GENETIC VARIABILITY AMONG BRAZILIAN SHEEP USING MICROSATELLITES

Paiva, S.R.[1]; Faria D.A.[2]; Silvério V.C.[1]; McManus C.[3]; Egito A.A.[1]; Dergam J.A.[2]; Guimarães S.E.F.[2]; Castro S.R.[1]; Albuquerque M.S.M.[1]; Mariante A.S.[1]

[1]Embrapa Genetic Resources and Biotechnology, Laboratory of Animal Genetics, 70770-900, Brasilia-DF, Brazil; samuel@cenargen.embrapa.br;
[2]University of Viçosa, Viçosa-MG, Brazil; [3]University of Brasilia, Brasília- DF, Brazil.

Summary

A total of 18 loci were examined in 297 animals in five naturalised breeds and three exotic breeds of sheep in Brazil. Results show that 12.87% of total variation (p<0.001) was due to inter-breed differences. Inter-breed results suggest low genetic differentiation between the breeds studied, while intra-breed results indicate the genetic quality of the herds examined and permit management decisions to be taken.

Keywords
Animal genetic resources, conservation genetics, gene flow, genetic distance, *Ovis aries*.

Introduction
Sheep were introduced to Brazil 5 centuries ago and at present, after years of natural selection, these are known as "crioulas", "local" or "Brazilian naturalised" (Mariante *et al.*, 1999). Nevertheless, some breeds are threatened with extinction due to absorbent crossing with commercial breeds. The molecular characterization of existing naturalised herds is a desirable initial step to aid management and conservation strategies of Brazilian breeds. The objective of this study was to evaluate genetic diversity between eight breeds of *Ovis aries* in Brazil using microsatellite markers.

Material and Methods
Blood was collected from 297 sheep of the breeds Santa Inês, Bergamácia, Rabo Largo, Morada Nova, Somalis, Ile de France, Corriedale and Hampshire. After DNA extraction, PCR reactions (*Polymerase Chain Reaction*) were carried out for 18 micro satellite *loci* (*OarFCB20, ILSTS05, OarFCB48, ILSTS11, ILSTS87, INRA35, INRA05, INRA63, OarAE129, OarFCB304, OMHC1, OarHH35, OarJMP29, INRA23, MAF65, MAF214, BM827, HUJ616*). Genotyping were carried out using an ABI Prism 310 automatic sequencer and analysed using Genescan software (*Applied Biosystems*). Statistical analyses were carried out using Arlequin (Schneider *et al.*, 2000), Genepop (Raymond e Rousset, 1995) and Dispan (Ota, 1993) softwares.

Results and Discussion
Data from the analysis of molecular variance (AMOVA) show that 12.87% of total observed variance (p<0.001) was due to inter-breed differences. Intra-breed variability (Table 1) showed that the Santa Inês breed had highest heterozygosity values as well as mean number of alleles per *locus* (0.7580 and 8.39 respectively) while the Somali and Corriedale breeds had the lowest values for these indices respectively (0.5752 and 4.22). With the exception of the Hampshire, all breeds had inbreeding coefficients (F_{IS}) less than 10%.

TABLE 1. Number of samples (N); Expected heterozygosity (HE); Observed heterozygosity (HO); Mean number of alleles per breed (N.A.); Inbreeding coefficient at individual level within breed (Fis), for the 18 micrsatellite loci studied in eight sheep breeds in Brazil.

BREED	N	HE	HO	N.A.	F_{is}
Santa Inês	48	0,7580	0,7203	8,39	0,050
Bergamácia	46	0,7232	0,6711	7,11	0,073
Rabo Largo	48	0,6491	0,6272	6,28	0,034
Morada Nova	48	0,7188	0,6592	7,33	0,084
Somalis	48	0,5752	0,5687	5,50	0,012
Hampshire	24	0,7027	0,6282	7,06	0,108
Ile de France	24	0,7151	0,6822	5,94	0,047
Corriedale	11	0,6011	0,6031	4,22	-0,004

The dendrogram (Figure 1) shows the breeds divided into two main groups. In the first group, formed by naturalised Brazilian breeds, the Santa Inês was closer to the Bergamácia and these closer to the Rabo Largo than the Morada Nova. In spite of this, the Morada Nova showed lower genetic distance in ration to the Santa Inês. The second group was made up of the exotic wool breeds.
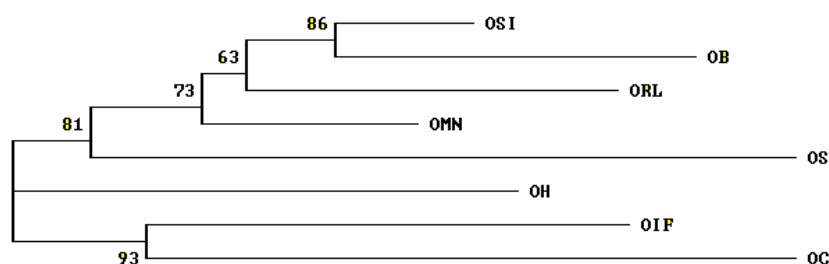

FIGURE 1. Dendrogram of genetic relationship between sheep breeds in Brazil using Nei´s genetic distance (1983), and Neighbour joining algorithm, from 18 microsatellite loci. OSI: Santa Inês; OB: Bergamácia; ORL: Rabo Largo; OMN: Morada Nova; OS: Somalis; OH: Hampshire; OIF: Ile de France; OC: Corriedale.

Inter-breed results and AMOVA suggest small genetic differences between sheep breeds in Brazil, in agreement with earlier results using RAPD markers (Paiva *et al.*, 2003). The implementation of management and conservation measures is necessary to reduce inbreeding in the Morada Nova and increase variability in the Somali breeds. New markers and breeds shall be included in this study to maximise knowledge on genetic variability and breed origin of Brazilian sheep.

REFERENCE LIST

[1] MARIANTE A. da S., ALBUQUERQUE M. do S.M., EGITO A.A. & McMANUS C. Advances in the Brazilian animal genetic resources conservation progamme. Animal Genetic Resources Information 25, 109-123, 1999.

[2] OTA T. DISPAN: genetic distance and phylogenetic analysis. Pennsylvania State University Park, PA. 1993.

[3] PAIVA, S.R.; SILVÉRIO, V.C.; EGITO, A.A.; MACMANUS, C.; FARIA, D.A.; MARIANTE, A.S.; CASTRO, S.R.; ALBUQUERQUE, M.S.M.; DERGAM, J. Caracterização Genética da Raça Santa Inês. In: 2ND International Symposium on Sheep and Goat Production, 2003, João Pessoa. Anais do Segundo Sincorte. João Pessoa: Empresa Estadual de Pesquisa agropecuária da Paraíba, 2003. v. Único, p. 487-499.

[4] RAYMOND, M.L. & ROUSSET, F. An exact test for population differentiation. Evolution 49, 1280-1283. 1995.

[5] SCHNEIDER S., ROESSLI D. & EXCOFFIER L. Arlequin, ver.2.000: A software for population genetic data analysis. Genetics and Biometry Laboratory, University of Geneva, Switzerland, 2000. 113p.