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Genetic diversity of the two main Moroccan goat breeds: phylogenetic relationships with four breeds reared in France

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Abstract

Two Moroccan goat breeds (Draa and Noire-Rahalli) and four breeds reared in France (Alpine, Saanen, Poitevine and Pyrénéenne) were screened using five microsatellite loci and the highly polymorphic milk protein gene encoding α_{s1}-casein. A total of 1975 animals were tested. Allelic frequencies were calculated in order to study genetic variability and phylogenetic relationships. The Moroccan goat breeds and the Pyrénéenne showed the highest diversity values (average number of alleles per locus). The correspondence analysis procedure (CAP) showed that the Pyrénéenne breed is the French goat breed most closely related to the Moroccan breeds. Unrooted Neighbor–Joining phylogenies were constructed using Nei and Cavalli-Sforza genetic distance estimates. The Phylogenetic trees showed almost the same pattern except for the Poitevine branching position. Genotyping at the α_{s1}-casein locus revealed that alleles associated with a high expression level (mainly A and B) are predominant (74 and 94% in Draa and Noire-Rahalli, respectively), whereas allele E, which is rather frequently found (11–60%) in European goat breeds, is rare (2–3%) in the Moroccan goat breeds.

Keywords: Microsatellites; Genetic structure; Phylogeny; α_{s1}-Casein; Moroccan and French goat breeds

1. Introduction

Different aspects of genetic diversity, breed characterization, phylogenetic history and evolution have been addressed in many studies on economically important domestic mammalian species, including the goat (*Capra hircus*). Previous research papers on goats have described the phenotypic classification of different breeds in southern Europe (Lauvergne, 1988), in central and western Africa (Lauvergne et al., 1993; Zeuh et al., 1997; Missohou et al., 2000) and in Brazil (Machado et al., 2000). Polymorphisms of milk proteins, such as α_{s1}-casein, have been characterized in different goat populations at the protein as well as at the genomic level (Grosclaude et al., 1987; reviewed by Martin, 1993). Recently, molecular studies

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analyzing mitochondrial DNA (mtDNA) have shown three distinct evolutionary lineages in *Capra hircus* (Luikart et al., 2001), whereas microsatellites and AFLP markers have been used either to assess the phylogenetic relationships of some Chinese and Swiss goat breeds (Yang et al., 1999; Saitbekova et al., 1999) or to investigate the genetic diversity within and between seven Italian goat populations (Ajmone-Marsan et al., 2001), respectively.

Data available on the genetic structure and diversity of the Moroccan goat populations are sparse. This question remains difficult to address since goat rearing and breeding are not well organized in Morocco, with the exception of a few experimental stations. Goat populations in the Northern regions show some phenotypic resemblance to Spanish breeds such as the Murciana-Granadina, the Malaguena or the Andalusia breeds (Benlekhal and Tazi, 1996). In the Central and Southern regions, two breeds are mainly found: the Noire-Rahalli and the Draa breeds. Noire-Rahalli goats are indigenous to the High and Midlle Atlas mountains and are a reliable source for meat production, whereas the Draa breed is restricted to oases of the Draa Valley and considered as the only breed for milk production in Morocco.

In this study, the two main Moroccan goat breeds (Draa and Noire-Rahalli) have been surveyed for genetic diversity and compared to four European breeds, reared in France (Alpine, Saanen, Poitevine and Pyrénéenne) using a set of six polymorphic markers made of five microsatellites and a highly polymorphic structural gene encoding the α_{s1}-casein. Our objectives were to: (1) obtain a better description and knowledge of genetic resources in the Moroccan goat populations; (2) provide necessary elements to monitor and manage biodiversity and (3) understand the phylogenetic relationships between Moroccan and some European goat breeds.

2. Material and methods

2.1. Samples and breeds

Blood samples were obtained from 132 Draa and 102 Noire-Rahalli goats. Draa goats were from the Skoura station at Ouarzazate and Zagora (south-west of Morocco). These goats have heterogeneous colours and are highly prolific. Noire-Rahalli goats were from a provincial market of the Mean Atlas mountains where all neighboring farmers sell their animals. Noire-Rahalli goats are small and have long hair, but their milk production level is very low. European goat breeds analyzed were from France. These correspond to French local and now rare breeds (Poitevine and Pyrénéenne) and cosmopolitan Swiss breeds (Alpine and Saanen) that have been intensively selected for milk production traits and widely spread all around the world. Blood samples from 243 Poitevine, 213 Pyrénéenne, 712 Alpine (400 and 312) and 573 Saanen (312 and 261) were collected. Numbers between brackets correspond to two samples collected in the early 1990s and in 2000, respectively.

