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Research Article

Genetic diversity between herds of Alpine and Saanen dairy goats and the naturalized Brazilian Moxotó breed

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Abstract

Brazilian naturalized goat breeds are adapted to the semiarid conditions prevalent in the Northeast region of the country (which has the largest Brazilian goat heard) and represent an as yet uninvestigated source of genetic diversity. Currently, imported goat breeds are crossed with Brazilian naturalized goat breeds, endangering the genetic potential of the naturalized breeds. We used 11 microsatellite markers to determine the genetic diversity among imported (non-naturalized) dairy Alpine and Saanen goats and naturalized Brazilian Moxotó goats. We genotyped 292 goats from three herds (one private, one from the University of Minas Gerais and the Moxotó conservation herd from Embrapa Caprinos) and found that the general heterozygosity was 0.6952 for Alpine, 0.7043 for Saanen and 0.4984 for Moxotó goats. The number of alleles ranged from 5 (*INRA005*) to 11 (*BM3205*), with an average of 7 alleles per locus in the imported breeds and 3.5 alleles per locus in the Moxotó breed. Mean differentiation between populations was higher for herds ($F_{ST}S = 0.0768$) than for breeds ($F_{ST}P = 0.0263$), indicating similarity between the imported breeds and the existence of crosses between them. Nei's genetic distance was highest between the Moxotó breed and the imported breeds. These indicate that further studies using these molecular markers would be fruitful.

Key words: conservation, DNA microsatellite, genetic distance, genetic diversity, goats.

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Introduction

In Brazil the most important dairy goat (*Capra hircus*) breeds are of European origin, mainly imported from France. The Saanen breed is intensively reared, especially in the Southeastern region, while the Alpine breed is very numerous in the dairy herds of the Northeast where it is widely employed for crossing with naturalized breeds to produce groups of goats called 'Parda Sertaneja' in Portuguese (Machado, 2000).

The semiarid Northeastern region of Brazil has the largest goat flock with almost all small farms having at least one goat, most of which are of undefined breed resulting from crosses between the different goats brought into the country during colonization. Another large group is the Brazilian naturalized standard breeds such as the Moxotó, Marota, Canindé and Repartida groups which are classified as naturalized because they are descendants of those animals introduced during colonization and have undergone strong natural selection in order to adapt to the semiarid conditions. Although both undefined breeds and standard breeds descend from imported goats the recent breeding history of the standard breeds is known and their characteristics are more standardized than goats of undefined breed.

The most traditional Brazilian naturalized standard goat breed is the Moxotó breed, originally developed in the Brazilian state of Pernambuco (Machado, 2000) and characterized by desirable traits such as disease resistance, fecundity and the ability to produce high quality leather, although this breed produces only small amounts of milk and meat. However, crosses between imported breeds and Moxotó goats make this breed vulnerable and might lead to

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the loss of genetic resources in goat farming in the future, because of which conservation studies are urgently needed to determine the genetic diversity of this and other naturalized breeds which constitute important genetic resources.

Because their high polymorphism, DNA simple sequence repeats (SSRs, microsatellites) are a valuable tool for the study of genetic diversity between populations (Moioli *et al.*, 2001). Takezaki and Nei (1996) and Diez-Táscon *et al*. (2000) have emphasized the importance of microsatellites in the study of evolutionary relationships of closely related populations. However, some problems may arise with the use of these markers for reasons such as irregularities in the mutation pattern and polymorphism differences between populations, because of which caution is required in extending inferences to populations other than those used in a specific study (Takeazaki and Nei, 1996).

Igarashi *et al*. (2000a) published the first study on the genetic structure of naturalized and imported Brazilian goat breeds using protein polymorphisms and used two microsatellite *loci* to analyze a subsample of this data, obtaining the same results (Igarashi *et al*., 2000b) as in the earlier study. Machado *et al*. (2000) investigated morphological traits suitable for the construction of phylogenetic trees involving a traditional undefined breed goat population from the Brazilian Northeast and Mediterranean goat breeds.

The study reported in our present paper proposes a microsatellite system that might be useful not only for the analyses of genetic distances between goat breeds in Brazil but also for determining diversity in Alpine, Saanen and Moxotó herds.

