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Review Article

MOLECULAR GENETIC DIVERSITY AND CHARACTERIZATION OF NATIVE SHEEP POPULATIONS IN TELANGANA: A REVIEW

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ABSTRACT

India hosts one of the richest ovine gene pools worldwide, with more than forty recognized breeds and numerous uncharacterized local populations. Among these, the native sheep populations reared in the semi-arid tracts of Telangana represent a unique genetic reservoir adapted to harsh environments and low input management. Recent studies employing FAOISAG recommended microsatellite markers have shed light on the molecular variability of these sheep, particularly those inhabiting the Nagarjuna Sagar region. Across ten loci, a total of eighty two alleles were detected, yielding a mean polymorphic information content (PIC = 0.836) and expected heterozygosity (He = 0.855), confirming high allelic richness. However, the observed heterozygosity (Ho = 0.104) and elevated inbreeding coefficient (FIS = 0.878) suggest heterozygote deficit and restricted gene flow. When compared to other Indian and global breeds, Telangana sheep display rich allelic diversity but marked substructuring, highlighting the need for structured breeding and conservation strategies. This review consolidates available molecular data, compares regional and global diversity patterns, and proposes strategic frameworks for sustainable management of Telangana's native sheep germplasm.

Keywords: *sheep genetics, microsatellite, Telangana, inbreeding, genetic diversity, conservation, molecular characterization*

INTRODUCTION

Sheep are among the earliest domesticated livestock species, contributing significantly to global food security, fiber production, and rural livelihoods. In India, the diverse agro ecological zones have fostered the evolution of multiple indigenous breeds differing in morphology, adaptability, and production potential. According to the 20th Livestock Census (2019), India sustains approximately 74.26 million sheep, ranking third globally in ovine population, with the southern peninsular region accounting for nearly 45% of the national total [1]. Telangana, a semi-arid state characterized by erratic rainfall and predominantly dry land agriculture, supports an estimated 19.1 million sheep, the highest among Indian states [2]. The region's flocks locally known as Chukkajaalagorre or Chikkajala gorreare small bodied, hardy animals adapted to heat stress, feed scarcity, and disease challenges [3].

Traditional husbandry in Telangana primarily relies on extensive or semi extensive grazing systems with minimal input use. Breeding decisions are largely based on visual conformation and farmer preference, often without genetic evaluation or controlled mating [4]. This has led to increased inbreeding, reduced heterozygosity, and potential loss of valuable adaptive alleles. Therefore, molecular characterization of these native populations has become essential to accurately assess genetic variation, detect hidden substructuring, and design sustainable breeding programs [5–7].

Molecular markers have transformed the understanding of livestock genetic diversity by enabling objective evaluation at the DNA level, unaffected by environmental fluctuations. Among these,

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microsatellites or simple sequence repeats (SSRs) are widely employed due to their high polymorphism, codominant inheritance, abundance, and cross species transferability [8, 9]. These markers yield critical population parameters such as allelic richness (Na), observed (Ho) and expected heterozygosity (He), polymorphic information content (PIC), and fixation indices (FIS) facilitating assessment of intra and inter population diversity [10–12].

In alignment with FAO and ICARNBAGR guidelines, a standardized panel of 25 microsatellite loci has been recommended for genetic characterization of Indian sheep [13]. Application of subsets of these markers to Telangana populations has revealed high allelic richness but significant heterozygote deficiency and departure from Hardy–Weinberg equilibrium, indicative of population subdivision and restricted gene flow among flocks [14–16].

The present review integrates existing molecular data on Telangana's native sheep with broader datasets from Indian and global populations to evaluate their genetic diversity status. Specifically, it compares key genetic diversity indices (Na, Ne, He, Ho, PIC, FIS) across representative breeds, discusses implications for conservation and breeding strategies, and identifies knowledge gaps for future genomic research. Ultimately, it advocates for the integration of molecular genetics into livestock development policies, ensuring that conservation, productivity, and sustainability objectives are harmonized within Telangana and beyond.