2.2. Genotyping at microsatellite and α_{s1}-casein loci

Microsatellites used were INRA005 (Bishop et al., 1994), INRA006, INRA063, INRA172 (Vaiman et al., 1994) and ILSTS87 (Kemp et al., 1995). DNA was extracted from blood samples either as described by Jeanpierre (1987) or using a rapid alkaline procedure on small volume (70 μl) blood samples, treated in 96 multiwell plates. Multiplex amplification was carried out using fluorescent primers and amplicons were analyzed with an ABI Prism 310 automated sequencing system (Applied Biosystems Inc.) equipped with GeneScan (version 2.1) and the Genotyper software (Babilliot and Amigues, Personal communication).

Genotyping at the α_{s1}-casein locus was performed either by PCR/RFLP and allele-specific amplification as described earlier (Leroux et al., 1990, 1992; Jansa Pérez et al., 1994) or using a multiplex amplification procedure developed by Labogena (Jouy-en-Josas, France), followed by analysis of the PCR products with the same automated sequencing system as described earlier.

2.3. Statistical analysis of data

Allelic frequencies were determined by direct counting. The Genetix program (Belkhir, 1999) was used to calculate the heterozygosity and estimates of F_{st}, following the Weir and Cockerham (1984) method. The distance matrix was measured according to Cavalli-Sforza and Edwards (1967) and Nei (1978). Phylogenetic trees were constructed using the

Neighbor–Joining method of the Phylip package (Felsenstein, 1995). A correspondence analysis procedure (CAP) was performed according to Benzécri (1973) using the SAS Package, version 6 (SAS Institute, 1989).

3. Results

3.1. Allelic frequencies of α_{s1}-casein

All samples of Moroccan and French breeds were genotyped at the α_{s1}-casein locus that is remarkable, in the goat, for its high degree of polymorphism and for the existence of large differences in expression level. A, B and C are considered as "strong" alleles, since they are associated with a high level of protein synthesis, E as an intermediate allele and F as a weak allele. Allele O, however, has to be considered as a true null allele without any expression of the α_{s1}-casein gene (Grosclaude et al., 1987; Leroux et al., 1990; Martin, 1993). The results are reported in Table 1. Allele E is rare in the Moroccan goat populations analyzed (2–3%), whereas it was rather highly represented in French and Swiss breeds (11–60%), even though its frequency in the French Alpine population has decreased significantly during the last decade, due to selection programs for the "strong" alleles which now account for up to 83 and 34% in the Alpine and the Saanen, respectively. The frequency of allele F is similar in the Moroccan Draa (19%) and both Swiss breeds (Alpine and Saanen) reared and collected in France in the early 1990s (16 and 19%). Conversely, the second Moroccan goat breed (Noire-Rahalli) displays the lowest frequency (2%) for the F allele. Strong alleles are predominant in the Moroccan breeds (74 and 94%). Whereas, in Alpine and Saanen breeds, allele A became the major strong allele, it is almost absent in the Pyrénéenne and Poitevine populations. The Poitevine breed shows a high frequency of strong alleles (58%), with B1 (27%) and B3/B4 (18%) types predominating. These latter alleles (B3/B4) are by far the main strong alleles in Draa (50%), Noire-Rahalli (66%) and to a lesser extent in Pyrénéenne (14%). Null alleles are found in both Moroccan and European goat populations. A novel null allele has been identified in the Moroccan breeds. It has also been found in other African goat populations (Mahé et al., unpublished data).