Materials and Methods

Animal sampling and DNA extraction

The following groups of goats were sampled: 121 Alpine and 94 Saanen goats from the herd at the Federal University of Viçosa (Universidade Federal do Viçosa (UFV), Minas Gerais state, Brazil), these goats being designated as Alpine-UFV and Saanen-UFV; 36 Alpine and 19 Saanen goats from a private herd in Minas Gerais state, designated as Alpine-private and Saanen-private; and 22 Moxotó goats from the Embrapa Goat conservation herd, Ceará State, Brazil.

For each Alpine and Saanen goat, a vacuum system was used to collect jugular blood which was then stored at 4 °C for 12 h before extracting the DNA using the phenol/chloroform protocol of Sambrook *et al*. (1989).

For each Moxotó goat, hair samples collected from the distal region of the tail and DNA extracted from the follicles using the cetyltrimethylammonium bromide (CTAB) protocol (Ferreira and Grattapaglia, 1998) in which the DNA samples were prepared by macerating 10-30 hair follicles in 0.5 mL of 2% (w/v) aqueous CTAB at 65 °C for 60 min with vortexing every 20 min. After maceration the mixture was centrifuged for 2 min at 14,000 revs min^{-1} and the supernatant transferred to a fresh micro-tube containing 0.5 mL of isoamyl alcohol, re-centrifuged and the supernatant transferred to another micro-tube containing 0.5 mL of isopropanol and incubate for 30 min at 4 °C to precipitate the DNA which was pelleted by centrifugation, washed and dehydrated in ethanol and resuspended in 50 to 100 μL of Tris-EDTA.

Microsatellite and genotyping system

The loci tested are shown in Table 1, all primers have previously been used for the construction of the goat genome linkage map (Vaiman *et al.*, 1996). The reverse primers were fluorescence labeled with Tet, 6-Fam and Hex (Applied Biosystem).

Each PCR mixture contained 25 ng genomic DNA, 20 mM Tris-HCl, pH 8.3, 50 mM KCl, 0.2 mM dNTPs, 1.25 to 2.5 mM $MgCl_2$ and 1 unit of *Taq* polymerase in a final volume of 20 μL. The concentration of each primer was adjusted to permit good readings of the fluorescent peaks and ranged as describe in Table 1. The amplification proto-

Table 1 - Locus, alleles (*kb) and allele frequencies (F) for the Alpine, Saanen and Moxotó breeds. The last column shows the overall allele frequency. Alleles undetected in a specific population are indicated by a dash (-) and PCR conditions are given as a footnote.

	Allele frequency for the different goat populations			
Locus and alleles	Alpine	Saanen	Moxotó	Overall
BETACAP				
*160	0.334	0.345	-	0.318
*162	0.073	0.133	0.361	0.115
*164	0.064	0.040	0.222	0.064
*166	-	-	0.333	0.021
*168	0.013	0.013	-	0.012
*170	0.516	0.465	0.083	0.469
*174	-	0.004	-	0.002

	Allele frequency for the different goat populations			
Locus and alleles	Alpine	Saanen	Moxotó	Overall
INRA005				
*113	0.003	0.004	-	0.003
*115	0.494	0.571	0.800	0.545
*117	0.102	0.252	0.125	0.162
*119	0.366	0.102	0.075	0.243
*121	0.035	0.071	-	0.047
ILSTS0087				
*135	0.010	-	-	0.005

Table 1 (cont.)

