reflects genetic differences between breeds, populations within a breed, and individuals within the same population, and is necessary for the survival of future generations of domesticated species (Groeneveld et al., 2010). Today, this diversity faces numerous human and natural threats, such as climate change, disease, and admixture driven by economically motivated population exchanges, as well as the lack of programs to preserve indigenous breeds (Wanjala et al., 2023).

Punctuation problem when using sources

Sheep were among the earliest animals to be domesticated and used as a source of meat and wool because they are easy to raise and tame (Ryder, 1983). Similar to other animal species, sheep domestication has resulted in significantly lower phenotypic variability than that of wild species (Simm, 1998; Clutton-Brock, 1999). They are the species with the largest number of documented breeds worldwide. According to Rege and Gibson (2003), there are over 850 recognized breeds globally, representing 25% of all mammalian breeds adapted to a variety of habitats (Gizaw et al., 2008), illustrating the diversity of the *Ovis aries* species. According to FAO (2021) there are currently around 1,284.82 million sheep kept in different parts of the world. The share of sheep kept in each of these regions is as follows (in millions): Asia (571.21), Africa (416.96), North America (5.96), Central America (9.41), Caribbean (1.99), South America (63.82), Europe (121.65), and Oceania (93.82).

Although morphological characteristics are essential and commonly used to classify animals into breeds (type of production, coat color, and the presence or absence of certain characteristics), other criteria, such as geographical location or genetic characteristics, are by far the most reliable to use. Microsatellite markers are one of the most valuable resources for assessing genetic divergence and diversity within and between populations (FAO, 2011). The cost-benefit ratio of microsatellites remains relevant in genetic diversity studies. SNPs are not inherently more accurate than microsatellites, which often provide higher per-locus information content. In addition, the frequent reliance on 'Global South' arguments obscures the scientific rationale behind marker choice, while SNP array ascertainment bias, largely driven by European breeds, constrains their applicability to local Maghrebian sheep populations (Vashistha, Rundla, and Om, 2020). Conservation genetics is in a transitional phase, moving from microsatellite DNA markers to single nucleotide polymorphisms. Microsatellite markers have many advantages, including locus specificity, abundance, and high level of repeat number expressed as the occurrence of many alleles per locus, and co-dominant inheritance (FAO, 2011). However, the variability of microsatellites must be taken into account.

In North Africa, the sheep population is estimated at 78 million head (FAO, 2021), 78% of which is located in three countries (Algeria, Tunisia, and Morocco) and represents an important economic pillar for the local population. While total population figures are based on the most recent FAO

estimates, the breed proportions reported for each country are largely derived from historical descriptions and should therefore not be regarded as precise or up-to-date estimates. The Algerian sheep population is about 31.126 million head (FAO, 2021), divided into 13 major breeds, and distributed differently throughout the country, with four main breeds; Ouled Djellal, Berbere, Rembi, and Hamra representing 63%, 25%, 11%, and 0.3%, respectively. Other small breed populations include D'man, Sidaoun, Barbarine, Tazegzawt, Taadmit, Ifilene, Sardi, Daraa, and Berguia, which together account for less than 0.2% (Chellig, 1992; MADR, 2016). In Libya and Mauritania, the sheep population is about 7.546 and 11.002 million head, respectively (FAO, 2021), with 95% dominated by the fat-tailed Barbary sheep (Barbarine). In Morocco, the sheep population is about 22.726 million head (FAO, 2021), classified into 14 sheep breeds. The main breeds are Timahdite, Beni Guil, Sardi, Beni Ahsen, D'man, and Boujaad, representing 12%, 11%, 10%, 3%, 3%, and 2.5%, respectively. The remaining fraction consists of other small breeds that have no breed standard and few or no studies, including: Doukkala, Zoulay, Zemrane, Talilat, Ait Barka, Aknoul, Rehamna-Sraghna, and Ouled Djellal (Bourfia and Touchberry, 1988). The Tunisian sheep population is about 6.243 million head (FAO, 2021), divided into four main breeds: the Barbarine, the Western thin tail, the Black of Thibar, and the Sicilo sarde, which represent 60.3%, 34.6%, 2.1%, and 0.7% of the total population, respectively (Rekik et al., 2005). D'man was introduced in Tunisia in 1994 to improve herd productivity (El Hentati, Hamouda, and Chriki, 2012). Other foreign breeds, such as Comisana, Moroccan Sardinian, and Lacaune, are present in small numbers (Rekik et al., 2005). In Libya, 95% of the sheep are fat-tailed barbary sheep (Barbarine) (El-Gabbas, Barghouth, and Ahtash, 1999), and in Mauritania, there are Toaubine (hair sheep) and thin-tailed hair sheep (black Maure) in addition to Peuth or Poulfouli breeds.

Current literature on the genetic diversity of North African sheep breeds remains highly fragmented and is characterized by substantial methodological heterogeneity, which collectively hampers any holistic assessment of Animal Genetic Resources (AnGR) in the Maghreb. Most studies rely on microsatellite markers, a gap that partly motivated the present study. In this study, we aim to critically synthesize, compare, and harmonize the available literature data on the genetics of sheep breeds in the Maghreb using microsatellite markers. By systematically reviewing and integrating published genetic diversity studies, this work seeks to provide a coherent and comparative framework for understanding existing knowledge and identifying gaps in the assessment of regional Animal Genetic Resources. Our analysis integrates published articles from several North African countries, allowing us to build an accurate picture of genetic diversity in the region. The results of our analysis will be crucial in guiding future efforts to preserve and conserve sheep breeds. This knowledge will be essential for the development of effective policies, as it will enable more targeted interventions for endangered breeds.

Materials and Methods

Study design

This study was conducted as a systematic review that followed the established guidelines of the Preferred Reporting Items for Systematic Reviews and Meta-analyses (PRISMA) framework (Page et al., 2021) to ensure the accuracy of the reporting process. By carefully reviewing and summarizing the available literature, the study aimed to analyze and consolidate knowledge on the genetic diversity of sheep populations in North Africa. This comprehensive approach allowed a better understanding of the patterns and trends associated with the evolution of genetic diversity of local breeds, providing valuable insights into admixture and its impact on sheep populations.

Information Sources and Search Strategy

In our study, a comprehensive and systematic search strategy was applied in four major databases (Google Scholar, PubMed, Web of Science, and Science Direct) to ensure a thorough exploration of the available literature. To increase the comprehensiveness of our search, we used general and specific search terms, namely 'genetic diversity', 'sheep', 'microsatellite', 'breed', 'North Africa', 'Maghreb',

`Algeria`, `Libya`, `Mauritania`, `Morocco`, and `Tunisia`, either individually or in combination. This approach aimed to collect all relevant studies in North Africa.

The initial search was conducted on 04/06/2024 and an updated and final search was conducted on 29/09/2024. After retrieving the results from the databases, all references were imported into Mendeley, a reference management software, for organization and analysis. Duplicates were identified and removed. The remaining unique references were then screened against a set of predetermined eligibility criteria to determine whether they could be included in the review.

Selection procedure

The following predefined criteria were used to identify accepted articles:

- 1) articles in French or English;
- 2) the year of the study was between 1990 and 2023;
- 3) microsatellites were used;
- 4) publications from North Africa;
- 5) target species was sheep;
- 6) materials and methods were well explained.

Papers that did not meet these six criteria were not accepted.

Data extraction and quality assessment

Using a predesigned form, two impartial expert reviewers extracted the data and a third reviewer resolved any discrepancies. We collected the following data from each publication: the name of the first author, the year of publication, the year of sampling, the geographical area (determined by the country and place where the study was conducted), the breeds selected, the type of molecular markers used, and the total number of samples. In addition, reported estimates of genetic diversity, such as mean number of alleles (MNA), observed heterozygosity (Ho), expected heterozygosity (He), inbreeding coefficient (Fis), fixation index (Fst), number of alleles per locus (Na), and polymorphism information content (PIC), as well as the number of microsatellites, were collected.

