

Analysis of STR Markers Reveals High Genetic Structure in Portuguese Native Cattle

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Genetic structure and diversity of 13 Portuguese native and 3 imported cattle breeds were assessed with 39 microsatellites. Allelic richness per locus was high, with an overall average of 8.3 ± 2.5 . The mean observed and expected heterozygosities were 0.673 ± 0.043 and 0.691 ± 0.034 , respectively. The mean number of alleles per breed ranged between 5.36 ± 1.27 and 7.87 ± 2.66 . Brava de Lide and Mirandesa breeds had the lowest genetic diversity, whereas Minhota, Arouquesa, and Mertolenga had the highest. Significant ($P < 0.05$) heterozygote deficit was detected in all breeds except Garvonesa, Marinhoa, Minhota, and Limousin. Hardy-Weinberg deviations are most probably due to inbreeding, particularly in Alentejana, Brava de Lide, Mertolenga, and Ramo Grande ($F_{is} > 0$, $P < 0.0001$). Based on the principal component and the Neighbor-Net analyses, Mirandesa was the most genetically distinct breed. Even though admixture was detected across all breeds (6.7%, $q < 0.800$), the molecular structure was consistent with original breed designations, with the exception of Cachena that had a clear influence of Barrosã ($K = 15$). Mertolenga showed substructure with independent clustering of red speckled animals. The percentage animals correctly assigned was ≥ 90 in all breeds except Cachena, Garvonesa, and Preta ($q \geq 0.800$). The results obtained here confirmed that high levels of genetic diversity exist within Portuguese native cattle and that the breeds are highly structured. Conservation measures should be implemented for all native breeds to minimize inbreeding.

Key Words: native cattle • microsatellites, genetic structure • admixture • breed assignment