Locus and alleles	Allele frequency for the different goat populations			
	Alpine	Saanen	Moxotó	Overall
*137	0.006	0.018	-	0.010
*139	0.019	0.004	0.237	0.028
*141	0.041	0.195	0.079	0.104
*143	0.067	0.004	0.289	0.057
*145	0.083	0.066	0.105	0.078
*147	0.357	0.323	0.289	0.339
*149	0.363	0.389	-	0.349
*153	0.054	-	-	0.029
INRA006				
*106	0.029	0.031	0.200	0.041
*108	0.013	0.053	0.100	0.034
*112	0.272	0.195	0.125	0.224
*114	0.066	0.173	-	0.102
*116	0.140	0.088	-	0.110
*118	0.226	0.323	0.575	0.288
*120	0.143	0.075	-	0.107
*122	0.124	0.035	-	0.081
*124	0.003	0.018	-	0.009
*126	-	0.009	-	0.003
INRABERN172				
*136	-	0.075	-	0.029
*140	0.003	0.009	0.053	0.009
*142	0.131	0.075	0.684	0.145
*144	0.369	0.425	0.105	0.374
*146	0.140	0.031	-	0.088
*148	0.197	0.137	-	0.161
*150	0.156	0.234	0.132	0.185
*152	0.003	0.013	0.026	0.009
ILSTS005				
*175	0.023	0.071	0.075	0.045
*177	-	0.022	-	0.009
*179	0.623	0.554	0.875	0.615
*181	0.266	0.326	0.050	0.274
*183	-	0.004	-	0.002
*185	-	0.008	-	0.003
*187	0.084	0.013	-	0.051
ILSTS011				
*262	-	0.004	-	0.002
*264	0.010	0.053	-	0.026
*266	0.094	0.097	0.278	0.107
*268	0.260	0.053	-	0.161
*270	0.003	0.004	-	0.003
*272	0.006	0.013	-	0.009
*274	0.399	0.407	-	0.377
*276	0.110	0.296	0.583	0.214
*278	0.114	0.071	0.139	0.098
*280	0.003	-	-	0.002
SRCRSP05				
*157	0.003	0.044	0.219	0.032
*159	0.026	0.084	-	0.048
*163	0.221	0.035	-	0.134
*165	0.153	0.270	-	0.191
*167	0.562	0.451	0.219	0.498
*169	0.032	0.097	-	0.056
*173	0.003	0.012	0.562	0.041
INRA063				
*162	0.032	-	-	0.017
*164	0.093	0.027	-	0.061
*166	0.045	0.203	0.158	0.115
*168	0.400	0.310	0.632	0.380
*170	0.281	0.460	0.210	0.347
*172	0.145	-	-	0.078
*207	0.003	-	-	0.002
OARFCB48				
*152	0.074	0.069	-	0.071
*154	0.011	0.037	0.100	0.024
*156	0.182	0.259	-	0.212
*158	0.230	0.250	-	0.234
*160	0.137	0.222	0.900	0.189
*162	0.352	0.162	-	0.262
*164	0.015	-	-	0.008
BM3205				
*215	0.077	0.054	-	0.067
*217	0.008	0.086	-	0.044
*219	0.008	0.014	-	0.010
*223	0.339	0.364	-	0.350
*225	0.115	0.150	-	0.131
*227	0.350	0.200	-	0.281
*229	0.004	0.073	-	0.035
*231	0.092	0.023	-	0.060
*233	0.004	-	-	0.002
*235	0.004	0.014	-	0.008
*237	-	0.023	-	0.010

PCR conditions: *BETACAP* = Mix, 1; t_a, 55; Mg^{2+}, 1.25; pr, .16; dye, Tet); *INRA005* = Mix, 1; t_a, 55; Mg^{2+}, 1.25; pr, 0.16; dye, 6-Fam; *ILSTS0087* = Mix, 1; t_a, 55; Mg^{2+}, 1.25; pr, 0.12; dye, 6-Fam; *INRA006* = mix, 2; t_a, 55; Mg^{2+}, 2.25; pr, 0.16; dye, Hex; *INRABERN172* = mix, 1; t_a, 55; Mg^{2+}, 1.25; pr, 0.2; dye, Hex; *ILSTS005* = Mix, 3; t_a, 56; Mg^{2+}, 2; pr, 0.16; dye, Tet; *ILSTS011* = mix, 3; t_a, 56; Mg^{2+}, 2; pr, 0.16; dye, 6-Fam; *SRCRSP05* = mix, 3; t_a, 56; Mg^{2+}, 2; pr, 0.16; dye, Hex; *INRA063* = Mix, 3; t_a, 56; Mg^{2+}, 2; pr, 0.2; dye, 6-Fam; *OARFCB48* = mix, 4; t_a, 58; Mg^{2+}, 3; pr, 0.2; dye, Tet; and *BM3205* = mix, 5; t_a, 50; Mg^{2+}, 1.25; pr, 0.2; dye, Hex. (Key: Mix = PCR mix number; t_a = annealing temperature (°C); Mg^{2+} = magnesium concentration (mM); pr = primer concentration (μM); dye = type of florescent marker).