The quality of the selected studies was assessed using criteria based on the GRADE (Grading of Recommendations Assessment, Development, and Evaluation) method (Atkins et al., 2004; Guyatt et al., 2008). GRADE is a framework for assessing the quality of evidence and grading the strength of recommendations. Each publication received one point for each satisfactory criterion:

- 1) method clearly described;
- 2) assessment of at least four parameters;
- 3) sample size;
- 4) number of microsatellites;

Based on this score, each publication was classified as high quality (score >3), moderate quality (score = 2 or 3), or low quality (score = 0 or 1). The scores were not used to exclude publications as they were reported to support future studies.

Results

Study selection and characteristics of included studies

Our search returned 5,930 studies, of which 314 met the selection criteria. A total of 42 published studies included research articles that used different techniques (e.g., single nucleotide polymorphisms and mitochondrial DNA) and had incomplete information or only phenotypic analysis. After removing these articles, a total of 17 articles remained, all of which were written in English. Blood and hair samples were collected from adult and young males and females. The largest sample size was 330, while the smallest was 24, and the number of breeds ranged from 1 to 12. The average number of microsatellite markers used in the 17 studies was 16.41, with the highest and lowest being 31 and 4, respectively (Figure 1 and Table 1).

Table 1. Characteristics of the studies reviewed on the genetic diversity of North African sheep breeds

First Author	Year	Country	GRADE score	MS N	Sample size	Number of Breeds	MS	Breeds
Gaouar. SBS	2005	Algeria	Medium	12	85	2	INRA49; OarFCB20; OarFCB11; MCM527; ILSTS5; CSSM66; MCM42; TGLA53; MAF65; OarCP49; OarHH56; and MAF36.	Hamra/ Ouled Djellal
Gaouar. SBS	2014	Algeria/ Tunisia	Medium	6	330	6	OarFCB11/ OarCP49/ OarHH56/ MAF36/ ILSTS5/ CSSM66	Hamra/ Ouled Djellal/ Beni Ighil (Hamra)/ D'men / Corse/ Lacaune/ Foro-Foro
Ressaissi. Y	2014	Tunisia	low	4	24	1	BM1824, DYMS1, HUIJ616 and ILSTS11	Barbarine
Ben Sassi Zaidy. Y	2014	Tunisia	Medium	17	249	7	Inra023/ Inra063/ OarCP49/ OarFCB304/ OarFCB20/ MAF65/ ILST087/ OarAE119/ MCM527/ MAF214/ OarAE129/ OarCP34/ OarAE54/ TGLA53/ URB058/ CSRD247/ HSC	Barbarine/ Queue Fine de l'Ouest"/ Crossbred/and Black Thibar/ Sicilo-Sarde/ D'men/ Appenninica
Kdidi. S	2015	Tunisia	high	30	186	5	MAF65, OARFCB193, OARFCB304, OARJMP29, OARJMP58, MAF70, MAF209, BM1824, INRA063, BM8125, MAF214, ILSTS5, ILSTS11, ILSTS28, MCM140, MCM527, OARFCB226 , OARFCB128, OARCP34, OARAE129, BM1329, OARCP38, HUIJ616, MAF33, OARHH47 , OARVH72, SRCRSP1, SRCRSP05, SRCRS09, DYMS1	Barbarine/ Queue Fine de l'Ouest/ Black Thibar/ Sicilo-Sarde/ Spanish Merino
Gaouar. SBS	2015	Algeria	Medium	31	158	6	OarFCB128 /OarCP34 /INRA063/BM1824/OarFCB193/OarFCB304 /INRA49 /MCM527 /MCM42/MAF65/TGLA53/OarFCB20 /CSRD247 /HSC /SRCRSP9 / HUIJ616/ILSTS11/ OarAE129/MAF209/MAF214/OARJMP58/ILSTS5/INRA035/ETH10/TGLA122/CSSM66/BM8125/DYMS1/M AF33/MCM140/CSR	Hamra/ Rembi/ Ouled Djellal/ Sidaoun/ Taadmit/ D'men
Ben Sassi-Zaidy. Y	2016	Tunisia	high	17	110	3	Inra023/ Inra063/ OarCP49/ OarFCB304/ OarFCB20/ MAF65/ ILST087/ OarAE119/ MCM527/ MAF214/ OarAE129/ OarCP34/ OarAE54/ TGLA53/ URB058/ CSRD247/ HSC	Barbarine/ Queue Fine de l'Ouest/ Crossbred
Gaouar SBS	2016	Morocco	high	22	171	5		Sardi/ Boujaad / Timahdite/ Beni Guil/ D'men
Harkat. S	2017	Algeria	high	23	152	2	OarCP34/ ILSTS11/ INRA035/ CSSM66/ BM8125/ DYMS1/ MAF33/ MCM140/ CSRM60/ OarFCB128/ OarFCB193/ MAF209/ INRA063/ OarJMP129/ OarFCB304/ MAF65/ HUIJ616/ MAF70/ OARJMP58/ OARHH47 / OARVH72 / OARCB226 /OarAE129/ SRCRSP1	Rembi/ Ouled Djellal
Ben Sassi-Zaidy. Y	2017	Tunisia	Medium	17	250	6	Inra023/ Inra063/ OarCP49/ OarFCB304/ OarFCB20/ MAF65/ ILST087/ OarAE119/ MCM527/ MAF214/ OarAE129/ OarCP34/ OarAE54/ TGLA53/ URB058/ CSRD247/ HSC	Barbarine , Queue Fine de l'Ouest , Noire de Thibar , Sicilosarde , D'men and the crossbred
Abdelkader. A	2018	Algeria	Medium	15	296	12	McM527, CSRD247, OarFCB128, BM1329, HSC, OarJMP29, MAF214, OarFCB304, INRA023, OarCP34, INRA0132, D5S2, BM1818, BM8125, OarFCB193	Barbarine; Ouled djellal; Ifilene; Sardi; Daraa; Rembi; Berbere; Taadmit; Hamra; Sidaoun; Tazegzawt; D'men
Ouinten. Y	2018	Algeria	Medium	7	54	3	INRA023/ MAF65/ McM527/ OarCP49/ INRA063/ HSC/ OarAE129	Ouled Djellal/ D'men / Sidaoun
Ata. N	2019	Algeria	low	15	180	5	OarFCB193/ OarFCB304/ INRA0123/ OarCP34/INRA0132/ D5S2/ BM1818/ BM8125/ McM527/ CSRD247/ OarFCB128/ BM1329/ HSC/ OarJMP29/ MAF213	Barbarine/ Rembi/ Berbere/ Taadmit/ D'men
Ameur. AA	2020	Algeria	high	14	240	4	OarFCB193/ OarFCB304/ INRA023/ OarCP34/ D5S2/ BM1818/ BM8125/ McM527/ CSRD247/ OarFCB128/ BM1329/ HSC/ OarJMP29/ MAF214	Hamra/ Ouled Djellal/ Sidaoun/ Tazegzawt
Ben Sassi Zaidy. Y	2022	Tunisia	high	17	52	1	Inra023/ Inra063/ OarCP49/ OarFCB304/ OarFCB20/ MAF65/ ILST087/ OarAE119/ MCM527/ MAF214/ OarAE129/ OarCP34/ OarAE54/ TGLA53/ URB058/ CSRD247/ HSC	Sicilo-Sarde
KDIDI. S	2023	Tunisia	high	22	90	3	OARHH47, MCM527, MAF65, ILSTS5, OARCP38, MAF209, OARFCB304, INRA63, MAF214, SRCRS09, MAF70, OARVH72, BM1824, OARJMP58, OARJMP29, DYMS1, OARFCB193, MCM140, ILSTS28, HUIJ616, OARFCB226, MAF33.	Barbarine, Western Thin Tail (Ouled Djella), and Black Thibar.
Ouinten. Y	2023	Algeria	Medium	10	183	8	OarFCB11, INRA063, HSC, OarCP49, McM527, MAF65, OarAE129, INRA023, McM42, OarFCB193	Sidaoun, D'men, Ouled Djellal, Hamra, Rembi, Sardi, Daraa, Berguia

MS: Microsatellite. **MS N:** Number of microsatellite.

