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Genetic distances and taxonomic trees between goats of Ceará State (Brazil) and goats of the Mediterranean region (Europe and Africa)

Théa M.M. Machado[1], Mohamed Chakir[2] and Jean Jacques Lauvergne[2]

Abstract

Goats of an undefined breed (called UDB) from the State of Ceará, northeastern Brazil (N = 447), European Mediterranean goats (N = 3,847) and African Mediterranean goats (N = 325) were compared to establish genetic distances and taxonomic trees. Allelic frequencies in each population for presence or absence of the following traits were used: horns, reduced ears, long hair, wattles, beard, roan color, brown eumelanin and eumelanic standard pigmentation. The genetic distance, applying the method developed by Nei (1972), was: least between goats from different meso-regions of the State of Ceará (0.0008 to 0.0120); small between all UDB of Ceará and French goats of Rove and Haute Roya (0.0236 and 0.0459); greater between all UDB of Ceará and northern Spanish goats (0.1166), and greatest between all UDB of Ceará and northern African goats (Moroccan of Drâa, Rhâali and Zagora), Balkan goats (Sakhar from Bulgaria and Macedonia from Greece) and some insular Mediterranean populations (Corsica, Sicily and Sardinia), which ranged from 0.1237 to 0.2714. Brazilian UDB goats are more closely related to Continental and Western European populations than to North African, Balkan or Insular Mediterranean populations.

INTRODUCTION

Goats were first introduced to Brazil by the Portuguese settlers. Today it is difficult to identify the origins of the populations, and one may ask how closely the Brazilian animals are to their origins. The nomenclature "undefined breed" (UDB) represents approximately 95% of the present total Northeast Brazilian goat population (Programa, 1979). The UDB concept is not recognized as a breed by the Ministry of Agriculture in Brazil; however, these animals represent a "criole" or mixture of breeds. As the name suggests, this population is not standardized.

Using genetic distances, it is possible to evaluate the degree of genetic similarity between two populations by measuring the probability of one or more characters appearing in one of the populations but not in the other (Sournia, 1991). In the calculation of distances from the allelic frequencies, Nei's genetic distance method is unique in having an evolutionary meaning. Since this distance has been intensively examined at the statistical level, it is frequently chosen. The genetic distance method developed by Nei (1972) is the distance among vectors of the allelic frequencies x_i and y_i:

$$D = -\text{Log} \cos \theta, \text{ where } \theta = \text{arc} \cos \sum (x_i y_i)^{1/2}.$$

In calculating the distance matrices by the unweighted pair group method of arithmetic averages, UPGMA, the most similar populations are found and grouped. Next, each new distance is obtained by dividing the mean weight by the number of populations considered. This process is repeated until all populations are regrouped into one hypothetical population. It is possible to convert a distance matrix, once elaborated, into a tree for visualizing the similarity among the organisms.

The objective of this study was to evaluate the possibility of identification of the origins of the traditional goat population in Brazil. The importance of the work is historical and it involves an identification of the genetic resources available and the intrinsic characteristics of the genetic sources involved.

MATERIAL AND METHODS

Allelic frequencies of phenotypic traits were compared to determine the genetic distances between northeastern Brazilian goats and Mediterranean goat populations.

Populations or taxons compared

European Mediterranean goats had already been studied at the time of the 47th French Conference Institut National de la Recherche Agronomique (INRA) (Lauvergne, 1988). Data for these goats are available at the Laboratoire of Génétique Factorielle of INRA, in Jouy-en-Josas. Animals from Greece (Macedonia), Bulgaria (Sakhar), Italy (Basilicata, Calabria, Sicily, Sardinia and Malta), France (Corsica, Haute Roya and Rove) and Spain (northern region) were included. Data for these goats on Portuguese goats were not available.

Macedonia: A characteristic population from the Ceres region, Greece, in which individuals with long black hair predominate. The animals analyzed belong to the Experimental Farm of Salonika University (Boyazoglu *et al.*, 1988).

