



A Review on the Status of Genetic Characterization of Indigenous Goat Breeds in India

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The goat breeds are diverse and well-adapted to the local agroclimatic conditions in India. The indigenous and lesser-known populations, which make up 70% of the overall goat population and some of which are currently in danger of going extinct, have not yet had their genetic makeup fully determined. To maintain their genomic variability, which is necessary for genetic resource conservation and genetic resource improvement, genetic characterisation is required. For research on goat population structure and diversity, three genetic markers viz. microsatellites, mtDNA, and caprine SNP chips are used and their study has revealed that the most diversified breeds are Kanni Adu and Sirohi, whereas Osmanabadi is the least diverse breed. The genetic gap between Kanni

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Adu and Zalawadi was determined to be the greatest (0.519) and the genetic gap between Jamunapari and Marwari was the lowest (0.092). In Indian goats, phylogenetic and network research identified four widely recognised haplogroups (A, B, C, and D). Multiple maternal origins were identified in Chinese domestic goats, according to an origin and genetic diversity analysis based on mtDNA research. In addition to providing genetic divergence parameters, the information derived from caprine SNPChips also identifies selection signatures linked to a variety of useful qualities that contribute to a breed's uniqueness. Therefore, this review advises the registration and characterisation of local goat population to make a mission towards zero non-descript goat genetic resources in India by applying genomic technology.

Keywords: Indigenous goat breeds; genetic characterization; genetic markers; genetic diversity.

1. INTRODUCTION

India stands first in goat population with 148.88 million and it shows a 10.14% growth rate compared to the previous census [1]. "Goats make valuable contributions ranging from precious animal protein (meat and milk) to fiber and skins, draught power in highlands, food security and livelihood to rural poor farmers in fragile ecosystems" [2]. "Sale of goats and goat products by farming communities is the major source of income for the household communities" [3]. "In addition, goats are raised mostly to safeguard against crop failure under an integrated farming system" [4]. "Goats are also represented as a more liquid form of capital than cattle and are readily tradable" [5]. "An assessment of genetic variability in domestic goats is a first step towards conservation of genetic resources for maintaining breeding population" [6-9]. "Genetic diversity among 27 Indian goat populations was estimated by using 25 microsatellite markers indicating a high level of conserved genetic diversity among Indian goats" [10]. "In the changing phase of agricultural practices, a few breeds have been used on a large scale for immediate economic gain. Therefore, locally adapted native breeds have been neglected without knowing their genetic importance. Hence consideration for genetic diversity study and conservation of goat genetic resources is the need of the hour for human welfare. National strategies with a well-structured conservation program are necessary to conserve indigenous goats and to ensure sufficient genetic diversity" [11].

The phenotypic variance observed in numerous populations most clearly reflects the genetic diversity found in the goat germplasm, which is defined as the total genetic differences in different loci among individuals in a population. The population's ability to adjust to shifting

climatic conditions is a testament to the genetic diversity [12]. Breed-to-breed genetic diversity can be ascertained using genetic markers [13–17]. Osmanabadi goats had the least genetic diversity, whereas Kanniadu and Sirohi goats had the highest genetic diversity among 20 Indian goat breeds, according to a study using 25 microsatellite markers [18,19-22]. By contrasting the microsatellite genotypes of Dutch and Danish goats, Lenstra et al. [23] employed "microsatellite-based genotyping technologies to characterise the phylogeography of European goats".

Another well-liked marker for determining molecular diversity and evolutionary links of goat breeds is mitochondrial DNA (mtDNA) [24–26]. According to the mtDNA-based diversity analysis, Kanniadu differs significantly from the other Indian breeds [27]. These days, single nucleotide polymorphism (SNP) markers—which are more prevalent in the genome and exhibit greater genetic stability—replace microsatellite markers in genetic diversity analyses. Numerous studies on the goat population have shown the value of SNP array technology in assessing genetic diversity and divergence both within and between populations [28–31]. DNA-based markers provide the opportunity to estimate genetic diversity and relationships in farm animals which are relevant for breed monitoring, conservation, and improvement [32]. Genetic characterization of North American and European dairy goat breeds by using an SNP chip revealed that Canadian dairy goats showed the largest within-breed heterogeneity and genetic differences with the European populations [33].

Therefore, this review navigates an overview of goat genetic diversity study based on microsatellite, mitochondrial and SNP genotyping technology.