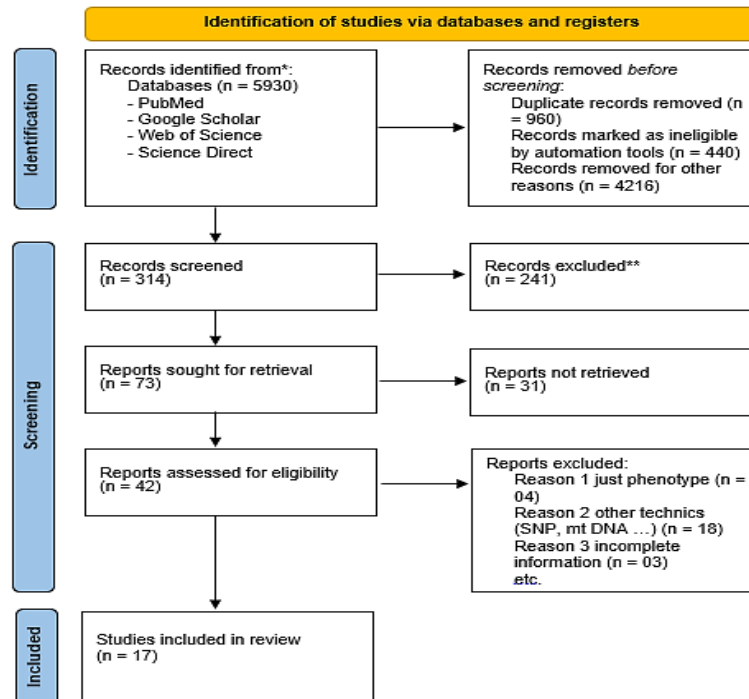


Figure 1. Flow chart for selecting studies.

Some breeds have been studied extensively, such as Ouled Djellal (13 studies), D'men, Barbarine, and Hamra (with 9, 8, and 7 studies, respectively), while others have been studied less, such as Daraa, Tazegzawt, and Berbere with 2 studies, and Boujaad, Timahdite, Ifilene, and Berguia with only one study. Articles were classified into four categories based on the number of breeds studied and the microsatellite used (Table 2).

In addition, although publications on sheep genetic diversity studies in North Africa have started to gain ground, the number has remained low over the past decades. For example, the number of articles published on this subject has remained low (17 articles), with 1 to 3 articles published per year (Figure 2A). There was also a difference in the number of articles published per country, with Algeria and Tunisia dominating with a share of 50% and 44%, respectively, and no data available for Libya and Mauritania (Figures 2B and 3). Regarding the number of microsatellites, the majority of published articles used a number between 10 and 20, while only 2 studies used more than 30 microsatellites (Figure 2C). Finally, 5 of the 17 publications used a sample size of less than 30 per breed, and 65% of the studies were performed on 5 or fewer breeds (Figure 2D and 2E).

Different parameters used to measure genetic diversity Give numbers to titles

The reported MNA results ranged from moderate to highly variable (Table 3). Five of the studies had MNA below 10 and nine had high MNA above 10. This suggests significant genetic diversity, which is beneficial for the resilience and adaptability of populations. Heterozygosity estimates were above 0.5 in all reviewed articles and ranged from 0.59 to 0.92 for H_o and 0.72 to 0.88 for H_e . This shows that there is high genetic diversity, indicating a large and genetically diverse population, which is often a sign of high genetic flow and low in breeding. Ideally, H_e should be close to H_o , since large differences between H_e and H_o indicate inbreeding or selection pressure.

Table 2. Sheep species studied using published species-specific microsatellite DNA markers