col consisted of a denaturation step of 3 min at 94 °C, followed by 27 cycles of 1 min at 94 °C, 1 min at 50-58 °C (Table 1), 1 min at 72 °C, and a final extension step of 20 min at 72 °C. All reactions were carried out in a MJ Research PTC-100 thermocycler. Single reactions were used for the *INRA006*, *OARFCB48* and *BM3205* loci, the other loci being amplified using two multiplex PCR reactions. The single and multiple PCR products were joined together and prepared for overall multiplex electrophoresis. Each final sample contained 1.0 μL of the amplified material and 0.25 μL of the internal size standard (TAMRA 500, Applied Biosystem). This reaction was then denatured in 24 μL deionized formamide (HI-DI, Applied Biosystem), incubated at 94 °C for 5 min and kept on ice. The amplified fragments were applied to a 9 V capillary electrophoresis system and subjected to electrophoreses at 60 °C for 22 min. Bands were analyzed using an ABI 310 Genetic Analyzer the Genescan® software (Applied Biosystem).

Statistical analysis

Allele frequencies, expected (H_E) heterozygosity considering Hardy-Weinberg equilibrium (HWE) and observed heterozygosity (H_O) estimates for each locus and the average over all loci were obtained with the Tools for Population Genetic Analyses v 1.3 (TFPGA) program (Miller, 1997). Analyses was performed for breeds and herd of origin as a within-breed population as follows: Alpine-UFV, Alpine-private, Saanen-UFV, Saanen-private, and Moxotó.

For the analysis of genetic differentiation between populations, Wright's fixation indices were computed (Weir and Cockerham, 1984) by bootstrapping with a 95% confidence interval (1000 replicates), where: F_{IS} (consanguinity or loss in heterozygosity within population), F_{ST} (measure of differentiation among populations), and F_{IT} (global loss in heterozygosity). The exact test of Hardy-Weinberg proportion for multiple alleles (Guo and Thompson, 1992) was performed using the Markov chain procedure (10 batches, 1000 iterations, 1000 dememorization steps).

The genetic distance (D_A) was estimated according to the method of Nei (1978). The unweighted pair group method with arithmetic mean (UPGMA) was used for dendrogram construction. To include a confidence interval in the constructed tree, a TFGPA bootstrap (1000 replicates) was performed which provided a percentage of replicates that were similar to the original data.

Results

292 goats were analyzed from three breeds with 11 molecular markers (Table 1). The overall proportion of non-analyzed *loci* was about 5% and the *BM3205* locus was not genotyped in Moxotó animals.

The number of alleles per locus ranged from five for the *INRA005* locus to 11 for the *BM3205* locus, the average per breed being 7.2 for Alpine and Saanen and 3.5 for the Moxotó goats . The observed heterozygosity H_O and expected heterozygosity (H_E) for each locus and goat population are shown in Table 2, from which it can be seen that H_E was generally close to H_O (direct counting) indicating no overall loss in heterozygosity (allele fixation). The H_E values were 0.6952 for the Alpine, 0.7043 for the Saanen and 0.4984 for the Moxotó populations. The Alpine and Saanen goats showed a high degree of observed diversity (*i.e.* high

Table 2 - Effective sample size (n) and expected and observed heterozygosity (H_E and H_O) at each locus for the populations and for the overall sample. Alleles undetected in a specific population are indicated by a dash (-).