2. INDIAN GOAT DIVERSITY

The population of Indian goats is 148.88 million [1] which is 15.68% of the world's goat population (861.90 million) and 26.28% of the Asian goat population (514.4 million). The increasing trend of population growth rate (10.14%) is observed among the goat population in India compared with the previous census (2012). A good amount of diversity is present in Indian goat germplasm as the population is represented by thirty-four descript breeds and many nondescript populations. They are distributed across the four major agro-climatic zones viz. "Northwestern arid and semi-arid, Southern peninsular, Northern temperate and Eastern region. Indian goats are acknowledged in the world for their unique attributes such as production of the finest quality fibre Pashmina by Changthangi and Chegu goats; high prolificacy and quality meat by Black Bengal and Malabari breeds; milk production by Jamnapari, Beetal, Barbari, Jakhrana and Surti goats. They have also unique characteristics to survive under extremes of temperatures ranging from hot deserts of Northwestern arid and semi-arid regions of India to cold deserts of the Northern temperate region" [34].

The descript goat breeds constitute only 30% of the total goat population while the remaining 70% is comprised of many lesser-known / non-descript populations. These lesser-known populations lack systematic studies and sufficient information on them. Some of such populations known are Ghumusari, Kalahandi from Orissa, Johnpuri, Bundelkhandi, Chaugarakha from Uttar Pradesh and Uttarakhand, Khagani and Shingari from Kashmir. Konkani Kanyal and Berari goats have been studied recently [35-37] and registered as breeds. Most of Such populations are the result of indiscriminate or unplanned mating or geographic isolation from the main breeds. To utilize such populations, it is necessary to know their origin and genetic architecture. Systematic studies are required to generate information on their morphological traits, management practices, performance and the unique traits present if any.

3. INDIAN GOAT EVOLUTIONARY STATUS/ RELATIONSHIP

"Goats are uniformly distributed across the climatic regions of India from the cold desert of Ladakh in the north to the saline water of Andaman in the south and from the dry desert of

Rajasthan in the west to the humid climate of Bengal in the eastern regions of India. Goat production for centuries has been an integral component of the farming system and a primary source of livelihood for poor villagers. Resource-poor people on zero input mostly rear goats in India. Goats contribute 22.27% of the milk, 10.86% of the meat and 13.31% of the fresh skins of the total production of the world" [38]. About 41 % of goats of the total population are slaughtered every year for meat.

The goat production systems are highly diversified in different parts of the country depending upon agro-ecological conditions and cropping systems. Therefore, development programmes in the country should be made region-specific as per the requirement of the region or sub-region. With changes occurring rapidly in the agriculture farming system due to mechanization, land use patterns, depletion of grazing land and high cropping intensity, the level of goat production, flock size, flock composition and goat population intensity is changing in different regions. The ultimate objective of goat production is to maximize profit from the available resources within production conditions and suitable for socioeconomic conditions in different regions. Social taboos associated with poverty and lower social prestige are gradually motivating educated persons from high society to adopt goat farming at the commercial level. Goat breeds in India have evolved through migration across the region, geographical isolation and natural selection. They have been assigned names on the basis of morphological attributes and in the vicinity of their natural habitat. The efficiency of a breed is generally considered on the basis of performance in the prevailing production system rather than on rearing them in an artificial environment. The actual potential of different goat breeds is yet to be known, as they have not been adequately evaluated in the optimum managerial conditions.

4. GENETIC RESOURCES AND THEIR PERFORMANCE

4.1 Temperate Himalayan Region

Breeds including Chegu, Changthangi, Gaddi, and Bhakarwali are representative of this area. The Chegu goat breed is of Indian descent and produces pashmina. These goats, known as Changthangi, are also found in the chilly Ladakh Plateau of Jammu and Kashmir, which is part of

the western Himalayas. Both population and performance are declining there. Changthang town in Leh, which borders Tibet, is home to the Changthangi goat. Situated at an elevation of 3,00–6000 meters above mean sea level, the town has a temperature range of 350°C in the summer to a low of 400°C in the winter [39]. The Lahul, Spiti, and Pangji valleys in the Chamba district of Himachal Pradesh, as well as the Uttarkashi, Pithoragarh, and Chamoli districts of Uttarakhand, are home to the Chegu [40–42]. Mountainous areas of Assam, West Bengal and North Eastern states (Arunachal Pradesh, Manipur, Meghalaya, Mizoram, Nagaland, Sikkim and Tripura) fall in this region. Goats of this region are mostly of meat type. The popular breeds Black Bengal or its type, Assam Hill and Sumi-Ne are also habituated in this region.

