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Genetic structure and diversity in a Guzerat metapopulation (*Bos indicus*) estimated from microsatellite markers

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The Guzerat breed (*Bos indicus*) is original from India, particularly from the dry lands of the region of Kankrej. Animals from this breed demonstrated good beef and dairy potentials under the environmental conditions in Brazil, after their introduction in this country by the end of the nineteenth century. Guzerat was prevalent in Brazil until the 1930s, when the effective population size of this breed started being considerably reduced because of their intense use in crossbreeding schemes. In 1994, the National Brazilian Guzerat Dairy Breeding Program started with the objective of improving the productivity of this breed, which is an important tropical genetic resource. The possibility of a reduction in the number of sires used by the breeders became a concern, concurring to the reduction of the genetic variability in the population, because breeders would focus on a small number of superior individuals identified under the genetic evaluations. The objective of this study was to evaluate the genetic diversity in a metapopulation from the Guzerat breed in Minas Gerais state. Population structure was accessed using molecular information within two approaches, among herds or among lineages. Blood samples from 10% of the animals within 15 major herds have been collected randomly, in a total of 744 animals. Most herds had been usually selected for dual purpose, beef and milk, while some were selected for beef only. Individual DNA samples obtained were amplified by PCR and submitted to capillary electrophoresis in MegaBACE 1000 equipment (GE Healthcare), for genotyping on 21 microsatellite markers, previously tested regarding their polymorphism and heterozygosity. Population structure in herds or lineages was analyzed with F_{ST} statistics from individual genotypes using the FSTAT program (version 2.9.3.2) (Goudet, 2001). Additionally, each subpopulation F_{IS} and pair-wise F_{ST} values were calculated using the software Molkin v3.0 (Gutiérrez et al., 2005). Average F_{ST} was 0.027 (± 0.002) for the herd approach, or 0.034 (± 0.002) for the lineage approach. These results indicated the existence of a structured population in both cases, but a more evident structure was observed in the approach where the subpopulations were differentiated according to lineages, which could be an evidence of a current increased gene flow among herds. In general, dual purpose lineages showed smaller values of average pair-wise F_{ST} when compared to beef lineages. These results indicated that dual purpose lineages would present superior gene flow within the metapopulation. One lineage selected for milk production showed the biggest average F_{ST} , indicating it was the subpopulation with the smallest gene flow within the metapopulation. F_{IS} statistics ranged from -0.048 to 0.077, indicating heterozygosity loss in some lineages, which could be caused by inbreeding. It was concluded that the studied metapopulation was structured in subpopulations with various degrees of genetic diversity. Keywords: Financial Support: Fapemig e CNPq.

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