Locus		Alpine-UFV (n = 116)	Alpine-private (n = 35)	Saanen-UFV (n = 93)	Saanen-private (n = 19)	Moxotó (n = 18)	Overall sample (n = 288)
BETACAP	H_E	0.640	0.489	0.668	0.555	0.693	0.663
	H_O	0.661	0.556	0.660	0.526	0.333	0.618
INRA005	H_E	0.628	0.527	0.621	0.422	0.339	0.617
	H_O	0.628	0.611	0.617	0.526	0.400	0.600
ILSTS087	H_E	0.711	0.632	0.688	0.632	0.759	0.742
	H_O	0.752	0.694	0.681	0.737	0.684	0.716
INRA006	H_E	0.817	0.760	0.810	0.731	0.604	0.825
	H_O	0.901	0.861	0.883	0.947	0.650	0.876
INRABER 172	H_E	0.764	0.725	0.706	0.796	0.500	0.772
	H_O	0.843	0.861	0.766	0.737	0.579	0.796
ILSTS005	H_E	0.542	0.469	0.585	0.525	0.226	0.542
	H_O	0.542	0.611	0.495	0.474	0.150	0.503
ILSTS011	H_E	0.749	0.675	0.710	0.737	0.563	0.765
	H_O	0.797	0.694	0.681	0.842	0.722	0.744

Table 2 (cont.)

Locus		Alpine-UFV (n = 116)	Alpine-private (n = 35)	Saanen-UFV (n = 93)	Saanen-private (n = 19)	Moxotó (n = 18)	Overall sample (n = 288)
SRCRSP05	H_E	0.588	0.629	0.712	0.663	0.588	0.690
	H_O	0.636	0.583	0.649	0.632	0.500	0.625
INRA063	H_E	0.731	0.663	0.665	0.554	0.532	0.713
	H_O	0.571	0.444	0.372	0.526	0.263	0.467
OARFCB48	H_E	0.777	0.672	0.765	0.661	0.180	0.792
	H_O	0.657	0.818	0.483	0.579	0.200	0.601
BM3205	H_E	0.732	0.561	0.794	0.690	-	0.771
	H_O	0.740	0.667	0.834	0.706	-	0.767
All *loci*	H_E	0.698	0.618	0.702	0.633	0.498	0.717
	H_O	0.702	0.673	0.648	0.657	0.448	0.665

heterozygosity) whereas Moxotó goats were less diverse in terms of the analyzed *loci*.

The alleles shared by the populations are listed in Table 3. Alpine goats showed some exclusive alleles at *loci ILSTS087* (135 and 153 bp) and *INRA063* (162,172, and 207 bp) while Moxotó goats presented a high frequency (0.333) 166-bp fragment at the *BETACAP* locus. The *INRA006* locus was the most polymorhic, sharing an average 5.2 of a total of 10 alleles between populations, while the *ILSTS005* locus was less polymorphic in that it shared an average 2.7 of a total of 7 alleles. For all the three breeds, *INRA005* and *ILSTS005* loci presented the same alleles at higher frequency. For the other five *loci* (*BETACAP*, *ILSTS087*, *INRABER172*, *ILSTS011* and *SRCRSP05*) the most frequent allele in Alpine goats was also the most frequent in Saanen goats, with both these breeds differing from the Moxotó breed. Only at *locus OARFCB48* did the most frequent allele differ for the three breeds (Table 3).

The *BETACAP*, *INRABER172*, *SRCRSP05*, *INRA063* and *OARFCB48* loci showed significant deviation ($p < 0.01$) from the overall expected Hardy-Weinberg equilibrium (HWE). Within breeds, the *INRABER172* locus showed disequilibrium only for Alpine goats ($p < 0.01$), while the *SRCRSP05* locus showed disequilibrium only for Saanen goats ($p < 0.05$) and the *BETACAP* locus only for Moxotó goats ($p < .01$).

Wright's F statistics for the different goat populations are given in Table 4. The highest within-population fixation index (F_{IS}) was observed for the *INRA063* and *OARFCB48* loci. The global F_{IS} did not differ from zero (95% confidence interval). Mean differentiation among populations (F_{ST}) was 0.0717 when considering the five population separately and 0.0263 when considering subpopulations according to herd. This finding suggests that most variability occurs between herds of the same breed ($F_{ST}S = 0.0768$) rather than between different breeds. Bootstrapping at the 95% confidence interval showed an F_{ST} value different from zero, indicating a significant difference between the populations studied.

The calculated genetic distance matrix (Nei, 1978) is shown in Table 5 and is a measure of the diversity between herds. The similarity between the Alpine-UFV and Saanen-UFV herd was higher than between the Alpine-UFV and Alpine-private herds and between the Saanen-UFV and Saanen-private herds.