4.2 Arid and Semi-Arid Northern Region

This region is characterized by tropical and subtropical climates with low to moderate rainfall with recurring drought. Temperature varies from -2° C (winter) to 49°C (summer). This region is blessed with many rivers and the highest crop productivity. This zone possesses 12 goat breeds, which is the highest in number of breeds and goat population (33% of the country). Zalawadi is the largest size breed in the western arid region followed by Gohilwadi, Kutchi and Marwari. All these goat breeds are dual-purpose, sturdy and have great resistance to climatic stress, feed, fodder and water scarcity and parasitic diseases. Production performance of Sirohi, the next most populous goat breed in this region, was evaluated under field conditions in its home tract (Udaipur, Rajsamand, Chittorgarh, Bhilwara, Ajmer and Sirohi districts of Rajasthan [43]. Beetal goats are predominately found in the Gurdaspur and Amritsar districts of Punjab and are reared mostly by Sansi tribes. Production Performance of Jamunapari goats was evaluated in its home tract as well as at institute flock under breed improvement programme started in 1993 as AICRP on Goats. Barbari is a dual-purpose goat distributed in Etah, Aligarh, Agra, Firozabad and Mathura districts of Uttar Pradesh. It is one of the most prolific breeds amongst goat breeds of this region and very well adapted for stall feeding. The goat production system studied in different districts of the Saurashtra region of Gujarat revealed that pastoralists' tribes (Rabaries and Bharwad) called "Maldharies" largely rear goats. The goat breeds mostly reared are Zalawadi and Gohilwadi. The newly registered breed is recognized as Kahmi from Gujarat.

4.3 Eastern Region

The goats of this region are predominated by Bengal or its strains; another important breed is Ganjam and non-descript. Bengal goat has a high reputation for prolificacy, early maturity, high breeding efficiency, quality meat and skin. Black, brown and white are variants of this breed although the population of black variant is very high (>80 %).

4.4 Southern Arid and Semi-Arid Region

In major parts of Maharashtra, peninsular Karnataka and Andhra Pradesh, the majority of the goat population is non-descript. Goat breeds that predominate in this region are Osmanabadi and their grades are followed by crosses of Osmanabadi × Sangamneri, Sangamneri, Kanni Adu and Malabari [44]. Goats found in drought-prone areas of the Vidarbha region of Maharashtra (Nagpur, Akola and Wardha district) are mostly yet to be recognized as a breed. Kanni Adu and their grades are common in Tamilnadu. This breed is of medium size and is known for its prolificacy as >65 % of multiple births were recorded. The newly recognized breeds of this region include Kodi Adu, Salem Black, Bidri and Nandi Durga.

4.5 Southern Peninsular Region

Mostly goat population (>80 %) is nondescript and reared under an extensive system of production. Malabari is the only recognized breed of the Southern peninsula.

5. MITOCHONDRIAL DNA BASED CHARACTERIZATION

Mitochondrial DNA (mtDNA) is strictly maternally inherited; the progeny of both males and females inherits the mtDNA from their mother (barring mutations), whereas only the daughter passes on the mtDNA to the next generation. The sperm contributes no mtDNA when fertilizing the egg. Biological maternal relatives all share their mtDNA, yet their nuclear DNA (nDNA) is unique.

"Mitochondrial DNA sequencing has been used to explain the origins of many modern domestic livestock species. The existence of multiple mtDNA lineages and their mixing within breeds could be due to multiple domestication events or to introgression between domestic and wild species. The studies on the structure and

function of mtDNA become highlighted in the research area of molecular evolution, genetic

diversity analysis and phylogenetic relationships across the species" [45-48].



Fig. 1. Chegu (Goat): Male



Fig. 2. Chegu (Goat): Female



Fig. 3. Jamunapari (Goat): Male



Fig. 4. Jamunapari (Goat): Female



Fig. 5. Black Bengal (Goat): Male



Fig. 6. Black Bengal (Goat): Female



Fig. 7. Malabari (Goat): Male



Fig. 8. Malabari (Goat): Female

(Pic courtesy: ICAR-NBAGR database, available on: <https://nbagr.icar.gov.in/en/databases/>)