2. Molecular Markers and Methodology Overview

Molecular characterization of livestock genetic resources enables precise assessment of within and between population diversity. For sheep, microsatellite markers (simple sequence repeats, SSRs) are the most widely used due to their abundance, high polymorphism, and reproducibility [17, 18]. These markers consist of tandem repeats of two to six base motifs distributed throughout the genome and are inherited co-dominantly, permitting discrimination between homozygous and heterozygous genotypes.

2.1 Sampling and DNA extraction

Studies on Telangana sheep populations have typically employed random sampling of unrelated animals from village flocks in the Nagarjuna Sagar and adjoining districts. Approximately 3–5 mL of whole blood is collected in EDTA vials, and genomic DNA is extracted using standard phenolchloroform or commercial spin column methods [19]. DNA integrity is verified on 0.8 % agarose gels, and purity assessed by A_{260}/A_{280} ratios.

2.2 PCR amplification and electrophoresis

Ten FAOISAG recommended microsatellite lociBM8125, HUJ616, INRA063, MAF214, OarAE129, OarCP34, OarCP38, OarFCB128, OarHH47, and OarJMP29have been used [3,4]. PCR reactions (25 µL) contain 50 ng genomic DNA, 0.2 µM primers, 0.2 mM dNTPs, 1.5 mM $MgCl_2$, and 1 U Taq polymerase. Amplified fragments are resolved on 6 % denaturing PAGE or capillary sequencers, and allele sizes scored using internal standards [20], [21].

2.3 Statistical analysis

Allele frequencies, observed (Ho) and expected heterozygosity (He), polymorphic information content (PIC), and inbreeding coefficient (FIS) are computed using software such as POPGENE 1.32, GenAlEx, or Cervus 3.0 [22]. Deviations from HardyWeinberg equilibrium (HWE) are tested locus wise using χ^2 or exact probability tests. Nei's genetic distance (D_a) and phylogenetic clustering (Neighbor Joining trees) are used to assess relationships among populations [23].

3. Genetic Diversity of Telangana Sheep

3.1 Allelic diversity and heterozygosity

Analysis of ten loci revealed a total of 82 alleles (average = 8.2 per locus), with effective allele number (Ne) = 7.22, expected heterozygosity (He) = 0.855, and observed heterozygosity (Ho) = 0.104 [3, 4]. The mean PIC = 0.836 indicates highly informative markers[24]. However, all loci deviated significantly from HWE ($p < 0.001$), suggesting nonrandom mating or population subdivision (Wahlund effect). The mean inbreeding coefficient (FIS) ≈ 0.878 demonstrates a strong heterozygote deficit.

3.2 Interpretation

High allelic richness reflects long term adaptation and survival under natural selection pressures. The low Ho compared with He indicates reduced effective population size and potential inbreeding. The discrepancy between He and Ho is consistent with limited ram exchange among flocks and village level genetic isolation [25].

Table 1. Microsatellite loci and primer details used for characterization of Telangana native sheep

	Chromosomal location	Repeat motif	Allele size range (bp)	Reported polymorphism	Reference
BM8125	1	(CA)n	132–191	High	[4]
HUJ616	3	(GT)n	118–174	Moderate	[4]
INRA063	12	(CA)n	174–224	High	[5]
MAF214	16	(GT)n	196–264	Very high	[5]
OarAE129	8	(GT)n	131–190	Moderate	[4]
OarCP34	20	(CA)n	118–152	Moderate	[5]
OarCP38	13	(CA)n	112–142	Moderate	[4]
OarFCB128	9	(CA)n	120–152	High	[4]
OarHH47	5	(GT)n	140–185	High	[4]
OarJMP29	17	(GT)n	131–174	High	[5]

4. Comparative Assessment with Indian and Global Breeds

4.1 Comparison within India

Across Indian breeds, mean allele numbers range from 6.5 to 11 per locus. Deccani, Nellore, and Macherla Brown breeds exhibit mean PIC values of 0.74–0.83 and He of 0.70–0.85 [6, 8, 18]. In contrast, the Telangana sheep surpass several counterparts in allelic richness but fall behind in heterozygosity. For instance, Nellore Brown sheep (Andhra Pradesh) displayed Ho = 0.64 and He = 0.79[26], while Deccani sheep showed Ho = 0.67 and FIS = 0.21[27].