3.2. Genetic diversity between Moroccan and European goat breeds

Genetic diversity of the Moroccan and European breeds has been analyzed taking into account allele frequencies occurring at the α_{s1}-casein locus and polymorphism data arising from five microsatellites. Allelic frequencies for these microsatellites are reported in Table 2. A higher number of alleles (11–13) was found at the INRA006, INRA172 and ILSTS87

Table 1
Allelic frequencies at the α_{s1}-casein locus in Moroccan[1] and French[2] goat breeds

α_{s1}-Casein alleles	Draa[1]	Noire-Rahalli[1]	Alp.85[2]	Alp.90[2]	Alp.00[2]	Poit.[2]	Pyr.[2]	Saa.85[2]	Saa.90[2]	Saa.00[2]
All A	0.2384	0.2691	0.14	0.5163	0.7083	0.0802	0.0939	0.07	0.1724	0.2720
B1	0.0000	0.0000		0.0250	0.0401	0.2695	0.0047		0.0086	0.0038
B2	0.0077	0.0096		0.0000	0.0016	0.0247	0.0000		0.0043	0.0383
B3/B4	0.5000	0.6587		0.0075	0.0288	0.1852	0.1432		0.0302	0.0249
All B	0.5077	0.6683	0.05	0.0325	0.1122	0.4794	0.1479	0.06	0.0431	0.0670
C	0.0000	0.0048	0.01	0.0150	0.0545	0.0226	0.0000		0.0022	0.0000
Strong alleles										
(A + B + C)	0.7461	0.9422	0.20	0.5638	0.8350	0.5822	0.2418	0.13	0.2177	0.3371
E medium	0.0192	0.0337	0.34	0.2650	0.1090	0.3354	0.6033	0.41	0.5862	0.5824
F low	0.1962	0.0192	0.41	0.1650	0.0545	0.0802	0.1244	0.43	0.1940	0.0766
Nulls	0.0385[a]	0.0049[a]		0.0150	0.0032	0.0021	0.0305		0.0022	0.0019

Alp., Alpine; Saa., Saanen; Poit., Poitevine; Pyr., Pyrénéenne. 85: data from Grosclaude and Martin (1997); 90 & 00: samples collected in 1990 and 2000, respectively.

[a] Including the novel null allele identified in African goat populations.

Table 2
Allelic frequencies of five microsatellites in Moroccan[1] and French goat breeds[2]

Locus alleles	Draa[1]	Noire-Rahalli[1]	Alp.90[2]	Alp.00[2]	Poit.[2]	Pyr.[2]	Saa.90[2]	Saa.00[2]
N[a]	132	105	400	312	243	213	232	261
INRA006								
G	0.0038	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
H	0.0038	0.0190	0.0000	0.0000	0.0000	0.0000	0.0000	0.0019
I	0.1250	0.0381	0.0288	0.0385	0.0103	0.0211	0.1207	0.0690
J	0.0189	0.0333	0.0075	0.0000	0.2222	0.0047	0.0000	0.0000
K	0.0076	0.0333	0.0088	0.0032	0.1111	0.0070	0.0065	0.0000
L	0.2955	0.2476	0.0850	0.1154	0.0597	0.4460	0.1595	0.2529
M	0.1515	0.1333	0.2950	0.2949	0.0432	0.1174	0.1853	0.1686
N	0.0379	0.0810	0.0962	0.0417	0.1728	0.0634	0.1250	0.0977
O	0.2348	0.2619	0.3050	0.3269	0.2160	0.1573	0.2953	0.2510
P	0.0909	0.1000	0.1388	0.1234	0.0658	0.1080	0.0603	0.1015
Q	0.0189	0.0286	0.0275	0.0561	0.0679	0.0446	0.0409	0.0498
R	0.0114	0.0095	0.0075	0.0000	0.0309	0.0305	0.0065	0.0077
X	0.0000	0.0143	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
INRA005								
K	0.0000	0.0000	0.0250	0.0256	0.0000	0.0023	0.0065	0.0000
L	0.5947	0.6202	0.5138	0.5288	0.3621	0.6808	0.5517	0.4808
M	0.2197	0.1394	0.1112	0.0529	0.1276	0.1925	0.3427	0.3774
N	0.1667	0.1731	0.2937	0.3429	0.4156	0.1127	0.0819	0.1188
O	0.0189	0.0673	0.0562	0.0497	0.0947	0.0117	0.0172	0.0230
ILSTS87								
H	0.0114	0.0048	0.0037	0.0032	0.0123	0.0000	0.0022	0.0019
I	0.0076	0.0667	0.0000	0.0000	0.0000	0.0047	0.0022	0.0000
J	0.0303	0.0714	0.0200	0.0128	0.0082	0.1056	0.0560	0.0670
K	0.5985	0.6714	0.1425	0.1426	0.6049	0.2019	0.3211	0.2778
L	0.2727	0.1143	0.0838	0.0817	0.0226	0.3944	0.0280	0.0766
M	0.0000	0.0048	0.1538	0.2404	0.0000	0.0399	0.0711	0.0517
N	0.0341	0.0333	0.2212	0.1763	0.1687	0.1620	0.2866	0.2701
O	0.0114	0.0095	0.3750	0.3237	0.1831	0.0728	0.2241	0.2452
P	0.0000	0.0048	0.0000	0.0000	0.0000	0.0023	0.0000	0.0000
Q	0.0189	0.0095	0.0000	0.0192	0.0000	0.0164	0.0086	0.0096
R	0.0152	0.0095	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
INRA172								
I	0.0038	0.0048	0.0000	0.0000	0.0021	0.0023	0.0797	0.0479
J	0.0000	0.0190	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
K	0.1477	0.1000	0.0100	0.0321	0.0535	0.3122	0.0409	0.0594
L	0.0871	0.2048	0.5913	0.5288	0.5206	0.2441	0.3707	0.2950
M	0.1780	0.0571	0.0688	0.0769	0.0103	0.0329	0.0841	0.1073
N	0.1326	0.1190	0.1725	0.1683	0.4095	0.1315	0.1659	0.1992
O	0.2008	0.2762	0.1563	0.1939	0.0041	0.2512	0.2565	0.2874
P	0.2197	0.1571	0.0012	0.0000	0.0000	0.0235	0.0022	0.0038
Q	0.0303	0.0524	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
R	0.0000	0.0095	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
T	0.0000	0.0000	0.0000	0.0000	0.0000	0.0023	0.0000	0.0000
INRA063								
J	0.0379	0.0095	0.0562	0.0465	0.0638	0.0728	0.0022	0.0000
K	0.0265	0.0571	0.0100	0.0048	0.0082	0.0188	0.0086	0.0077
L	0.1136	0.2143	0.1975	0.1795	0.0741	0.0657	0.1659	0.1226
M	0.4356	0.2952	0.4963	0.3766	0.7407	0.5493	0.4871	0.4732
N	0.3864	0.4190	0.1688	0.2228	0.1132	0.2864	0.3254	0.3716
O	0.0000	0.0048	0.0712	0.1699	0.0000	0.0070	0.0108	0.0249

