1. Introduction

India is considered as reservoir of diverse cattle genetic resources represented by 30 well recognized and many uncharacterized populations. The Indian zebu cattle (Bos indicus) are broadly categorized into dairy, draft and dual purpose breeds depending upon their utility. Most of these native cattle breeds have evolved over the years for their utility under particular agro-climatic conditions that ranged from good milch animals to extreme draught type, tall to small stature and highland cattle to those adapted to arid climate. Some of the features like adaptability to extreme climatic conditions, subsistence on poor feed and fodder and better capabilities to withstand environmental stress/diseases make Indian native cattle a rich source of highly evolved gene pool of immense economic importance.

The indigenous cattle form an important and integral component of Indian agriculture system which is essentially ‘organic’ in nature. Moreover, these cattle are well adjusted to low input production system and are important to the respective regions of our country. Indian cattle breeds are excellent resource for genetic evaluation as they present traits different from those of the highly selective taurine/exotic breed (Bos taurus). In the past, important native breeds like Ongole, Gir, Sahiwal, Krishnavalley having excellent adaptability traits had attracted several countries (Brazil, USA, Argentina, Mexico etc.) to import this germplasm for upgradation of their native breeds.

Although cattle in India is the most important livestock species and plays a major role in agricultural economy, yet population of some of the important cattle breeds is either declining or breed characters are being diluted under the present production system. With the emergence of cross breeding, several traditionally reared indigenous breeds have suffered genetic erosion with a steep decline in the pure bred populations. Preference for few selected breeds has also been leading to
the continuous displacement of many of the breeds. Although maintaining cost for cross-bred cattle in tropical country like India is high due to problems of feed and fodder scarcity, frequent incidence of parasitic infestations and other disease infections, and high mortality etc., yet there has been unplanned cross breeding in lieu of getting higher milk production.

This dilution in cattle genetic resources might result in loss of important gene combinations responsible for adaptive traits, further leading to loss in genetic variability. It is now realized that preserving these naturally evolved gene pool would be important for long-term genetic improvement and meeting the future challenges. Selection of the breeds for conservation or improvement programs so as to maintain maximum genetic diversity through an objective breed classification based on phylogenetic distinctness is a globally accepted criterion (May, 1990; Hall and Bradley, 1995). This approach has also an integral part of Food and Agricultural Organization’s (FAO’s) global strategy for measurement of domestic animal diversity (MoDAD) to facilitate conservation and management of farm animal genetic resources.

However, the genetic relationship between the native cattle breeds of India is largely unknown. Over the years, assignment of these cattle breeds had often been based on morphological data and information gained from the local sources (Nivsarkar et al., 2000). With the limited national resources, inclusion of each breed for genetic improvement and conservation might not be a feasible proposition. Thus the key issues like deducing the genetic structure and distinctness amongst the Indian native cattle breeds becomes pertinent. Consequently, a comprehensive effort to undertake genetic characterization of Indian cattle breeds has become an essential prerequisite for development of rational genetic management strategies.

Arrays of molecular markers have opened new vistas to exploit DNA polymorphism in genetic characterization and molecular evolution studies. Amongst the current genomic technologies, microsatellites also known as simple tandem repeats (STRs) or short simple repeats (SSRs) are the most preferred markers for diversity analysis of animal genetic resources due to their highly
informative nature, abundance and amenability to automation. The discovery of numerous species specific microsatellite markers has revolutionized the genetic linkage mapping efforts for bovine, ovine, porcine, and chicken (Bishop et al., 1994; Eggen and Fries, 1995, Archibald et al., 1995; Rohrer et al., 1996; Barendse et al., 1997, Kappes et al., 1997, Groenen et al., 2000). This has led to applications in QTL identification, fine mapping, marker assisted selection and genetic diversity analysis in livestock species.

Several microsatellite marker based studies on genetic structure, relationships and introgression have been reported in different cattle populations from Africa, Europe and Asia (MacHugh et al., 1998; Martin-Burriel et al., 1999; Mommens et al., 1999; Beja-Pereira et al., 2003; Jordana et al., 2003; Ibeagha-Awemu and Erhardt, 2005). In contrast, not many studies have been undertaken to define the evolutionary relationship amongst the native Indian cattle breeds of different agroclimatic zones and geographical regions of India. More recently, few isolated efforts had been made to characterize the genetic variability in one or two Indian cattle breeds but comprehensive genetic structure and their relationship has not been taken up.

Recently, in addition to microsatellites (type-II) markers, much attention has been given to utilize type I (gene based) marker system which has become an integral strategy to reveal the holistic picture of the existing genetic diversity and relationships amongst the livestock breeds. The exploitation of type-I markers has attracted researchers to characterize the variations in and around candidate genes predisposing to traits of economic importance (Moody et al., 1995; Lagzeil et al., 2000; Chrenek et al., 2003; Thaller et al., 2003; Winter et al., 2005) as in livestock, the phenotypic differences between breeds might be due to differences in few gene loci. The typing of allelic variations of the genes of importance might be a promising strategy for trait specific gene characterization, genetic differentiation and population structure of native cattle breeds.

Several gene based polymorphisms have been reported in different exotic Bos taurus cattle. Such efforts are negligible in Indian native cattle breeds which may harbour unique alleles, different from those of exotic cattle. Characterization
of the polymorphism at major genes affecting economic traits in native cattle breeds would unravel their status in terms of gene frequencies/gene diversity. The allelic profile thus available would allow comparisons with *Bos taurus* genome which portray traits different from *Bos indicus*. Further, such study would lead to evaluate different allelic variants for marker-phenotype association in Indian cattle breeds. Thus systematic and concerted efforts should therefore be made to characterize the polymorphisms occurring at candidate genes influencing milk production/composition and growth traits in native cattle breeds. The variation in allele/genotypic frequencies at these economically important gene loci may provide valuable information related to the functional differences, if any, between the investigated cattle breeds.

The present work has thus been intended to assess the overall genetic diversity in six Indian zebu cattle breeds from Rajasthan and Gujarat states based on SSR/microsatellite markers and functional gene based markers. The cattle breeds included in this study represented all the three utility classes such as milch type (Tharparkar, Rathi and Gir); dual type (Kankrej) and draught type (Nagori and Mewati) which have immense regional importance in sustaining the livestock keepers of the respective region.

Considering the above issues, an effort has been made to reveal overall genetic diversity and structure of relationships of six Indian native cattle breeds with the following objectives:

- To characterize genetic diversity in Indian zebu cattle breeds using microsatellite (SSRs) DNA markers
- To identify and characterize the genetic variations in Indian zebu cattle breeds at selected candidate gene loci affecting traits of economic importance
- To reveal the overall genetic diversity, breed structure and relationships amongst the investigated cattle breeds based on analyzed molecular markers.