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A genetic dissection of breed composition in well-known taurine, indicine, and crossbred cattle by using SNP genotyping.

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Abstract : In this study, the genotype data (50K SNP bead chip data) was used for a total of 156 representative animals belonging to seven indicine and four taurine breeds of cattle. A total of 43,041 SNPs common for all the breeds were taken into account for the present study. Using the Bayesian approach, STRUCTURE software was run on the data set. Under each value of K (2-12), the indicine and taurine breeds were distinctly separated, with poor differentiation of breeds within the two lineages. The results from principal component analysis were in accordance with separate identities of the two lineages. The study was extended under similar conditions to hybrid Santa Gertrudis individuals, with 10 individuals included from hybrid and purebred constituent populations and the tools used in the study efficiently differentiated the individuals from pure breed and crossbred populations. It may be concluded that these Bioinformatics and statistical softwares are efficient in determination of clustering, introgression and admixture levels in different purebred and crossbred populations of India.

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Indexing terms for this abstract:

Organism descriptor(s) : cattle, Santa Gertrudis, zebu

Descriptor(s) : Bayesian theory, bioinformatics, breed differences, breeds, cattle breeds, crossbreds, crosses, genotypes, hybrids, population genetics, principal component analysis, single nucleotide polymorphism, zebu breeds

Identifier(s) : animal breed, animal breeds

Geographical Location(s) : India

Broader term(s) : Bos, Bovidae, ruminants, Artiodactyla, mammals, vertebrates, Chordata, animals, eukaryotes, cattle, Commonwealth of Nations, lower-middle income countries, medium Human Development Index countries, South Asia, Asia

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