See legend in Table 1.
[a] *N*: number of animals analysed.

Table 3
Allele number (N_m), heterozygosity (Hs) and F_{st} for each locus

Locus	N_m	H_s	F_{st}
INRA006	13	0.825	0.047
INRA005	05	0.458	0.061
ILSTS87	11	0.667	0.111
INRA172	11	0.708	0.083
INRA063	06	0.586	0.049
α_{s1}-Casein	13	0.562	0.161
All loci			0.088

loci. By contrast, only 5–6 alleles were found at the INRA005 and INRA063 loci. In addition, 13 different alleles have been detected at the α_{s1}-casein locus (Table 3). Thus, these markers are polymorphic enough to estimate genetic distances between the goat populations (Barker et al., 1993). However, as shown in Table 3, the allele number per microsatellite is not correlated to the locus involvement in the population variability. For example, microsatellites INRA006 and INRA063 display different allele numbers (13 versus 6). Nevertheless, with a F_{st} value close to 5%, they would be equally involved in the population variability. The highest value (11%) observed for the coefficient of gene differentiation (F_{st}) with a microsatellite (ILSTS87) remains significantly lower than that shown by the α_{s1}-casein locus (16%). The F_{st} for the loci taken together is close to 9%.

Comparing different goat populations, Table 4 shows that the highest average allele number per locus (8.333) is found in the Noire-Rahalli breed, followed by the Draa and Pyrénéenne breeds. The lowest value (6.833) is observed with the Poitevine breed. In order to shed light on the impact of selection programs on the genetic structure of goat populations, two samples of the Alpine and Saanen breeds were collected and analyzed independently in the early 1990s and 2000. The average allele number has slowly decreased in these populations during the course of the last decade.