Sheep breed	localization	Microsatellite markers	Publications
Ouled Djellal (Western thin tail)	Algeria, Morocco, Tunisia	OarCP34/ ILSTS11/ INRA035/ CSSM66/ BM8125/ DYMS1/ MAF33/ MCM140/ OarFCB128/ OarFCB193/ MAF209/ INRA063/ OarJMP129/ OarFCB304/ MAF65/ HUJ616/ MAF70/ OARJMP58/ OARHH47/OARVH72 /OARCB226 /OarAE129/ SRCRSP1/ ILSTS28/ BM1824/INRA49 / MCM527/ MCM42/ TGLA53/ OarFCB20 /CSRD247 /HSC /SRCRSP9 /MAF214 /ILSTS5/ETH10/ TGLA122/ CSRM60/ INRA0132/ INRA023/ D5S2/BM1818/BM1329/OarJMP29/OarCP49/OARCP38/ ILST087/ OarAE119/OarAE54/ URB058/ OarFCB11/ OARFCB226/ OarHH56/ MAF36/ SRCRS09/ SRCRSP05	Gaouar (2005,2014,2015), Ben Sassi-Zaidy (2014, 2016,2017), Kdidi (2015,2023), Harkat (2017), Abdelkader (2018), Ameur (2020), Ouinten (2018,2023),
Hamra (Beni Ighil)	Algeria, Morocco	OarFCB128 /OarCP34 /INRA063/BM1824/OarFCB193/OarFCB304 /INRA49 /MCM527 / MCM42 / MAF65/ TGLA53/ OarFCB20/ CSRD247 /HSC /SRCRSP9 / HUJ616/ILSTS11/INRA0132/ OarAE129 /MAF209/MAF214/OARJMP58/ILSTS5/INRA035/ ETH10/TGLA122/ CSSM66/ BM8125/ DYMS1/ MAF33/ MCM140/CSRM60/ INRA023/ D5S2/ BM1818/ BM1329/ OarJMP29/ OarFCB11/ OarCP49/ OarHH56/ MAF36/ OARHH47/ OARCP38/ SRCRS09/ MAF70/ OARVH72/ ILSTS28/ OARFCB226	Gaouar (2005, 2014,2015, 2016), Abdelkader (2018), Ameur (2020), Ouinten (2023),
D'men	Algeria, Morocco	OarFCB128 /OarCP34 /INRA063/BM1824/OarFCB193/OarFCB304 /INRA49 /MCM527 /MCM42/MAF65/TGLA53/OarFCB20 /CSRD247 /HSC /SRCRSP9 / HUJ616/ILSTS11/ OarAE129/MAF209/MAF214/OARJMP58/ILSTS5/INRA035/ETH10/TGLA122/CSSM66/BM8125/ DYMS1/MAF33/MCM140/CSRM60/ INRA023/ INRA0123/INRA0132/ D5S2/ BM1818/ BM1329/ OarJMP29/ MAF213/ OarFCB11/ OarCP49/ OarHH56/ MAF36/ ILST087/ OarAE119/ OarAE54/ URB058	Gaouar (2014,2015, 2016), Ben Sassi-Zaidy (2014, 2017), Abdelkader (2018), Ouinten (2018,2023), Nezih Ata (2019)
Rembi	Algeria	OarFCB128 /OarCP34 /INRA063/BM1824/OarFCB193/OarFCB304 /INRA49 /MCM527 /MCM42/MAF65/TGLA53/OarFCB20 /CSRD247 /HSC /SRCRSP9 / HUJ616/ILSTS11/ INRA023/ OarAE129/ MAF209/ MAF214/ OARJMP58/ILSTS5/ INRA035/ ETH10/ TGLA122/ CSSM66/BM8125/ DYMS1/MAF33/MCM140/CSRM60/ OarJMP129/ MAF70/ OARHH47 / OARVH72 / OARCB226 /SRCRSP1/ INRA0123/INRA0132/ D5S2/ BM1818/ BM1329/ OarJMP29/ MAF213/ OarFCB11/ OarCP49	Gaouar (2015), Harkat (2017), Abdelkader (2018), Nezih Ata (2019), Ouinten (2023)
Barbarine	Algeria, Tunisia	OarFCB193/ OarFCB304/ INRA0123/ OarCP34/INRA0132/ D5S2/ BM1818/ BM8125/ MCM527/ CSRD247/ OarFCB128/ BM1329/ HSC/ OarJMP29/ MAF213/ INRA023/ OarCP49/ OarFCB20/ MAF65/ ILST087/ OarAE119/ MAF214/ OarAE129/ OarAE54/ TGLA53/ URB058/ OARHH47/ ILSTS5/ OARCP38/ MAF209/ INRA063/ SRCRS09/ MAF70/ OARVH72/ BM1824/ OARJMP58/ DYMS1/ MCM140/ ILSTS28/ HUJ616/ OARFCB226/ MAF33/ ILSTS11/ SRCRSP1, SRCRSP05	Ressaissi (2014), Ben Sassi-Zaidy (2014, 2016,2017), Kdidi (2015,2023), Abdelkader (2018), Nezih Ata (2019)
Crossbred	Tunisia	INRA023/ INRA063/ OarCP49/ OarFCB304/ OarFCB20/ MAF65/ ILST087/ OarAE119/ MCM527/ MAF214/ OarAE129/ OarCP34/ OarAE54/ TGLA53/ URB058/ CSRD247/ HSC	Ben Sassi-Zaidy (2014, 2016,2017)
Black Thibar	Tunisia	OARHH47/ MCM527/ MAF65/ ILSTS5/ OARCP38/ MAF209/ OARFCB304/ INRA063/ MAF214/ SRCRS09/ MAF70/ OARVH72/ BM1824/ OARJMP58/ OARJMP29/ DYMS1/ OARFCB193/ MCM140/ ILSTS28/ HUJ616/ OARFCB226/ MAF33/ INRA023/ OarCP49/ OarFCB20/ ILST087/ OarAE119/ OarAE129/ OarCP34/ OarAE54/ TGLA53/ URB058/ CSRD247/ HSC/ BM8125/ ILSTS11/ OARFCB128, BM1329/ SRCRSP1, SRCRSP05	Ben Sassi-Zaidy (2014, 2017), Kdidi (2015,2023),
Sidaoun	Algeria	OarFCB128 /OarCP34 /INRA063/BM1824/OarFCB193/OarFCB304 /INRA49 /MCM527 / MCM42/ MAF65/TGLA53/OarFCB20 /CSRD247 /HSC /SRCRSP9 / HUJ616/ILSTS11/ INRA0132/ OarAE129/ MAF209/ MAF214/ OARJMP58/ ILSTS5/ INRA035/ ETH10/ TGLA122/ CSSM66/BM8125/ DYMS1/MAF33/MCM140/CSRM60/ INRA023/ D5S2/ BM1818/ BM1329/OarJMP29/ OarCP49/ OarFCB11	Gaouar (2015), Abdelkader (2018), Ameur (2020), Ouinten (2018,2023),
Taadmit	Algeria	OarFCB128 /OarCP34 /INRA063/BM1824/OarFCB193/INRA49 /MCM527 /MCM42/ MAF65/ TGLA53/OarFCB20 /CSRD247 /HSC /SRCRSP9 / HUJ616/ILSTS11/ INRA023/ OarAE129/ MAF209/ MAF214/ OARJMP58/ ILSTS5/ INRA035/ETH10/TGLA122/CSSM66/ BM8125/ DYMS1/ MAF33/MCM140/CSRM60/ INRA0123/ INRA0132/ D5S2/ BM1818/ BM1329/ OarJMP29/ MAF213	Gaouar (2015), Abdelkader (2018), Nezih Ata (2019)
Sardi	Algeria, Morocco	McM527/ CSRD247/ OarFCB128, BM1329/ HSC/ OarJMP29/ MAF214/ OarFCB304/ INRA023/ OarCP34/ INRA0132/ D5S2/ BM1818/ BM8125/ OarFCB193/ OarFCB11/ INRA063/ OarCP49/ MAF65/ OarAE129/ McM42	Gaouar (2016), Abdelkader (2018), Ouinten (2023)
Boujaad	Morocco		Gaouar (2016)
Timahdite	Morocco		Gaouar (2016)
Sicilosarde	Tunisia	INRA023/ INRA063/ OarCP49/ OarFCB304/ OarFCB20/ MAF65/ ILST087/ OarAE119/ MCM527/ MAF214/ OarAE129/ OarCP34/ OarAE54/ TGLA53/ URB058/ CSRD247/ HSC/ OARFCB193/ OARJMP29/ OARJMP58/ MAF70, MAF209, BM1824/ BM8125/ ILSTS5/ ILSTS11/ ILSTS28/ MCM140/ OARFCB226/ OARFCB128/ BM1329/ OARCP38/ HUJ616/ MAF33/ OARHH47/ OARVH72/ SRCRSP1/ SRCRSP05/ SRCRS09/ DYMS1	Ben Sassi-Zaidy (2014,2017, 2022), Kdidi (2015)
Ifilene	Algeria	McM527/ CSRD247/ OarFCB128/ BM1329/ HSC/ OarJMP29/ MAF214/ OarFCB304/ INRA023/ OarCP34/ INRA0132/ D5S2/ BM1818/ BM8125/ OarFCB193	Abdelkader (2018),
Daraa	Algeria	McM527/ CSRD247/ OarFCB128, BM1329/ HSC/ OarJMP29/ MAF214, OarFCB304, INRA023/ OarCP34/ INRA0132/ D5S2/ BM1818/ BM8125/ OarFCB193/ OarFCB11/ INRA063/ OarCP49/ MAF65/ OarAE129/ McM42	Abdelkader (2018), Ouinten (2023)
Berbere	Algeria	OarFCB193/ OarFCB304/ INRA0123/ OarCP34/INRA0132/ D5S2/ BM1818/ BM8125/ McM527/ CSRD247/ OarFCB128/ BM1329/ HSC/ OarJMP29/ MAF213/ MAF214, INRA023	Abdelkader (2018), Nezih Ata (2019)
Tazegzawt	Algeria	OarFCB193/ OarFCB304/ INRA023/ OarCP34/ D5S2/ BM1818/ BM8125/ McM527/ CSRD247/ OarFCB128/ BM1329/ HSC/ OarJMP29/ MAF214/ INRA0132	Abdelkader (2018), Ameur (2020)
Berguia	Algeria	OarFCB11/ INRA063/ HSC/ OarCP49/ McM527/ MAF65/ OarAE129/INRA023/ McM42/OarFCB193	Ouinten (2023)

Nb: Daraa and Berguia are considered by some authors as sub breed.

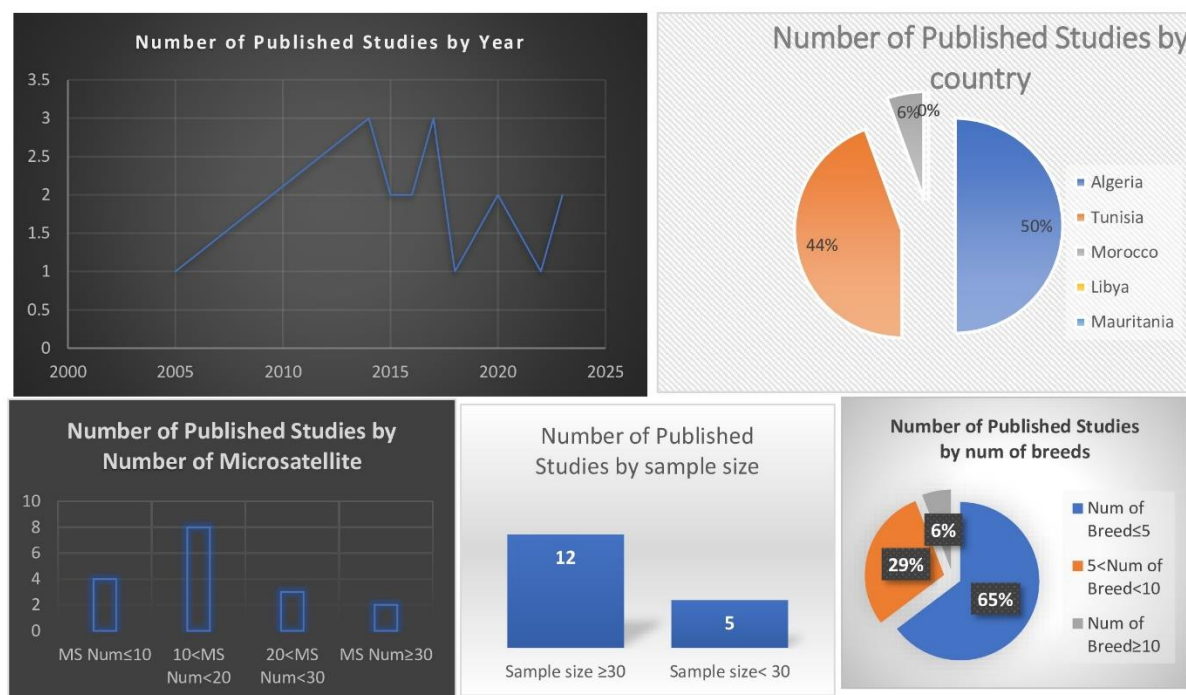


Figure 2. Published studies analyzing the use of microsatellite markers in sheep diversity studies, based on sampling data provided by the authors. The studies were classified according to the sample data extracted from the different studies: A. Number of published studies by year; B. Number of published studies by country; C. Number of microsatellites used; D. Sample size; and E. Number of breeds.

