

GENETIC DISTANCES AMONG ABERDEEN ANGUS, CANCHIM, CARACU, NELLORE AND  
SIMMENTAL BEEF CATTLE BREEDS.

L. C. A. Regitano<sup>1</sup>; L.P.M.K. Vasconcellos<sup>2</sup>, E. Jacinto<sup>3</sup>, M. Tambasco-Studart<sup>2</sup>, D. D. Tambasco<sup>2</sup>,  
K. Euclides Filho<sup>4</sup>, P. F. Barbosa<sup>1</sup>; I. U. Packer<sup>5</sup> and L. L. Coutinho<sup>5</sup>.  
<sup>1</sup>Embrapa Pecuária Sudeste, CP 339, CEP: 13560-970, São Carlos, SP, Brazil. <sup>2</sup>Departamento de  
Genética e Evolução – UFSCar, São Carlos, SP. <sup>3</sup>Curso de Medicina Veterinária,  
UFPR – Campus de Palotina. <sup>4</sup>Pesquisador da Embrapa Gado de Corte.  
<sup>5</sup>Departamento de Produção Animal – ESALQ/ USP, Piracicaba, SP, Brazil.  
luciana@cppse.embrapa.br

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### Introduction

Bovine breeds started to be selected in the old world, during the 19th century. The starting populations were varieties of cattle adapted by natural selection to the local environment. Now a days, a large quantity of specialized bovine breeds are spread all over the world. Several of these are exploited for meat production in Brazil. The objective of the present work was to investigate the genetic relationship among some of these breeds, representing beef cattle from different categories: Caracu, a European breed adapted to tropical environment, Simmental, a continental European breed, Aberdeen Angus, a representative of British Isles breeds, Canchim, a crossbred (5/8 Charolais, 3/8 *Bos indicus*) and Nellore, the most relevant *Bos indicus* beef cattle breed in Brazil.

### Material and methods

DNA samples were collected from 46 Caracu, 52 Aberdeen Angus, 52 Simmental, 180 Nellore and 142 Canchim cattle. Genotypes for 3 Restriction Fragment Length Polymorphisms (CSN3- *Hinf*I, LGB-*Hae*III and GH-*Alu*I) and two microsatellite loci (CSFM50 and Texan15) were determined after polymerase chain reaction (PCR). Reactions were set up with 200 ng of DNA template, 0,2  $\mu$ M each dNTP, 0,4  $\mu$ M each primer, 0,5 unit of Taq DNA polymerase and PCR Buffer (20 mM Tris-HCl, pH 8,4; 1.5 mM MgCl<sub>2</sub>; 50 mM KCl), in a volume of 25  $\mu$ l. RFLP genotypes were determined by analysis of restriction endonuclease digestion of PCR products in 3% agarose gel electrophoresis, ethidium bromide stained. Microsatellites PCR products were scored in 6% polyacrilamide gels, either by silver staining, isotopic or fluorescent labelling. Allele frequencies, heterozygosity (H), gene diversity (D) and Nei's unbiased genetic distance (Nei, 1978) for the five molecular markers were calculated using the software Biosys (Swofford and Selander, 1989). Clustering analysis was performed using Unweighted Pair-Group Arithmetic Mean (UPGMA).

## Results and discussion

With the exception of GH- *AluI*, which was monomorphic in the Nellore breed, all markers were polymorphic in all populations. Allele numbers varied from two, in the RFLP systems, to 11 in Texan15. The highest H and D values were observed in Caracu, followed by Canchim, Simmental, Aberdeen Angus and Nellore. Genetic distances are shown in Table 1. All *Bos taurus* breeds were clustered together by the UPGMA analysis, with a closer genetic relationship between Canchim and Simmental, while Caracu and Aberdeen Angus were placed in a second group. Nellore, the only *Bos indicus* breed represented in this study, was set in a isolated group. The closer resemblance between Canchim and Simmental was expected since Canchim has 5/8 of genetic contribution of Charolais which, as Simmental, is also a short-horned European breed, probably descendent of *Bos longifrons* (Friend and Bishop, 1978).

Table 1. Genetic distances (Nei unbiased, 1978) among four *Bos taurus* and one *Bos indicus* bovine breed, with regard to five molecular markers.

	A. Angus	Caracu	Simmental	Nellore	Canchim
A. Angus					
Caracu	0.051				
Simmental	0.152	0.164			
Nellore	0.144	0.120	0.234		
Canchim	0.106	0.082	0.046	0.113	

## Conclusions

Genetic distances calculated for the five bovine breeds are in accordance with breed's history. The high genetic variability found for Caracu suggests successful conservation efforts.

## References

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