Elsewhere, it is worth noting that few alleles occurring at the five microsatellite loci studied seem to be characteristics for some breeds and potentially useful markers for breed assignment. This is particularly well exemplified by allele M at the ILSTS87 locus of which the frequency ranges between 0.15 and 0.24, in the Alpine breed, whereas it does not exceed 0.07 in the other breeds. Likewise, allele I at the INRA172 locus, even though occurring at a low frequency in most of the breeds studied is definitely absent in the Alpine breed for which more than 700 individuals were analyzed. Using allele frequency distributions at these two loci, Alpine breed assignment should be achieved with a good accuracy. Alleles J and K of INRA006 show large differences in frequency between the Poitevine breed (0.22 and 0.11, respectively) and the other breeds (<0.03).

Table 4
Within-population mean heterozygosity (H_T) with its standard error (S.E.) and average allele number (A_m)

Breeds	$H_T \pm$ S.E.	A_m
Draa	0.670 ± 0.053	7.833
Noire-Rahalli	0.635 ± 0.074	8.333
Alp.90	0.711 ± 0.037	7.333
Alp.00	0.728 ± 0.035	7.167
Poitevine	0.630 ± 0.072	6.833
Pyrénéenne	0.636 ± 0.040	7.833
Saa.90	0.698 ± 0.048	7.667
Saa.00	0.729 ± 0.043	7.000

All DNA markers (microsatellites and α_{s1}-casein) have been used to estimate heterozygosity. See legend in Table 1.

3.3. Pairwise genetic distances, multivariate and phylogenetic analyses

Pairwise genetic distances were estimated between breeds, using the same six DNA markers (five microsatellites and the α_{s1}-casein locus). Since the phylogenetic analysis of the Alpine and Saanen samples collected at different periods (1990 and 2000) did not provide any additional information, they have subsequently been regarded as a single population within each breed. Cavalli-Sforza and Nei distances (Tables 5 and 6) were applied to construct the

Table 5
Pairwise genetic distance among the six goat breeds according to Cavalli-Sforza and Edwards (1967)

	Draa	Noire-Rahalli	Alpine	Poitevine	Pyrénéenne
Noire-Rahalli	0.0181				
Alpine	0.0913	0.0854			
Poitevine	0.0996	0.0910	0.0750		
Pyrénéenne	0.0501	0.0587	0.0610	0.0791	
Saanen	0.0684	0.0690	0.0360	0.0719	0.0312

Table 6
Pairwise genetic distance among the six goat breeds according to Nei (1978)

	Draa	Noire-Rahalli	Alpine	Poitevine	Pyrénéenne
Noire-Rahalli	0.0499				
Alpine	0.4314	0.4369			
Poitevine	0.3747	0.3830	0.2698		
Pyrénéenne	0.2514	0.3436	0.3079	0.3577	
Saanen	0.3110	0.3529	0.1691	0.2614	0.1213

phylogenetic trees using the Neighbor–Joining method (Figs. 1 and 2). Whatever the distance used, Moroccan and European breeds are separated with the highest bootstrap value (>90%). The Pyrénéenne breed is closer to the Moroccan breeds. The other European breeds are not branched in the same way in both phylogenetic trees, depending on the genetic distance applied. Only the phylogenetic tree based on Cavalli-Sforza distance confirms the known geographical origin of both the Alpine and the Saanen breeds.

Since the Poitevine branching in the phylogenetic trees differs depending on how the genetic distance is estimated, a CAP was applied, using the individual genotypes to yield the representation shown in Fig. 3.

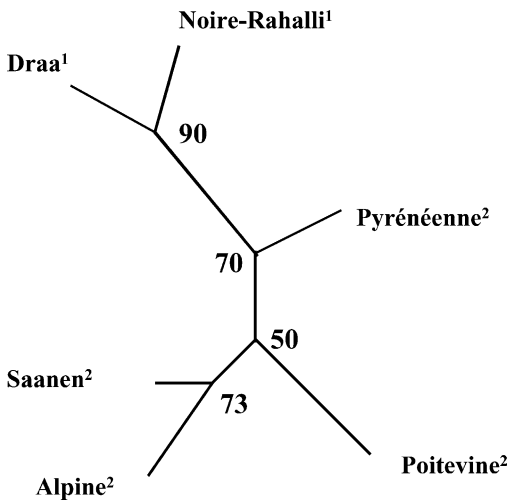

Fig. 1. The Neighbor–Joining dendrogram of two Moroccan[1] and four French[2] goat breeds based on the Cavalli-Sforza distance (Table 5). Numbers on the nodes are percentage bootstrap from 500 resamplings.