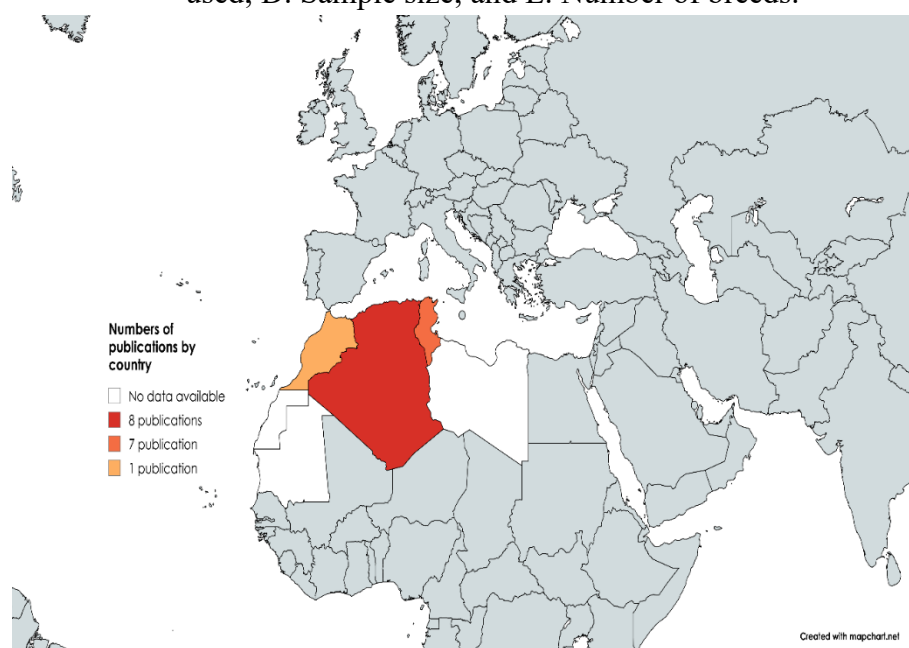


Figure 3. A summary of the number of studies by country that provided data for this study (<https://www.mapchart.net/world.html>)

The results PIC estimates did not vary significantly. All estimates were above 0.5 and ranged from 0.75 to 0.92, indicating that the markers used are highly polymorphic and highly informative. The estimate of Na represents the total count of different alleles observed at a given genetic locus in a population. In the studies reviewed, it ranged from 11.75 to 26.8, a high level of genetic diversity that is common in large and well-mixed populations.

Table 3. Various parameters used to measure genetic diversity

Author	MNA	Ho	He	PIC	Fis	Fst	Na
Gaouar. SBS 2005	9.54	////	////	////	////	////	11.75
Gaouar. SBS 2014	10.16	0.659	0.783	0.8075	////	////	18.17
Ressaissi. Y 2014	////	////	0.88 (0.02)	0.92	////	////	19
Ben Sassi-Zaidy. Y 2014	8.27	0.717 (0.144)	0.803 (0.092)	////	////	////	////
Kdidi. S 2015	10.03	0.655 (0.15)	0.773 (0.097)	0.756	////	////	14.27
Gaouar. SBS 2015	7.62 (2.61)	0.66 (0.18)	0.72 (0.16)	////	////	////	////
Ben Sassi-Zaidy. Y 2016	11.39	0.719(0.143)	0.798(0.08)	0.791	0.112	0.007	15.06
Gaouar. SBS 2016	8.82	0.662 (0.035)	0.742 (0.023)	////	0,142	0.036	////
Harkat. S 2017	11.36 (3.02)	0.78 (0.1)	0.78 (0.08)	0.75	0.05 [−0.002; 0.113]	////	12.70 ± 3.51
Ben Sassi-Zaidy. Y 2017	11.46 (3.73)	0.726 (0.144)	0.809 (0.095)	0.830	////	////	18.41
Abdelkader. A 2018	13.26	0.82 (0.025)	0.86 (0.01)	0.89	0.032	0.057	24.46
Ouinten. Y 2018	14.78	////	////	////	0.065	0.008	15.86
Ata. N 2019	////	////	////	0.89	0.061	////	23
Ameur. AA 2020	12.49	0.76 (0.04)	0.83(0.019)	0.90	0.104	0.068	24.29
Ben Sassi-Zaidy. Y 2022	9.74 (3.79)	0.725 (0.164)	0.79 (0.104)	0.810	0.1	0.01	12.47
Kdidi. S 2023	////	////	////	0.772	0.1664	0.0127	14.27
Ouinten. Y 2023	10.58 (0.62)	0.92 (0.01)	0.82 (0.01)	0.763	-0.014	0.062	26.8

MNA: Mean Number of Alleles, Ho: Observed Heterozygosity, He: Expected Heterozygosity, PIC: Polymorphism Information Content, Fis: Inbreeding Coefficient, Fst: Fixation Index, Na: Number of Alleles.

In our analysis, a few studies reported estimates of Fis and Fst. For Fis, small and positive values between 0.032 and 0.166 were observed in the studies reviewed, with the exception of one study that reported a negative estimate of -0.014 (Ouinten et al., 2024). These predominantly positive FIS values indicate a moderate excess of homozygosity, consistent with low to moderate inbreeding or population subdivision (Wahlund effect), while the negative value suggests a slight excess of heterozygosity. These results indicate a deficit of homozygosity, suggesting that related individuals have low inbreeding and can be considered a healthy random mating population. For Fst, which measures genetic differentiation between populations, low estimates between 0.007 and 0.068 were reported, indicating low genetic differentiation (Hall, 2022).

Discussion

The domestic sheep belongs to the genus *Ovis*, although its origin remains unclear. Several studies have found that species or subspecies of wild sheep are the ancestors of domestic sheep or at least contributed to this species, particularly the urial (*O. vignei*) and the mouflon (*O. musimon* or *O. orientalis*) (Ryder, 1983; Mereu et al., 2025). Classification within the genus *Ovis* is controversial, with the number of species varying from four to eight. Much of this controversy is due to the fact that all species can reproduce by producing fertile offspring (Franklin, 1997; Wanjala, Bagi, and Kusza, 2021). However, one argument for species differentiation is the difference in chromosome number (Supplementary Material 1). This is why molecular tools are so useful for characterizing different populations, origin determination, hybrid identification, and assessing inbreeding levels. Genotyping with microsatellites provides a higher level of information due to high polymorphism and Mendelian inheritance, and is also cost-effective, making it an appropriate choice with a significant impact on breeding programs and conservation efforts (Rasoarahona et al., 2023).

Supplementary material 1. Principal characteristics of the genus ovis

Species	Common name	Chromosome number
<i>Ovis aries</i>	Domestic sheep	2n= 54
<i>Ovis musimon/orientalis</i>	European mouflon	2n= 54
<i>Ovis vignei</i>	Urial	2n= 58
<i>Ovis ammon</i>	Argali	2n= 56
<i>Ovis Canadensis</i>	Bighorn sheep	2n= 54
<i>Ovis dalli</i>	Dall sheep	2n= 54
<i>Ovis nivicola</i>	Snow sheep	2n= 52

In North Africa, sheep breeding is an important economic activity and yet, the characterization and conservation of sheep populations remains weak. The first study on this subject was carried out in the 2000s, and data are not available in some countries (Mauritania, Libya, and Western Sahara). The total number of genetic studies focused on this topic was 42, of which 17 used the microsatellite technique. This number remains low, reflecting the fact that it has received less attention from the scientific community. The limited progress of genetic studies for the characterization of sheep breeds in North Africa can be explained by several factors, often related to structural, economic, and technical constraints.

