

A STUDY OF GENETIC VARIABILITY IN CANCHIM (5/8 CHAROLAIS, 3/8 ZEBU) BASED ON 8 MOLECULAR MARKERS

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Introduction

The canchim is a synthetic beef cattle breed, produced by crosses between Charolais (*Bos taurus*) and several *Bos indicus* breeds (Zebu). With a genetic composition of 5/8 Charolais + 3/8 Zebu, Canchim combines growth ability associated with a *Bos taurus* breed and tolerance to tropical environments that is attributed to Zebu breeds. The herd used in this study was formed in 1953 and subjected to phenotypic selection for yearling weight and fertility, under pasture management. Even though the average inbreeding coefficient was kept low by avoiding consanguineous mating (Alencar *et al.*, 1981), genetic variability losses could be expected as a result of selection and restricted effective number (N_e), since there was no introduction of outside animals. The objective of this study was to evaluate genetic variability parameters estimated from molecular data.

Material and methods

Molecular markers were selected to represent different chromosomes. From the eight markers analyzed, five were microsatellites (CSFM50, IGF-1, TEXAN15, BM1224 and INRA006) and three were RFLPs, in the coding region of κ -casein (CSN3), β -lactoglobulin (LGB) and growth hormone (GH), respectively. DNA samples from 142 Canchim animals were extracted from white blood cells. Polymerase chain reaction was performed in a volume of 25 μ l containing 200 ng of bovine genomic DNA, 0,2 μ M each dNTP, 0,4 μ M each primer, 0,5 unit of Taq DNA polymerase and PCR Buffer (20 mM Tris-HCl, pH 8,4; 1.5 mM $MgCl_2$; 50 mM KCl). With the exception of Texan15, microsatellite forward primers were end labeled with ³²P so that PCR products could be analyzed after electrophoresis in 6% denaturing polyacrylamide gels and autoradiography. TEXAN15 microsatellite marker was analyzed by silver staining of polyacrilamide gels and RFLPs in 3% agarose gels stained with etidium bromide. Allele frequencies were estimated for each locus by direct count. Population variability measures, heterozigosity (H) and genetic diversity (D) were estimated using the software Biosys.

Results and discussion

All loci analyzed were polymorphic and, with the exception of IGF-1 and GH, genotype distributions were in Hardy-Weinberg equilibrium. Disequilibrium at those two loci might be related to selection (Regitano et al., 1999). Values of observed heterozygosity (H) and expected heterozygosity or gene diversity (D) were high even for diallelic loci, such as CSN3 and LGB (Table 1). Mean values were comparable to the reported in Brangus Ibagé, another 5/8 *Bos taurus*, 3/8 *Bos indicus* crossbred (Almeida et al., 2000). Polymorphic information content (PIC) values, a measure of the utility of a marker for mapping applications, were higher for microsatellite loci (Table 1).

Table1 – Observed number of alleles (NA), heterozygosity (H), gene diversity (D) and polymorphic information content (PIC) for the eight markers.

Locus (marker) ¹	NA	H	D	PIC
CSN3 (RFLP)	2	0.479	0.452	0.350
LGB (RFLP)	2	0.507	0.494	0.372
GH (RFLP)	2	0.070	0.189	0.171
CSFM50 (M)	6	0.754	0.741	0.705
IGF-1 (M)	4	0.549	0.638	0.571
TEXAN15 (M)	9	0.606	0.807	0.780
BM1224 (M)	6	0.648	0.708	0.661
INRA006 (M)	7	0.739	0.686	0.627
Mean (s.d.) ²	4.75 (±0.9)	0.544 (± 0.076)	0.589 (± 0.072)	

¹Marker type is indicated by parenthesis (RFLP – Restriction Fragment Length Polymorphism, M – microsatellite); ²Standard deviation.

Conclusions

Estimates of genetic variability based in the analysis of eight molecular markers suggest that, even after 50 years of selection in a closed herd, this Canchim population still has a high genetic variability.

References

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