A SURVEY OF NELLORE BREED BASED ON NINE MOLECULAR MARKERS.

D. D. Tambasco[1]; M. M. de Alencar[2]; L. L. Coutinho[3] ; I. U. Packer[3]
M. Tambasco-Studart[1] and L. C. A. Regitano[2]
[1]Departamento de Genética e Evolução UFSCar, São Carlos, SP;
[2]Embrapa Pecuária Sudeste, São Carlos, SP;
[3]Departamento de Produção Animal – ESALQ/ USP, Piracicaba, SP.
luciana@cppse.embrapa.br

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Introduction

The Brazilian Nellore is a *Bos indicus* breed developed from animals imported from India up to the middle of this century. Due to its high tolerance to the tropical environment, the Nellore became the most popular beef cattle breed in Brazil. Besides its importance as pure breed, it has been successfully used in commercial crosses and in the composition of new breeds. Genetic variability provides the scenario for selection in animal breeding programs. Monitoring this variability through molecular marker analysis can be useful to prevent genetic erosion. The objective of this study was to characterize Nellore animals based on restriction fragment length polymorphisms (RFLP) and microsatellites.

Material and methods

Microsatellites TEXAN15, BM1224, BM8246, BM7160, BM6026 and CSFM50 and the RFLPs κ-casein (CSN3) - *Hinf*I, β-lactoglobulin (LGB) - *Hae*III and growth hormone (GH) - *Alu*I, were chosen to represent nine different chromosomes. With the exception of BM7160 and BM6026, for which 115 animals were escored, all markers were analyzed in 180 Nellore females representing 8 herds. DNA was obtained from white blood cells. Polymerase chain reactions were performed in a volume of 25 µl containing 200 ng of DNA template, 0,2 µM each dNTP, 0,4 µM 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). Microsatellites TEXAN15, BM1224, BM7160 and BM6026 were analyzed in a fluorescence automated sequencer. CSFM50 and BM8246 markers were analyzed by silver staining in 6% polyacrilamide gels. Allele frequencies were estimated for each locus by counting. Populational variability measures, heterozigosity (H) and genetic diversity (D), as well as the polymorphic informative content (PIC) and the paternity exclusion probability (PE), were calculated.

Results and discussion

Mean values of H and D (Table 1) were slightly lower than those observed for Simmental sample in a study using the same markers (Tambasco-Studart, in preparation), for Canchim and Charolais (Regitano, 1997) and for Brangus Ibagé (Almeida et al., 2000). The GH locus was

monomorphic in this sample. The allele L fixation was observed also in other Brazilian zebu herds (Kemenes et al., 1999). The PIC values observed for the eight polymorphic markers are in agreement with the expected since diallelic markers have lower polymorphic informative content than the multiallelic microsatellites.

Table1 – Observed number of alleles, heterozigosity (H), genetic diversity (D), polymorphic informative content (PIC) and paternity exclusion probability (PE) for the nine markers.

Locus (marker)[1]	Number of alleles	H	D	PIC	PE
CSN3 (RFLP)	2	0,111	0,105	0,101	0,051
LGB (RFLP)	2	0,244	0,365	0,298	0,165
GH (RFLP)	1	0,000	0,000	0,000	0,000
BM1224 (M)	10	0,311	0,729	0,685	0,521
BM6026 (M)	9	0,700	0,724	0,630	0,612
BM7160 (M)	10	0,645	0,715	0,715	0,557
BM8246 (M)	14	0,711	0,866	0,845	0,732
TEXAN15 (M)	9	0,577	0,589	0,554	0,389
CSFM50 (M)	5	0,669	0,661	0,641	0,466
Mean	6,890	0,441	0,528	-	0,994 [2]

[1]The marker is indicated by parenthesis (RFLP – Restriction Fragment Length Polymorphism, M – microsatellite). [2]CPE – combined paternity exclusion probability.

Conclusions

Mean values of H and D reveals a somewhat narrow genetic basis of the Brazilian Nellore breed, when compared to European continental breeds. With the exception of GH, all markers used in this survey could be useful to monitor genetic variability of Nellore breeding stocks. The PIC and PE parameters demonstrate the advantage of microsatellites over the RFLPs for genetic mapping and pedigree analysis.

References

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