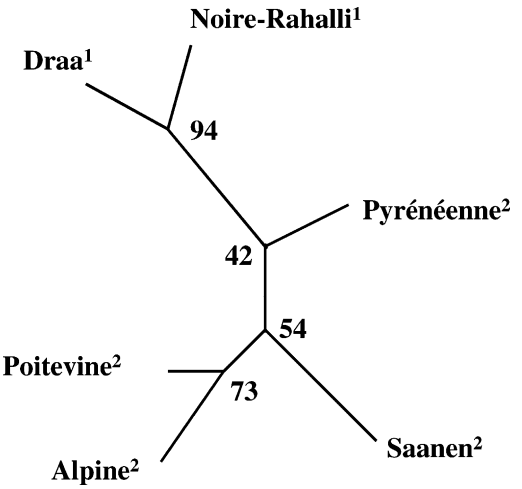

Fig. 2. The Neighbor–Joining dendrogram of two Moroccan[1] and four French[2] goat breeds based on the Nei (1978) distance (Table 6). Numbers on the nodes are percentage bootstrap from 500 resamplings.

Individual genotypes were prepared by scoring alleles of all loci. Such a representation provides additional information about the genetic structure of each population. The two main axes account for 66% of the underlying genetic variability between breeds that cluster rather loosely within breed-specific regions of the plot. The first axis summarizes 37% of the variability, essentially due to alleles B3/B4 at the α_{s1}-casein locus, and to P and K alleles at the INRA172 and ILSTS87 loci, respectively. The Moroccan breeds are branched out from Alpine and Saanen according to this axis. On the second axis, with 29% of the total variation mainly due to allele B1 at the α_{s1}-casein locus and to allele J at the INRA006 microsatellite locus, only the Poitevine breed is distinguished from all the other breeds. Alleles at both the loci would be equally involved in this breed distinction. Thus, it became clear from the CAP representation that the Poitevine can be differentiated from the other breeds, as suggested by the occurrence of different branching positions for this breed in the phylogenetic trees. The Moroccan breeds are close to each other, but comparatively rather distant from the other breeds except the Pyrénéenne which is the closest European breed. In order to discriminate between breeds, the contribution of each marker can be considered. The most important locus, α_{s1}-casein, explains 33% of the total