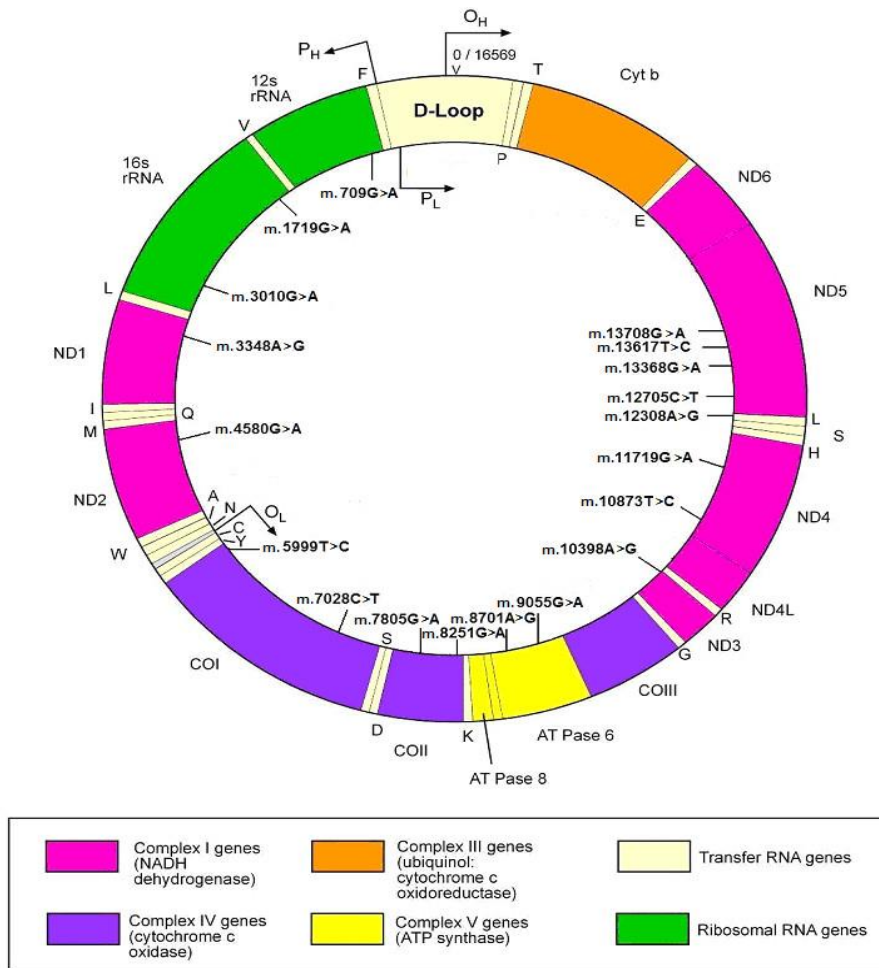


Fig. 9. The structure of Mitochondrial DNA (mtDNA)

“Over the last three decades, mitochondrial DNA has been the most popular marker of choice for molecular diversity. The reasons for the adoption of mtDNA as a marker of choice are well-known.

Experimentally, mtDNA is relatively easy to amplify because it appears in multiple copies in the cell. Mitochondrial gene content is strongly conserved across animals, with very little

duplication, no intron, and very short intergenic regions" [49]. "Mitochondrial DNA is highly variable in natural populations because of its elevated mutation rate, which can generate some signals about population history over short time frames. The presence of variable regions (control region) is typically flanked by highly conserved ones (e.g. ribosomal DNA), in which PCR primers can be designed. The only technical issues associated with the marker arise from illegitimate amplification of mitochondrial genes that have been inserted into the nuclear genome in some species" [50]. Clearly, mtDNA is the most convenient and cheapest solution for genetic diversity and population structure studies.

The highly polymorphic parts of the displacement region (D-loop) in the mtDNA structure (Hypervariable regions I and II) explain the origins and evolution of livestock species (Fig. 1). "The mitochondrial DNA contains 37 genes, all of which are required for proper mitochondrial operation. Thirteen of these genes provide instructions for making the enzymes involved in oxidative phosphorylation. The remaining genes code for the production of molecules known as transfer RNAs (tRNAs) and ribosomal RNAs (rRNAs), which are chemical cousins of DNA. The construction of functional proteins from amino acids, which are the building blocks of proteins, is facilitated by these RNA types. A mitochondrial fragment known as COX1 was recently selected as the benchmark tool for molecular taxonomy and identification" [51].

"Mitochondrial DNA studies on domestic goats identified at least four major mtDNA lineages. Lineage A is the most diverse and widely distributed across all continents. Lineage B is confined to eastern and southern Asia, including Mongolia, Laos, Malaysia, Pakistan and India. Lineage C is present in low frequencies in Mongolia, Switzerland, Slovenia, Pakistan and India. Finally, lineage D is rare and only observed in Pakistani and Indian local goats. The time since divergence among these four lineages (more than 200,000 years ago) far predated the time of domestication around 10,000 years ago" [52-55].