The Moxotó herd showed the highest distance compared to the other herds, except for the Saanen-private herd, probably due to the low number of sampled animals in both herds. A bootstrap of the branch points of the generated tree (Figure 1) showed 0.433 and 0.417 similarity at points 1 and 2, respectively, and 100% at points 3 and 4. The number of *loci* supporting each point were 2, 2, 6 for points 1 and 2 and 10 for points 3 and 4.

Discussion

The precision of estimated genetic diversity is a function of the number of loci analyzed, the heterozygosity of these loci and the number of animals sampled in each population (Barker, 1994). The Food and Agricultural Organization (FAO) recommends that at least 25 randomly selected animals should be used in population studies (FAO, 1998) and Barker (1994) suggests that in diversity studies loci with at least four different alleles should be used to reduce the standard error of the estimated distance.

Diez-Tascón *et al*. (2000) studied diversity among closely related Merino sheep populations with less than 400 years of separation, and showed that it was possible to distinguish related populations on the basis of microsatellite analysis.

Diversity studies on goats using microsatellite markers are rare in the literature, although Maudet *et al*. (2002) did investigate the usefulness of various statistical methods in biodiversity conservation management using *Capra ibex*

Table 3 - Number of alleles (N, see Table 1) per locus present in each goat population and shared between populations. Alleles undetected in an individual population or pair of populations are indicated by a dash (-).

Goat populations	Number of alleles (as positive primers) per locus found in the goat populations											
	BETACAP (N = 7)	*INRA005* (N = 5)	*ILSTS087* (N = 9)	*INRA006* *(N = 10)*	*INRABER17* (N = 8)	*ILSTS005* (N = 7)	*ILSTS011* (N = 10)	*SRCRSP05* (N = 7)	*INRA063* (N = 7)	*OARFCB48* (N = 7)	*BM3205* (N = 11)	Mean* (N = 8)
Individual populations												
Alpine-UFV	5	4	9	8	5	4	8	7	7	7	10	6.7
Alpine-private	4	4	6	8	7	3	6	5	5	6	6	5.5
Saanen-UFV	6	5	6	10	7	7	9	7	4	6	9	6.9
Saanen-private	4	3	5	5	6	3	4	4	3	5	8	4.5
Moxotó	4	3	5	4	5	3	3	3	3	2	-	3.5
Paired populations[#]												
1 and 2	4	3	6	7	5	3	5	5	5	6	6	5.0
1 and 3	5	4	6	9	5	4	7	7	4	6	8	5.8
1 and 4	4	3	5	5	4	2	4	4	3	5	2	3.7
1 and 5	3	3	5	4	3	3	3	3	3	2	-	3.2
2 and 3	4	4	5	8	6	2	6	5	4	6	6	5.0
2 and 4	3	3	5	4	5	2	4	3	3	5	5	3.8
2 and 5	3	3	5	3	5	3	3	1	3	2	-	3.2
3 and 4	4	3	4	5	5	3	4	4	3	5	6	4.2
3 and 5	3	3	4	4	4	3	3	3	3	2	-	3.1
4 and 5	2	3	4	3	4	2	2	2	3	1	-	2.6
Mean shared alleles	3.5	3.2	4.1	5.2	4.6	2.7	4.1	3.7	3.4	4.5	5.5	4.0

*This refers to the mean number of loci for the 11 alleles.
[#]Key: 1 = Alpine-UFV; 2 = Alpine-private; 3 = Saanen-UFV; 4 = Saanen-private; 5 = Moxotó.

as a model and demonstrated low genetic variability in this wild alpine goat species.

Yang *et al*. (1999) studied diversity among autochthonous goat breeds from China using microsatellite markers and obtained results that agreed with the history of the populations. Heterozygosity was high at 6 of the 13 ana-

Table 4 - Within population fixation index (F_{IS}), between population fixation index ($F_{ST}P$) and between subpopulations fixation index ($F_{ST}S$) and global consanguinity (F_{IT}) obtained for each individual *locus* and all *loci* combined.