North Africa has a large diversity of indigenous sheep breeds, the origin of which is linked to environmental characteristics and specific historical events in the region (Ben Jemaa et al., 2019). Of the 22 North African sheep breeds mentioned in the literature, only 18 were investigated in the 17 microsatellite studies, with a dominance of the four main breeds (Ouled Djellal, D'men, Hamra, and Barbarine) that have a large presence in the region (Belhaj et al., 2021), with percentages ranging from 11% to 63% depending on the country. This highlights the importance of these breeds not only for local agriculture but also for their genetic diversity, which is crucial for adaptation to changing environmental conditions. Furthermore, understanding the distribution and characteristics of these breeds can help in the development of targeted conservation strategies to preserve their unique traits.

The mean number of alleles per locus is a measure that can be used to analyze genetic diversity within a population. It is a useful measure for identifying genetic polymorphism within the population (Halima et al., 2014) and is dependent on sample size, as unique alleles may occur at low frequencies in the population (Qwabe, 2011; Aljumaah et al., 2012). The average number of alleles was reported in microsatellites studied for several sheep populations (Table 3), which showed relatively low estimates in the study of Gaouar et al. (2015) for some Algerian sheep populations, and relatively high values were reported, especially in Ouinten et al. (2018) and Abdelkader et al. (2018). A high number of alleles implies more genetic variation, and it is the key relevance in conservation programs (Nei, 1987). In addition, some of the studies used small numbers of animals, which is far from the FAO recommendations for microsatellite marker analysis (FAO, 2011). For example, Ouinten et al. (2024) used only four animals to represent a population which could lead to a bias in the calculation of genetic parameters, such as Hardy-Weinberg equilibrium (HWE) and MNA.

The other parameters most commonly used to measure the genetic diversity of a population are H_o , which is the proportion of heterozygotes observed in a population, and H_e , which is the proportion of heterozygotes expected in a population based on Hardy-Weinberg proportions (Ojango et al., 2011; Toro, Fernández, and Caballero, 2009). According to the published studies (Table 3), the reported heterozygosity estimates were higher than 0.5. The observed and expected values of heterozygosity are relatively high, indicating that the sheep populations studied have high genetic diversity within populations (Dávila et al., 2009; Dorji, Duangjinda, and Phasuk, 2012). With the exception of Ouinten et al. (2024), most H_o estimates were generally lower or close to H_e , indicating that there was no overall loss of heterozygosity (allele fixation) and that the populations are in HWE (Araújo et al., 2006).

The most commonly used markers in all studies were OarCP34, INRA063, OarFCB128, OarFCB304, MAF65, OarAE129, OarFCB193, MCM527, CSRD247, HSC, MAF214, and INRA023, while others used less frequently were OarJMP129, OARCB226, SRCRSP05, and MAF36. Only the studies on sheep breeds from Algeria and Tunisia (Kdidi et al., 2015; Gaouar et al., 2015) were covered by all 30 microsatellites, which is the maximum coverage recommended by (FAO, 2011). The usefulness of the

markers and primers used in the study for investigating the genetic variability of a population is represented by PIC. While $0.5 > \text{PIC} > 0.25$ is considered reasonably informative and below 0.25 is considered less informative, a marker with a $\text{PIC} > 0.5$ can be considered highly informative and highly polymorphic. Our results show that all estimates are higher than 0.5, indicating that highly polymorphic markers have been used for the majority of the sheep populations studied (Tables 2 and 3). According to (Aljumaah et al., 2012), heterozygosity and the total number of alleles determine the PIC, making microsatellite markers an excellent option for genetic characterization and diversity studies in Maghreb sheep breeds.

High positive F_{is} estimates indicate high homozygosity, while negative estimates indicate low levels of inbreeding (Dorji, Duangjinda, and Phasuk, 2012). F_{st} is the ratio of the total genetic variance in a subpopulation to the total genetic variance. A high F_{st} indicates a high degree of differentiation between populations. According to Kalinowski (2004), the lowest estimate is less than 0.05, the mean is between 0.05 and 0.25, and the highest genetic distance is greater than 0.25. With this background information, several authors have reported moderate to high levels of inbreeding in various sheep populations. For example, F_{is} estimates for four sheep breeds in Tunisia were 0.112 (Ben Sassi-Zaidy et al., 2016) and 0.1664 (Samia Kdidi et al. 2023), five breeds in Morocco were 0.142 (Gaouar, Kdidi, and Ouragh, 2016), and some local sheep breeds in Algeria were 0.142 (Abdelkader et al. 2020). This could be due to the small size of the sheep population, the controlled breeding system, and the extremely low number of breeding rams used continuously for several years. This conclusion is supported by the lowest heterozygosity and MNA values as shown in Table 3. Previous studies have reported acceptable mean F_{is} estimates of 0.065 for Algerian sheep breeds (Ouinten et al., 2018), 0.061 for Ata, Ameur, and Yilmaz (2019), and 0.032 for Abdelkader et al. (2018). These intermediate levels of inbreeding could be the result of unplanned or uncontrolled matings, whereas high levels of inbreeding could have resulted from moderate matings between closely related individuals (Mekuriaw et al., 2016). On the other hand, two studies on Algerian sheep breeds reported F_{is} estimates of -0.014 (Ouinten et al., 2024) and 0.05 (Harkat et al., 2017), indicating low levels of inbreeding and an excess of heterozygotes, while the other seven studies did not report F_{is} estimates.

The genetic distance estimates between populations in terms of F_{st} have been reported in many studies. For example, 0.068 (Abdelkader et al., 2020); 0.062 (Ouinten et al., 2024); 0.057 (Abdelkader et al., 2018); 0.036 (Gaouar, Kdidi, and Ouragh, 2016); 0.01 (Ben Sassi-Zaidy et al., 2022); 0.0127 (Kdidi et al., 2023); 0.008 (Ouinten et al., 2018); and 0.007 (Ben Sassi-Zaidy et al., 2016) are in the range of negligible estimates ($F_{ST} < 0.25$). There is no study with significant estimates of genetic distance between populations, while these parameters are absent in nine others. This suggests that genetic differentiation between sheep subpopulations is low to moderate. According to these reports, the average F_{st} estimate for all microsatellite loci in Algerian sheep populations was found to be 0.049, indicating a total genetic variation of 4.9% between populations and 95.1% between individuals. Based on the same studies, gene flow between regions with similar ecosystems and close geographical distances could be the cause of the lack of differentiation in these phenotypically distinct subpopulations. Similarly, Gaouar, Kdidi and Ouragh (2016) found that 3.6% of the total variation in the Moroccan sheep population was due to population subdivision, while 96.3% of the variation was between individuals within sheep populations, possibly due to migration of individuals between subpopulations. It was also confirmed by Kdidi et al. (2023), Sassi-Zaidy et al. (2016), and Ben Sassi-Zaidy et al. (2022) that traditional uncontrolled mating practices and policies, which encouraged or resulted in uncontrolled animal movements through different market routes and agricultural extension systems in Tunisia, may be responsible for the low genetic differentiation between subpopulations.

Conclusion

This study provided an overview of the current situation of sheep breeds in North Africa, using microsatellites as a useful tool for genetic characterization. The review also highlighted the lack of studies on the conservation of indigenous breeds, with results showing greater intra-population variation than inter-population variation, implying low genetic differentiation between sub-populations. It is therefore imperative to study the genetic structure and gene flow in these populations.

Molecular evaluation using microsatellites provides useful information for formulating effective conservation programs for critically endangered breeds (e.g. Hamra, Rembi, Taadmit, and Tazegzaout). Such programs can increase genetic diversity and resilience, ultimately ensuring the survival of these unique breeds. By focusing on both genetic characterization and conservation strategies, researchers can make informed decisions that support biodiversity and promote sustainable agricultural practices. This can be extended to the study of the effects of introduced genetic admixture and the identification of genetically diverse breeds to assist in the conservation and rehabilitation of sheep breeds. The study also highlights the need to strengthen future studies for a deeper understanding of flock structure based on well-designed sampling and using the latest technological advances in the field.

Acknowledgement

The authors would like to thank the research team members and technical staff for their valuable assistance during the fieldwork and data collection.

Funding Information

No funding was received for this work.

Institutional Review Board Statement: The study was conducted according to the guidelines of the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA).

