

Population Structure Analysis of Pakistani Indigenous Cattle Population by Using High Density SNP Array

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Abstract : Genetic differences associated with speciation, breed formation or local adaptation can help to preserve and effective utilization of animals in selection programs. Analyses of population structure and breed diversity have provided insight into the origin and evolution of cattle. In this study, we used a high-density panel of SNP markers to examine population structure and diversity among ten Pakistani indigenous cattle breeds. In total, 25 individuals from three cattle populations, including Achi (n=08), Bhagnari (n=04) and Cholistani (n=13) were genotyped for 777, 962 single nucleotide polymorphism (SNP) markers. Population structure was examined using the linkage model in the program STRUCTURE. After characterizing SNP polymorphism in the different populations, we performed a detailed analysis of genetic structure at both the individual and population levels. The whole-genome SNP panel identified several levels of population substructure in the set of examined cattle breeds. We further searched for spatial patterns of genetic diversity among these breeds under the recently developed spatial principal component analysis framework. Overall, such high throughput genotyping data confirmed a clear partitioning of the cattle genetic diversity into distinct breeds. The resulting complex historical origins associated with both natural and artificial selection have led to the differentiation of numerous different cattle breeds displaying a broad phenotypic variety over a short period of time.

Keywords : Pakistan, cattle, genetic diversity, population structure

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