Locus	F_{IS}	$F_{ST}S$	$F_{ST}P$	F_{IT}
BETACAP	0.0246	0.0835	0.0536	0.1060
INRA005	-0.0264	0.0873	0.0597	0.0632
ILSTS087	-0.0270	0.0788	-0.0213	0.0540
INRA006	-0.1041	0.0576	-0.0117	-0.0405
INRABER172	-0.0889	0.0850	0.0563	0.0036
ILSTS005	0.0474	0.0420	0.0200	0.0874
ILSTS011	-0.0324	0.0903	0.0705	0.0608
SRCRSP05	0.0310	0.1111	0.0852	0.1386
INRA063	0.3171	0.0679	0.0491	0.3635
OARFCB48	0.1955	0.0810	-0.0038	0.2606
BM3205	-0.0394	0.0550	-0.0543	0.0178
All *loci*	0.0252	0.0768	0.0263	0.1000
Upper bootstrap	0.1028	0.0873	0.0511	0.1726
Lower bootstrap	-0.0379	0.0672	-0.0014	0.0411

Limits were estimated by bootstrapping at the 95% confidence interval.

Table 5 - Nei's genetic distance between the populations studied.

Population	Population			
	Alpine-private	Saanen-UFV	Saanen-private	Moxotó
Alpine-UFV	0.1133	0.1010	0.1707	0.5456
Alpine-private		0.1236	0.1477	0.6358
Saanen-UFV			0.1220	0.4468
Saanen-private				0.6139

Figure 1 - Genetic distance (D_A) unrooted (UPGMA) dendrogram for the different goat pbased on the.

lyzed *loci*. Saitbekova *et al*. (1999) evaluated diversity among nine domestic Swiss goat herds, Wild Ibex goats and Bezoar goats. Heterozygosity was higher in the domestic breeds than in the wild goats, with the mean H_E ranging from 0.51 to 0.58 for domestic herds and from 0.17 to 0.19 for the wild species.

In the imported breeds sampled here, high and moderate ($H_E > 0.70$) polymorphism was observed for the set of loci studied. The Moxotó breed showed lower polymorphism, probably because of the smaller sample size and also due to a certain reduction in within-population genetic variability. Inbreeding was also indicated from pedigree information and the closed herd history of the Moxoto breeding nucleus. The low F_{ST} value observed for the UFV Alpine and Saanen herds (lower than that obtained for geographically isolated herds) suggests that the animals from the UVF herds resulted from matings between both breeds leading to genetic similarity between them, these suspicions being confirmed by their mating history. Laval *et al*. (2000) state that, for commercial populations, migration exerts a greater effect than mutation or drift on the reduction in genetic differentiation between populations.

Our data revealed no deficit or excess of heterozygosity. Deviations from HWE at microsatellite *loci* have been reported in various studies (Barker *et al*., 2001; Laval *et al*., 2000; Luikart *et al*., 1999) and indicate departure from random mating. This deviation might be the result of the presence of null or non-amplified alleles, allele grouping defects, a sampling structure effect, selection against heterozygotes or inbreeding.

The *INRA06*3 and *OARFCB48 loci* showed a higher within population Fixation index (F_{IS}) than the other *loci*, indicating allele fixation. However, analysis of the global F_{IS} indicated that there was no increase in inbreeding in these populations. The global consanguinity (F_{IT}) and F_{IS} were close (Table 4), indicating impairment of inbreeding within herds.

Wide genetic diversity between imported breeds and the naturalized Moxotó breed and close similarity between the Alpine and Saanen breeds were showed by data analysis. The Embrapa Moxotó herd is composed strictly of pure native animals, an extremely uncommon situation in commercial herds were crossbreeding has occurred over a long period of time. The F_{ST}P value indicates that only 2.6% of the genetic variability is due to differences between breeds. The UFV Alpine and Saanen herds were more closely related than the Alpine and Saanen private herds, demonstrating gene flow between the UFV Alpine and Saanen breeds. In general, the Saanen and Alpine breeds differed little from one another, probably because of their common origin. These results agree with those reported by Igarashi *et al*. (2000b) and with the history of the breeds.

Our study shows that the imported Alpine and Saanen breeds have separate genetic identities and are very distant from the naturalized Brazilian Moxotó breed. Also, the Moxotó herd showed low genetic diversity which compromises its potential. A further conclusion is that the microsatellites analyzed in this study were informative and should be used in future studies about the genetic diversity of goats in Brazil.

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