

ABSTRACT

For microsatellite genetic diversity study, there is a lack of concern for the conservation and improvement of goat breeds under field conditions. However, there is worldwide recognition of the need for the conservation of livestock diversity and for characterization of breeds and populations including their genetic differentiation and relationships. These unique characteristics are the result of evolutionary forces and their interactions over longer periods of time. However, these adaptation and unique characteristics might have been diluted due to intermixing, sub- structuring and/or consequent genetic drift in the population over the time. No studies has been done to estimate the inbreeding level in the field animals thus how various forces of genetic change are modifying the foundation genetic structure of the population is not known. Therefore, an investigation of genetic variation within and between breed, and its structure may help to evaluate these factors, and provide genetic information to be used for conservation prioritization and improvement of Jamunapari, Malabari, Osmanabadi and Sangamneri goat breeds having unique characteristics. In conservation prioritization it is important to know whether these breeds/populations are genetically unique or they are less differentiated to become OTU (Operational Taxonomic Units). Microsatellite loci out of many genetic markers now available are best suited for answering some of these questions.

In genetic differentiation and genetic distance this analysis showed that microsatellites analysis can be used to classify Indian goat populations into distinct genetic groups or breeds. Phylogenetic and principal component analysis showed the clustering of goats according to their geographical origin. Although the breeding tracts of goats are overlapping and they are spread over all the parts of the country, they still maintain genetic distinctness in their natural habitat; it would be prudent to manage the different populations individually to preserve their genetic uniqueness. The result also revalidates the heterologous microsatellite markers' effectiveness in analyzing close population/breeds.