Authors' Contributions

In order to recognize the authors' participation, we highlight each individual contribution: O.Y, M.B and G.M designed the study and supervised the experiments, I.L, M.B and K.B made contributions in acquiring the data, O.Y, G.M were responsible for data correction, O.Y, M.B and G.M assisted in writing and editing of the article. All these authors have substantial contributions to the final manuscript and approved this submission. All authors are aware of the order of authorship and that no further change in authorship will be performed after submission, excepting those previously authorized by the editor-in-chief.

Ethics

This research was conducted in accordance with national regulations and ethical guidelines.

References

- Abdelkader, Ameer Ameer, Nezih Ata, Mohammed Tahar Benyoucef, Amel Djaout, Noureddine Azzi, Onur Yilmaz, İbrahim Cemal, and Gaouar S.B.S. 2018. "New Genetic Identification and Characterisation of 12 Algerian Sheep Breeds by Microsatellite Markers." *Italian Journal of Animal Science* 17 (1): 38–48. <https://doi.org/10.1080/1828051X.2017.1335182>.
- Abdelkader, Ameer Ameer, Onur YILMAZ, Ibrahim CEMAL, and Gaouar S. B. S. 2020. "Assessment of Genetic Diversity of Turkish and Algerian Native Sheep Breeds." *Acta Agriculturae Slovenica* 115 (1): 5–14.
- Aljumaah, Riyadh S, Muneeb M Musthafa, Mohamed A Al-Shaikh, Osama M Badri, and Mansour F Hussein. 2012. "Genetic Diversity of Ardi Goat Based on Microsatellite Analysis." *African Journal of Biotechnology* 11 (100): 16539–45.
- Araújo, Adriana Mello de, Simone Eliza Facioni Guimarães, Thea Mirian Medeiros Machado, Paulo Sávio Lopes, Carmen Silva Pereira, Francisco Luiz Ribeiro da Silva, Marcelo Teixeira Rodrigues, Virgínia de Souza Columbiano, and Cleusa Graça da Fonseca. 2006. "Genetic Diversity between Herds of Alpine and Saanen Dairy Goats and the Naturalized Brazilian Moxotó Breed." *Genetics and Molecular Biology* 29: 67–74.
- Ata, Nezih, Abdelkader Ameer Ameer, and Onur Yilmaz. 2019. "Bottleneck Analysis of Turkish and Algerian Sheep Breeds Using Microsatellite Markers." In *Scientific-Expert Conference of Agriculture and Food Industry*, 122–31. Springer.
- Atkins, David, Martin Eccles, Signe Flottorp, Gordon H Guyatt, David Henry, Suzanne Hill, Alessandro Liberati, Dianne O'Connell, Andrew D Oxman, and Bob Phillips. 2004. "Systems for Grading the

- Quality of Evidence and the Strength of Recommendations I: Critical Appraisal of Existing Approaches The GRADE Working Group.” *BMC Health Services Research* 4: 1–7.
- Belhaj, Kamal, Farid Mansouri, Abdessamad Ben moumen, Marianne Sindic, Marie-Laure Fauconnier, Mohamed Boukharta, Hana Serghini Caid, and Ahmed Elamrani. 2021. “Proximate Composition, Amino Acid Profile, and Mineral Content of Four Sheep Meats Reared Extensively in Morocco: A Comparative Study.” *The Scientific World Journal* 2021 (1): 6633774.
- Bourfia, M, and R W Touchberry. 1988. “Litter Live Weight at Birth with Varying Levels of D’Man Germplasm.” *Agricultural and Food Science* 60 (6): 599–601.
- Chellig, R. 1992. “Algerian Sheep Breeds, Office of University Publications, Algeria.(Races Ovines Algériennes, Office Des Publications Universitaires, Algérie).”
- Clutton-Brock, T H, M Major, S D Albon, and F E Guinness. 1987. “Early Development and Population Dynamics in Red Deer. I. Density-Dependent Effects on Juvenile Survival.” *The Journal of Animal Ecology*, 53–67.
- Dávila, S G, M G Gil, P Resino-Talaván, and J L Campo. 2009. “Evaluation of Diversity between Different Spanish Chicken Breeds, a Tester Line, and a White Leghorn Population Based on Microsatellite Markers.” *Poultry Science* 88 (12): 2518–25.
- Dorji, Nedup, Monchai Duangjinda, and Yupin Phasuk. 2012. “Genetic Characterization of Bhutanese Native Chickens Based on an Analysis of Red Junglefowl (*Gallus Gallus Gallus* and *Gallus Gallus Spadecius*), Domestic Southeast Asian and Commercial Chicken Lines (*Gallus Gallus Domesticus*).” *Genetics and Molecular Biology* 35: 603–9.
- El-Gabbas, H M, A A Barghouth, and A E Ahtash. 1999. “The Potentiality of Wool Production in Libyan Barbary Sheep.” *Mansoura University Journal of Agricultural Science (Egypt)* 24 (5).
- FAO/DAD-IS. n.d. “Domestic Animal Diversity Information System (DAD-IS).” 2025. <https://www.fao.org/dad-is/browse-by-country-and-species/en/>.
- FAO. 2000. “FAO. (2000). Conserving and Developing Farm Animal Diversity. In State of the World Animal Genetic Resources. Retrieved.” 2000. <https://www.fao.org/faostat/en/#data/QCL>.
- FAOStat (2021) FAO Stat. Available at: [http://www.fao.org/fao stat](http://www.fao.org/fao%20stat) (accessed 30 March 2025)
- FAO, Rome. 2011. “Molecular Genetic Characterization of Animal Genetic Resources.” *FAO Animal Production and Health Guidelines*, no. 9.
- FAO/WB. 2024. “Moving Towards Sustainability: The Livestock Sector and the World Bank”. <https://www.worldbank.org/en/topic/agriculture/brief/moving-towards-sustainability-the-livestock-sector-and-the-world-bank>
- Frankham, Richard, Scientist Emeritus Jonathan D Ballou, David A Briscoe, and Jonathan D Ballou. 2002. *Introduction to Conservation Genetics*. Cambridge university press.
- Franklin, I R. 1997. “Systematics and Phylogeny of the Sheep.”
- Gaouar, S. B. S, Samia Kdidi, and Lahoussine Ouragh. 2016. “Estimating Population Structure and Genetic Diversity of Five Moroccan Sheep Breeds by Microsatellite Markers.” *Small Ruminant Research* 144: 23–27.
- Gaouar, S. B. S, Anne Da Silva, Elena Ciani, Samia Kdidi, Miloud Aouissat, Laziz Dhimi, Mohamed Lafri, Abderrahman Maftah, and Nadhira Mehtar. 2015. “Admixture and Local Breed Marginalization Threaten Algerian Sheep Diversity.” *PloS One* 10 (4): e0122667.
- Gizaw, Solomon, Hans Komen, Olivier Hanotte, and Johan A M Van Arendonk. 2008. “Indigenous Sheep Resources of Ethiopia: Types, Production Systems and Farmers Preferences.” *Animal Genetic Resources/Resources Génétiques Animales/Recursos Genéticos Animales* 43: 25–39.
- Groeneveld, L F, J A Lenstra, H Eding, M A Toro, B Scherf, D Pilling, R Negrini, E K Finlay, H Jianlin, and EJAG Groeneveld. 2010. “Genetic Diversity in Farm Animals—a Review.” *Animal Genetics* 41: 6–31.
- Guyatt, Gordon H, Andrew D Oxman, Gunn E Vist, Regina Kunz, Yngve Falck-Ytter, Pablo Alonso-

