



Genetic variability in Blanco Orejinegro breed cattle populations in Colombia

R. Martínez, A.P. Llinás and J.F. M.-Rocha

Centro de Biotecnología y Bioindustria,
Corporación Colombiana de Investigación Agropecuaria, Mosquera, Colombia

Corresponding author: J.F. M.-Rocha
E-mail: juanfelipemrocha@gmail.com

Genet. Mol. Res. 12 (2): 1083-1094 (2013)

Received June 1, 2012

Accepted September 12, 2012

Published April 10, 2013

DOI <http://dx.doi.org/10.4238/2013.April.10.4>

ABSTRACT. We analyzed population structure and genetic diversity in Blanco Orejinegro Creole cattle with 12 microsatellite markers, genotyping 138 individuals belonging to 7 commercial and 3 conservation herds. These markers showed a high level of polymorphism; 171 alleles were identified. The mean number of alleles per locus was 5.63 (3.82-6.58). The total number of alleles per marker was 14.2 and ranged from 16 (TGLA126) to 22 (TGLA227). The mean expected heterozygosity (0.73) was higher than the observed heterozygosity (0.65), with a significant excess of heterozygosity in almost all populations ($F_{IS} = 0.09$; $P < 0.05$). This may be due to crossing between different lines of this breed, affecting the inbreeding levels. Analysis of relationships among populations, assessed by principal component analysis and Nei's genetic distances, indicated a close relationship between some herds. Furthermore, analysis of population structure demonstrated a low probability of admixture with Zebu breeds, as it shows the cluster assignment and the F_{ST} values obtained. We conclude that there is high allelic diversity in this breed, even though a low effective population size has been maintained and the level of inbreeding has not been monitored. Therefore, appropriate conservation

efforts should be undertaken, such as adopting strategies aimed at minimizing inbreeding, to avoid losing genetic variability.

Key words: Genetic diversity; Microsatellite markers; Population genetic structure