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[1] *Departamento de Produção Animal da Universidade Federal de Uberlândia, Caixa Postal 593, Campus Umuarama, 38400-902 Uberlândia, MG, Brasil. Send correspondence to T.M.M.M. at Departamento de Zootecnia, UFV, 36571-000 Viçosa, MG, Brasil. E-mail: thea@mail.ufv.br*

[2] *Laboratoire de Génétique Factorielle de l'Institut National de la Recherche Agronomique, 78352 Jouy-en-Josas, France.*

Sakhar: A characteristic population from the Sakhar hills, Bulgaria, in which individuals with long black hair predominate. The animals analyzed belong to a goat herd which is maintained for preservation of the local genetic resources (Djorbineva *et al.*, 1988).

Basilicata, Calabria and Sicily: Most of the Italian goat population is found in the southern part of the country and is characterized by strong genetic variability (Renieri *et al.*, 1988).

Sardinia: Characterized by phenotypic variability, in spite of local attempts to select for long hair (Branca and Casu, 1988).

Malta: Since 1940, goats from Malta have been crossbred with the Saanen race (Gruppetta *et al.*, 1988).

Corsica: Goats from Corsica were recently crossbred with modern races such as the Alpine (Franceschi and Santusi, 1988).

Haute Roya: Goats from the Haute Roya valley, in French Maritime Alps, are raised in migratory mixed sheep and goat herds (Martrès and Benadjaoud, 1988).

Rove: Goats from French Provence traditionally followed migratory sheep. There have been local attempts at race standardization (Sadorge and Benadjaoud, 1988).

Northern Spain: Most goats from northern Spain present some phenotypic variability (Dunner and Cañon, 1988).

The group of African Mediterranean goats was composed of three Moroccan populations. This data was unpublished.

Drâa: Southern Moroccan goats are of a non-defined type. The animals analyzed were from the Center for Goat Research and the Sidi Fleh village, located in Skoura.

Rhâali: A black goat from Morocco, probably the Atlas Mountains. Its kinship to Mamber goats from the Middle East is arguable (Hossaini-Hilari and Benlamlih, 1995). The animals analyzed were from Zagora.

Zagora: A crossbred local population with Drâa goats. The animals were from Demnate, Ouarzazate, Center for Goat Research located in Tahnnaout and the Marrakech region.

Four sub-populations of Brazilian goats of undefined breed were selected according to their geographic locations in the State of Ceará - UDB CE. The sub-populations were identified as:

UDB N CE or UDB from northeastern Ceará: The National Center for Goat Research of the Brazilian Enterprise in Agricultural and Livestock Research (EMBRAPA/CNPC) is located in this meso-region. CNPC works with both native and exotic goats. Initial work was with the main native breeds and the Indian Bhuj goats; today they use the Brazilian Moxotó breed, as well as Anglo-Nubian and Alpine breeds. These recently introduced breeds may be influencing the genetics of goats in this meso-region.

UDB M-E CE or UDB from middle-eastern Ceará: The Enterprise for Agricultural and Livestock Research of Ceará State (EPACE) is located in this meso-region. EPACE works with Alpine, Anglo-Nubian and Canindé (a Brazilian goat). The largest goat fair of the State of Ceará is also located in this meso-region. The resulting mixture of local goats with those from outside region may influence local goat genetics.

UDB S CE or UDB from southern Ceará: This meso-region is the most isolated in the State of Ceará. It is humid and characterized by commercial agriculture with salaried workers. This system of production largely excludes interest in goat production.

UDB Fortaleza: This population, being very small in size, was not examined separately from the others.

The sample population (UDB) in the State of Ceará totaled 447 animals from 21 herds. Goat herds were selected by the local development service. This method is applied when randomized choice is impossible (Gutierrez *et al.*, 1981). One municipality was chosen from each homogeneous micro-region defined by the Brazilian Institute of Geography and Statistics (IBGE).