- Coello, and Holger J Schünemann. 2008. “GRADE: An Emerging Consensus on Rating Quality of Evidence and Strength of Recommendations.” *Bmj* 336 (7650): 924–26.
- Halima, Abir Ben, Raoudha Bahri, Esther Esteban, Mohamed Habib Ben Aribia, Pedro Moral, and Hassen Chaabani. 2014. “Ethnic Composition and Genetic Differentiation of the Libyan Population: Insights on Alu Polymorphisms.” *Annals of Human Biology* 41 (3): 229–37.
- Hall, Stephen J G. 2022. “Genetic Differentiation among Livestock Breeds—Values for Fst.” *Animals* 12 (9): 1115.
- Hanotte, Olivier, and Han Jianlin. 2006. “8. Genetic Characterization of Livestock Populations.” *The Role of Biotechnology in Exploring and Protecting Agricultural Genetic Resources*, 89.
- Harkat, Sahraoui, Abbes Laoun, Ibrahim Belabdi, Rédha Benali, Djouhar Outayeb, Nathalie Payet-Duprat, Véronique Blanquet, Mohamed Lafri, and Anne Da Silva. 2017. “Assessing Patterns of Genetic Admixture between Sheep Breeds: Case Study in Algeria.” *Ecology and Evolution* 7 (16): 6404–12.
- Hentati, Haifa El, Mohamed Ben Hamouda, and Ali Chriki. 2012. “Genetic Differentiation and Gene Flow between the Tunisian Ovine Breeds Barbarine and Western Thin Tail Using Random Amplified Polymorphic DNA-Polymerase Chain Reaction (RAPD-PCR) Analysis.” *African Journal of Biotechnology* 11 (96): 16291–96.
- Jemaa, S Ben, S Kdidi, A M Gdura, A S Dayhum, I M Eldaghayes, Mekki Boussaha, Emmanuelle Rebours, and M H Yahyaoui. 2019. “Inferring the Population Structure of the Maghreb Sheep Breeds Using a Medium-density SNP Chip.” *Animal Genetics* 50 (5): 526–33.
- Kalinowski, Steven T. 2004. “Counting Alleles with Rarefaction: Private Alleles and Hierarchical Sampling Designs.” *Conservation Genetics* 5 (4): 539–43.
- Kdidi, S, J H Calvo, L González-Calvo, M Ben Sassi, T Khorchani, and M H Yahyaoui. 2015. “Genetic Relationship and Admixture in Four Tunisian Sheep Breeds Revealed by Microsatellite Markers.” *Small Ruminant Research* 131: 64–69.
- Kdidi, Samia, Jorge Hugo Calvo, Gaouar S. B. S, Mohamed Dbara, Slah Belhadj, Ezzeddine Belfekih, Mohamed Hammadi, Touhami Khorchani, and Mohamed Habib Yahyaoui. 2023. “Genetic Structure and Assignment of Tunisian Meat Sheep Breeds.”
- MADR. 2016. “Statistique Agricole, Superficie et Productions Serie B.” 2016.
- Mahmoudi, B, M Sh Babayev, F Hayeri Khiavi, A Pourhosein, and M Daliri. 2011. “Breed Characteristics in Iranian Native Goat Populations.” *Journal of Cell and Animal Biology* 5 (7): 129–34.
- Mekuriaw, Zeleke, Habtemariam Assefa, Azage Tegegne, and Dagne Muluneh. 2016. “Estrus Response and Fertility of Menz and Crossbred Ewes to Single Prostaglandin Injection Protocol.” *Tropical Animal Health and Production* 48: 53–57.
- Mereu, Paolo, Monica Pirastru, Fabio Scarpa, Marco Zedda, Luisa Bogliolo, Salvatore Naitana, and Giovanni Giuseppe Leoni. 2025. “Mouflon and Domestic Sheep Phylogeny: Ancestry, Domestication, and Evolutionary Dynamics.” *Life* 15 (9): 1446.
- Nei, Masatoshi. 1987. *Molecular Evolutionary Genetics*. Columbia university press.
- Ojango, J M, N Mpofu, K Marshall, and L Andersson-Eklund. 2011. “Quantitative Methods to Improve the Understanding and Utilization of Animal Genetic Resources.” *Animal Genetics Training Resource, Version 3*: 2011.
- Ouinten, Y, P M Klenovitski, A A Nikichov, and E A Gladyr. 2018. “Genetic and Morphological Diversity in Algerian Sheep Breeds.” In *Innovative in Agriculture*, 117–22.
- Ouinten, Yacine, Sid Ahmed Aouadj, Bachir Medrouh, Imène Lafri, Dalila Ranebi, Gaouar S.B.S., Pavel Mikhailovich Klenovitskii, and Walid Benchiha. 2024. “The Genetic Diversity of Some North African Sheep Breeds Using Microsatellite Markers.” *Brazilian Journal of Animal and Environmental Research* 7 (4): e74802–e74802.

- Page, Matthew J, Joanne E McKenzie, Patrick M Bossuyt, Isabelle Boutron, Tammy C Hoffmann, Cynthia D Mulrow, Larissa Shamseer, Jennifer M Tetzlaff, Elie A Akl, and Sue E Brennan. 2021. "The PRISMA 2020 Statement: An Updated Guideline for Reporting Systematic Reviews." *Bmj* 372.
- Qwabe, Sithembile Olga. 2011. *Genetic and Phenotypic Characterisation of the South African Namaqua Afrikaner Sheep Breed*. University of Pretoria (South Africa).
- Rasoarahona, Ryan, Pish Wattanadilokchatkun, Thitipong Panthum, Thanyapat Thong, Worapong Singchat, Syed Farhan Ahmad, Aingorn Chaiyes, Kyudong Han, Ekaphan Kraichak, and Narongrit Muangmai. 2023. "Optimizing Microsatellite Marker Panels for Genetic Diversity and Population Genetic Studies: An Ant Colony Algorithm Approach with Polymorphic Information Content." *Biology* 12 (10): 1280.
- Rege, John Edward O, and John P Gibson. 2003. "Animal Genetic Resources and Economic Development: Issues in Relation to Economic Valuation." *Ecological Economics* 45 (3): 319–30.
- Rekik, M, I Ben Salem, H Diallo, H Ammar, and R Aloulou. 2005. "Productivité Numérique et Pondérale Des Brebis Produites Du Croisement Entre La D'man et La Race Locale Queue Fine de l'Ouest." *Revue d'élevage et de Médecine Vétérinaire Des Pays Tropicaux* 58 (1–2): 81–88.
- Ryder, Michael Lawson. 1983. *Sheep and Man*.
- Sassi-Zaidy, Y Ben, F Maretto, F Charfi-Cheikhrouha, A Mohamed-Brahmi, and M Cassandro. 2016. "Contribution of Microsatellites Markers in the Clarification of the Origin, Genetic Risk Factors, and Implications for Conservation of Tunisian Native Sheep Breeds." *Genetics and Molecular Research* 15 (1): 1–11.
- Sassi-Zaidy, Yousra Ben, Aziza Mohamed-Brahmi, Ghada Nouairia, Faouzia Charfi-Cheikhrouha, M'Naouer Djemali, and Martino Cassandro. 2022. "Genetic Variability and Population Structure of the Tunisian Sicilo-Sarde Dairy Sheep Breed Inferred from Microsatellites Analysis." *Genes* 13 (2): 304.
- Sheriff, Oumer, Berhanu Belay, and Aynalem Haile. 2013. "Characterization of Cattle Production System in Jimma Zone, Southwestern Ethiopia." *Ethiopian Journal of Animal Production* 13 (1): 17–30.
- Sheriff, Oumer, and Wondimu Bireda. 2016. "Characterization of Cattle Production System in Metekel Zone, Northwestern Ethiopia." *World Journal of Pharmaceutical and Life Sciences* 2: 1–14.
- Simm, Geoff. 1998. *Genetic Improvement of Cattle and Sheep*.
- Toro, Miguel A, Jesús Fernández, and Armando Caballero. 2009. "Molecular Characterization of Breeds and Its Use in Conservation." *Livestock Science* 120 (3): 174–95.
- Vashistha, Aakash, Manish Rundla, and Prabha Om. 2020. "Idiopathic Gigantomastia with Pseudoangiomatous Stromal Hyperplasia: A Case Report." *International Journal of Surgery Case Reports* 77: 915–19.
- Wanjala, George, Putri Kusuma Astuti, Zoltán Bagi, Nelly Kichamu, Péter Strausz, and Szilvia Kusza. 2023. "A Review on the Potential Effects of Environmental and Economic Factors on Sheep Genetic Diversity: Consequences of Climate Change." *Saudi Journal of Biological Sciences* 30 (1): 103505.
- Wanjala, George, Zoltan Bagi, and Szilvia Kusza. 2021. "Meta-Analysis of Mitochondrial DNA Control Region Diversity to Shed Light on Phylogenetic Relationship and Demographic History of African Sheep (*Ovis Aries*) Breeds." *Biology* 10 (8): 762.