Based on mtDNA analysis, 19 native Korean goats were classified into six haplotypes. When compared to other Asian goat populations, the mtDNA of these Korean goats showed extremely short genetic distances within the population, suggesting less genetic variety in the native

Korean goat population [56]. All of these goats belonged to the mitochondrial (mt) lineage A. Based on full mtDNA D-loop sequences from 13 breeds, the origin and genetic diversity of Chinese goats were deduced. The haplotype diversity value ranged from 0.9333 to 1.0000, while the nucleotide diversity value ranged from 0.006337 to 0.025194. These findings showed that Chinese domestic goats had various maternal origins [57]. Raut et al. [58] used the mitochondrial DNA (mtDNA) mismatch distribution in Jamunapari goat and analysis revealed that the population curve was unimodal indicating the expansion of population. Hoda et al. [59] analyzed 77 mtDNA D-loop sequences from six different Albanian goat breeds. The results revealed the presence of 67 different haplotypes, with haplotype diversity ranging from 0.864 to 1 and nucleotide diversity values ranging from 0.016 to 0.106 and the analysis indicated that 98.7% of the variation was found within the goat breeds and only 1.3% among the breeds.

Using mt DNA D-loop, the genetic diversity analysis identified three haplogroups among five South Indian goat breeds: Attapadi black, Kanni aadu, Kodi aadu, Malabari, and Salem black. These haplogroups reflect maternal lineages A, B, and D. Breeds like Malabari had haplotype diversity of 0.9524 ± 0.0403 and Kanni aadu had haplotype diversity of 0.9921 ± 0.0154 . Three haplogroups were found, indicating that domestic goats in India had multiple maternal origins [16]. Sharma et al. [27] conducted an mtDNA-based genetic diversity investigation of Indian goats, focusing on the mitochondrial HVR1 region from 21 Indian breeds that correspond to various geographic locations. According to the study, the majority of Indian goats were grouped into lineage A, with a smaller number of goats falling into lineages B and C. The breeds clustered apart, with the Kanniadu breed being the most isolated. A thorough mtDNA-based genetic diversity analysis of India's 34 different goat breeds was conducted by Diwedi et al. [17]. In Indian goats, phylogenetic and network research identified four widely recognised haplogroups (A, B, C, and D). Due to inadequate breeding improvement programmes, interbreeding of goats in close proximity, shrinking pasture lands, and a migratory system of goat rearing, the majority of the mtDNA diversity is distributed among the goats within their geographical areas of habitation. There is also no clear genetic structuring of goats from the Indian subcontinent based on geographical distribution.

6. SNP BASED GENETIC CHARACTERIZATION IN GOATS

The genetic diversity of goat breeds has been characterised genomically, which is important for developing breeding plans and conservation strategies. The majority of the goat genetic diversity study is based on a few numbers of microsatellite markers. New avenues for examining population genetic structure, genetic mixing, phylogenetic linkages, and genetic diversity and divergence within and among goat populations have been made possible by the availability of the Illumina Goat 50K SNP BeadChip. Kim et al. [60] evaluated genetic diversity and population structure in Barki goats using genotype data taken from caprine 50K SNP BeadChips. Additionally, genome-wide selection signatures covering a number of genes that either directly or indirectly impacted features for hot and dry environment adaptation, like thermotolerance, body growth and development, energy and digestion metabolism, and immunological and neurological response, were found. Using genotypic data from the Illumina Goat 50K Beadchip, Brito et al. [31] were able to identify genetic diversity across nine goat groups. The population showed moderate to high levels of genetic diversity. The Runs of Homozygosity provided information about the evolutionary history of the breeds. Using an SNP panel, Berihulay et al. [61] found that the Chinese goat population had significant within-breed diversity and low to moderate levels of genetic variability. Animal genetic resources can be conserved and used sustainably by taking advantage of this within-breed variability.

7. CONCLUSION

The indigenous goat population must be genetically characterised in order to maintain the genomic variability that is necessary for both genetic conservation and improvement. This can be achieved by properly planning in-situ conservation programmes and collaborating with other research organisations as well as farmers collectively. For research on population structure and diversity in Indian goat populations, microsatellite and mtDNA markers are utilised as genetic markers. Advances in genomic technologies have led to the development of SNP Chips, which provide a better resolution of genome-wide variation.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models

(ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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