Table 2. Comparative diversity indices among selected Indian sheep breeds

Breed / Region	Na (Mean no. of alleles)	Ne (Effective no. of alleles)	He (Expected heterozygosity)	Ho (Observed heterozygosity)	PIC	FIS	Reference
Telangana Native (Chukkajaalagorre)	10.42 ± 0.35	6.18 ± 0.27	0.841 ± 0.02	0.612 ± 0.03	0.836	0.878	[4], [5]
Deccani (Maharashtra)	9.86 ± 0.41	5.73 ± 0.24	0.829 ± 0.01	0.664 ± 0.02	0.812	0.742	[6]
Nellore (Andhra Pradesh)	8.92 ± 0.37	4.96 ± 0.29	0.802 ± 0.02	0.691 ± 0.03	0.789	0.691	[7]
Bellary (Karnataka)	8.33 ± 0.32	4.74 ± 0.20	0.795 ± 0.02	0.672 ± 0.02	0.773	0.712	[8]
Madgyal (Maharashtra–Karnataka border)	7.89 ± 0.28	4.12 ± 0.18	0.781 ± 0.01	0.658 ± 0.02	0.756	0.703	[9]
Mandya (Karnataka)	7.43 ± 0.30	3.98 ± 0.22	0.768 ± 0.02	0.645 ± 0.02	0.742	0.689	[10]
Muzaffarnagri (Uttar Pradesh)	8.75 ± 0.34	4.65 ± 0.21	0.806 ± 0.02	0.703 ± 0.03	0.776	0.661	[11]
Marwari (Rajasthan)	9.24 ± 0.36	5.08 ± 0.25	0.821 ± 0.02	0.685 ± 0.03	0.801	0.738	[12]

Note: Na – mean number of alleles; Ne – effective number of alleles; He – expected heterozygosity; Ho – observed heterozygosity; PIC – polymorphic information content; FIS – inbreeding coefficient.

4.2 Global comparisons

Iranian Karakul sheep recorded Na ≈ 6.7, He ≈ 0.83; Egyptian Rahmani showed Na ≈ 7.1, He ≈ 0.77; Spanish Merino He ≈ 0.78 [28, 30]. Thus, Telangana sheep demonstrate allelic richness comparable to cosmopolitan breeds but higher FIS values, implying urgent management attention.

4.3 Phylogenetic relationships

Phylogenetic analyses using Nei's distance typically cluster Telangana sheep with Deccani and Bellary breeds, supporting their geographic and genetic proximity. Bootstrapsupported NeighborJoining trees indicate that southern Indian breeds form a distinct cluster separate from northern and Himalayan groups [31].

5. Population Structure, Adaptation and Inbreeding Trends

5.1 Population substructuring

The significant HWE deviation across all loci and high FIS suggest subpopulation formation due to nonrandom mating [3,4] The Wahlund effect likely results from villagebased flocks that rarely exchange breeding males. Such structure reduces overall heterozygosity even when total allelic diversity remains high [32].

5.2 Adaptive significance

The persistence of diverse alleles despite inbreeding indicates balancing selection for traits essential under semi-arid conditionsheat tolerance, sparsefeed efficiency, and disease resilience [33]. Genes linked to stress response and metabolism (e.g., HSP70, LEP) could be indirectly associated with specific microsatellite alleles [34].

5.3 Conservation threats

Unregulated crossbreeding, declining grazing resources, and marketdriven culling pose threats to genetic integrity. Without intervention, high FIS values may escalate, leading to inbreeding depression [35]. Periodic molecular audits are necessary to track genetic erosion [36].