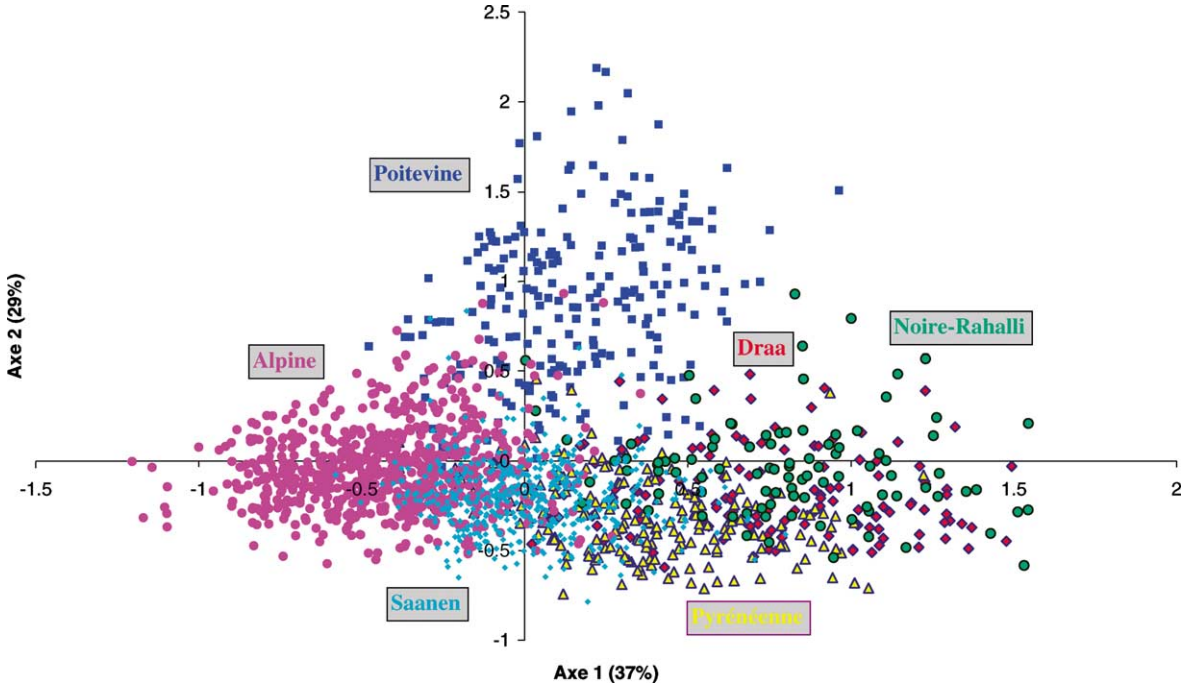

Fig. 3. Correspondence analysis procedure of the six goat breeds.

inertia. ILSTS87 and INRA172 each contribute about 19% whereas INRA006 explains 16% of total inertia.

4. Discussion

The data presented here contribute to a better genetic characterization and make it possible to gain an insight into the phylogenetic relationships of goat breeds reared in Morocco and France. Cluster analyses based on standard genetic distance between breeds indicated that both Moroccan breeds (Draa and Noire-Rahalli), though phenotypically distinct, appeared to be closely related and clustered from the four breeds reared in France. Of the European breeds studied here, the Pyrénéenne breed was the closest to the Moroccan breeds. By contrast, for goat breeds reared in France, the topology of the trees does not seem so clearly established. This instability was reflected in rather low bootstrap values (ranging between 42 and 73%) and branching positions which varied depending on the genetic distances used. This was particularly true for the Poitevine breed. Using Cavalli-Sforza distance, the bootstrap value (50%) remained low for this highly probable branching node that may have changed, using the Nei distance, if a larger number of markers had been studied, as was previously shown for bovine breeds (Moazami-Goudarzi et al., 1997). However, molecular studies, performed to assess genetic structure and phylogenetic relationships in goat populations using even a low number of anonymous marker loci, have proven to be useful in distinguishing geographically distant Chinese goat breeds (Yang et al., 1999) as well as geographically close Swiss goat breeds (Saitbekova et al., 1999). These data, as well as those provided here show clearly that six markers are enough to distinguish between goat populations.

The most striking aspect of the results presented here was the phylogenetic position of the Poitevine breed which seems separate from all the other breeds, especially using multivariate CAP (according to the second axis). This possibility is inconsistent with previous hypotheses suggesting that the Poitevine originates from Africa and would have been introduced in Europe during Arabic invasions (Toussaint, 1967). Since the B1 allele is regarded as the ancestral

α_{s1}-casein gene (Grosclaude and Martin, 1997), a high frequency of this allele in the Poitevine could be due to a bottleneck effect. Alternatively, allele B1 could have appeared more recently as a consequence of an interallelic recombination event having occurred at this locus (Bevilacqua et al., 2002). Multivariate data strongly suggest that the Poitevine may come from a different evolutionary lineage. Such a hypothesis is consistent with archeological and molecular genetic evidence supporting multiple maternal lineages in goats, possibly arising through independent domestications or originating via introgression from wild species (Luikart et al., 2001).

With respect to genetic diversity, both of the Moroccan breeds and the Pyrénéenne showed the highest average allele number per locus. In fact, these three breeds can be considered as native populations, although the Draa and the Pyrénéenne breeds may have been slightly selected for milk production. In contrast, Alpine and Saanen showed a lower average number of alleles per locus. When comparing these cosmopolitan breeds originating in Switzerland and sampled in France during the last decade, the genetic variability is decreased. This might be due to the selection program undertaken in France, particularly in the Alpine population, on the α_{s1}-casein locus, during this period. It is also worth noting that the six populations surveyed for microsatellite variation and for polymorphism at a coding locus (α_{s1}-casein) showed, in the multivariate analysis, a rather low degree of breed-specific clustering.

Finally, mean heterozygosity within population ranged between 0.630 and 0.729 and was not significantly different in the Moroccan and French goat populations. Similar values were obtained within the Chinese and Swiss populations (Yang et al., 1999; Saitbekova et al., 1999). This could be explained by a weak degree of genetic structuring of goat populations, as has been recently proposed (Luikart et al., 2001).

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