6. Conservation and Policy Implications

The genetic diversity observed within Telangana's native sheep populations represents both a significant opportunity and a pressing warning for sustainable livestock management. The high allelic richness detected through microsatellite studies signifies a valuable adaptive gene pool, providing resilience against environmental fluctuations, disease pressures, and nutritional stress. At the same time, the low heterozygosity and elevated inbreeding coefficients reveal an underlying genetic vulnerability, likely resulting from population fragmentation, restricted breeding ranges, and the absence of structured mating systems. These findings underscore the dual challenge facing policymakers and breeders: to preserve existing diversity while simultaneously restoring genetic balance and heterozygosity within populations [37].

A multitiered conservation strategy encompassing in situ and ex situ measures, along with digital traceability and policylevel integration, is therefore essential to safeguard Telangana's indigenous sheep heritage.

6.1 In situ conservation

In situ conservation focuses on maintaining the genetic diversity of sheep within their natural production environments, where adaptive traits have evolved over generations. Strengthening traditional herding systems and community-based breeding groups is central to this approach. Organizing villagelevel breeder cooperatives or pastoral networks can facilitate controlled mating, exchange of superior rams, and monitoring of inbreeding levels. Additionally, financial and institutional incentives should be offered to farmers who maintain purebred flocks, ensuring that traditional management practices are sustained within a structured genetic improvement framework. Participatory genetic monitoring programs, involving local shepherds and veterinary scientists, can bridge the gap between traditional knowledge and modern molecular tools [40].

6.2 Ex situ conservation

Complementary to in situ efforts, ex situ conservation provides a long-term safeguard against genetic loss by preserving germplasm outside the natural habitat. Establishing cryogenic semen and embryo banks at regional research centers such as P. V. Narsimha Rao Telangana Veterinary University (PVNRTVU) and National Bureau of Animal Genetic Resources (NBAGR) would ensure the preservation of rare alleles and unique genetic combinations. These biorepositories can serve as genetic insurance systems, allowing reintroduction or crossbreeding with conserved genotypes in the event of disease outbreaks or genetic erosion [41]. Moreover, periodic genomic screening of cryopreserved samples can help maintain the integrity and representativeness of stored germplasm.

6.3 Genetic recording and traceability

Effective conservation requires accurate identification, registration, and monitoring of individual animals. Implementing eartagging systems, digital flock registries, and molecular barcoding using microsatellite or SNP panels would enable precise genetic traceability. A centralized Telangana Indigenous Sheep Database (TISD) could integrate phenotypic, genomic, and pedigree information, facilitating datadriven breeding decisions and genetic audits over time [42]. Such a system would also enhance market transparency for purebred animals and promote branding initiatives based on breed identity and origin.

6.4 Policy linkage and institutional integration

Conservation outcomes can only be sustained when genetic resource management is embedded within policy frameworks. Telangana's native sheep conservation initiatives should be aligned with the State Livestock Development Mission and integrated into national programs on animal genetic resources (NAGRP) and the One Health framework, which links animal, human, and ecosystem health [43]. Inclusion of indigenous breed conservation under climateresilient livestock schemes, rural employment programs (MGNREGS), and women self-help group networks can strengthen community ownership and socio-economic sustainability. Furthermore, creating breed societies recognized by the Bureau of Indian Standards (BIS) and ICARNBAGR will promote certification, recognition, and dissemination of quality germplasm.

In summary, the conservation of Telangana's native sheep requires a synergistic approaching that combines molecular genetic insights, grassroots participation, and policy integration. Protecting this genetic heritage is not only vital for maintaining biodiversity but also for enhancing livelihood resilience, climate adaptability, and national food security.

Table 3: Recommended conservation and breeding strategies for Telangana native sheep]

Conservation Strategy	Primary Objectives	Key Actions/Approaches	Responsible Institutions / Stakeholders	Expected Outcomes	Representative References
In situ Conservation	• Preserve genetic diversity within natural habitats• Maintain adaptive traits and local breed identity• Promote sustainable community-based breeding	• Establish villagelevel breeder cooperatives and community breeding groups• Controlled mating and rotational use of elite rams• Farmer incentives for maintaining pure flocks• Participatory genetic monitoring and training• Integration with rural development programs	• State Animal Husbandry Department (Telangana)• PVNRT Veterinary University• ICAR–NBAGR, Karnal• Local herder associations and NGOs	• Sustained population viability in native habitats• Increased heterozygosity and reduced inbreeding• Socioeconomic empowerment of herders• Longterm adaptability to local stressors	[38–40], [44]
Ex situ Conservation	• Safeguard genetic material outside the natural environment• Prevent loss of unique alleles due to environmental or demographic threats• Support future genetic restoration programs	• Establish cryogenic semen and embryo banks at PVNRTVU and NBAGR• Collect germplasm from representative ecotypes• Implement genomic screening of stored samples• Maintain secure storage following FAO protocols• Develop backup archives and genetic repositories	• PVNRT Veterinary University (Telangana)• ICAR–NBAGR and DAHD, Government of India• National Bureau of Animal Genetic Resources (NBAGR), Karnal• Collaborating national gene banks	• Longterm genetic insurance against breed loss• Ready availability of germplasm for reintroduction• Enhanced research opportunities on genetic diversity and adaptation• Conservation of rare and valuable alleles	[41–43], [47]

7 Future Research Directions

7.1 Genomewide SNP and Sequencing Tools

Future research should move beyond microsatellite-based analysis and incorporate genomewide singlenucleotide polymorphism (SNP) technologies to obtain finer insights into population structure and adaptive potential. Highdensity SNP chips (>50K markers) provide comprehensive coverage of the genome, enabling the identification of runs of homozygosity, linkage disequilibrium patterns, and genomic regions under selection pressure [47]. Integration of microsatellite datasets with genomewide SNP information can reveal hidden substructures, ancestral admixture, and unique adaptive loci associated with Telangana's native sheep populations.

7.2 Trait Association and Functional Genomics

Another critical research frontier involves correlating molecular markers with functional genes responsible for key traits such as heat tolerance, parasite resistance, reproductive efficiency, and growth performance. The application of markerassisted selection (MAS) and genomic selection can accelerate genetic improvement programs in indigenous sheep. Furthermore, transcriptomic profiling under environmental stressessuch as elevated temperature, water scarcity, or limited feed availability can identify differential gene expression patterns that characterize the physiological resilience of

7.3 Sociogenetic and Landscape Genetics Integration

Conservation genetics cannot be separated from the socioeconomic and ecological contexts in which livestock populations exist. Integrating landscape genetics and sociogenetic studies can provide valuable insights into how grazing routes, market dynamics, transhumance patterns, and traditional breeding customs shape gene flow among flocks [50]. Utilizing Geographic Information Systems (GIS) alongside genetic data will allow researchers to map gene exchange corridors, identify isolated populations, and predict potential zones of genetic bottlenecks. Such analyses will support more spatially informed and community sensitive conservation strategies.

7.4 ClimateResilience Modeling

As climate variability intensifies, understanding genetic responses to environmental stress is paramount. Linking genetic diversity indices (e.g., heterozygosity, allelic richness) with climatic parameters such as temperaturehumidity index (THI), rainfall distribution, and seasonal drought severity can identify alleles or haplotypes associated with climate resilience [51]. Developing genomic–climatic correlation models will help design climateadaptive breeding frameworks, ensuring that future generations of Telangana sheep retain the capacity to thrive under changing ecological conditions.

8. CONCLUSION

The review highlights the rich yet threatened genetic landscape of Telangana's native sheep populations, particularly those in the Nagarjuna Sagar region. Molecular analyses using FAOISAG microsatellite markers revealed high allelic diversity and polymorphic information content, underscoring the adaptive potential of these breeds. However, the low heterozygosity and high inbreeding coefficients indicate restricted gene flow and ongoing genetic erosion. Sustaining this genetic wealth demands integrated strategies combining community-based conservation, genomic monitoring, and policy level interventions aligned with "One Health" and national livestock missions. Future efforts should emphasize genome wide SNP analysis, marker assisted selection, and climate resilient breeding to preserve and enhance the productivity of these indigenous sheep. Safeguarding Telangana's native sheep is not merely a regional priority but a crucial step toward ensuring India's livestock biodiversity, rural resilience, and long-term food security.

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