The sample was composed of 0.05% of the total registered goats of the micro-region (IBGE, 1988), chosen from one or more herds. The size of the sample was determined to be adequate considering that one million goats are registered in the State, an area of 145,000 km^2. In the case that the herd chosen had more than enough goats for sampling, animals were chosen at random. Otherwise, all animals were chosen and others, selected at random from a second herd. Data from each micro-region were grouped by meso-regions (UDB M-E CE, UDB N CE and UDB S CE), except for those from Fortaleza due to its small registered goat herd. Data from all meso-regions, including Fortaleza, were grouped for the total sampling of the State **(UDB CE)**.

Consideration of traits and alleles

Presence/absence of reduced ears: Ears approximately two centimeters in length, such as in the Lamancha breed. This trait is controlled by an autosomal locus with incomplete dominance. The ear length (EL) locus has the alleles reduced “R” and wild “+” (COGNOSAC, 1986).

Presence/absence of long hair: Long hair is due to the presence of an autosomal locus with incomplete penetrance. The hair length (HL) locus has the alleles long “L” and wild “+” (Lauvergne and Howell, 1978; Lauvergne, 1988).

Presence/absence of horns: The hornless character is due to the expression of a dominant autosomal locus. The hornless (Ho) locus has the alleles polled “P” and wild “+” (COGNOSAG, 1986).

Presence/absence of wattles: Wattles are due to a dominant autosomal locus with variable expression. The wattles (Wa) locus has the alleles wattled “W” and wild “+” (Lauvergne, 1988).

Presence/absence of a beard: The beard is due to a locus which is dominant in males and recessive in females. The beard (Br) locus has the alleles bearded “b” and wild “+” (Asdell and Buchanan-Smith, 1928; COGNOSAG, 1986). Only females were considered in the allelic frequency calculation.

Presence/absence of roan color: Roan color is the presence of white, black and red colors in the same hair due to an autosomal locus with incomplete dominance. The roan (Rn) locus has the alleles roan “R” and wild “+” (Queinnec and Queinnec, 1974; COGNOSAG, 1986).

Presence/absence of brown eumelanin: Brown eumelanin is a modification of black eumelanin due to an autosomal locus, which is probably recessive. Its expression gives a chocolate tonality which is fixed in the Toggenbourg breed. The brown (B) locus has the alleles wild “+” and brown “b” (Berge, 1967; COGNOSAG, 1989).

Presence/absence of eumelanic standard pigmentation: The locus *Agouti* controls the appearance of both eumelanin (black or brown) and pheomelanin (red) in mammal hair. In goats the total number of alleles at this locus is unknown, but it is known that the allele called *non-agouti* is recessive to the alleles *phaeomelanic, wild, eumelanic* and *tan* and *badger face* (Searle, 1968; Lauvergne, 1993). The locus *Agouti* (A) was considered to have the allele *non-agouti* “a” and any other allele different from “a”.

In this study Nei’s genetic distance method (Nei, 1972) was applied and the resulting values were used to construct “trees” as phenograms, designed by the unweighted pair grouping method of arithmetic averages (UPGMA). To obtain a representation of the concordant parts from several possible trees for a set of data, it is necessary to construct a “tree of consensus”. In this process, each consensual tree was obtained by the majority consensus method (or majority rule consensus tree). Monophyletic groups were present in at least 50% of the 500 trees which were possible for the data set (PHILIP, 1993).

There were no data available on the brown eumelanin character for Rove goats and all goats from northern Spain. Thus, two sets of analyses were elaborated, one with 16 populations and 16 alleles and the other with 18 populations and 14 alleles.

RESULTS

Allelic frequencies for each population (Table I) were used to obtain their genetic distances from each other (Table II) and the taxonomic trees (Figure 1) were subsequently constructed. The shortest genetic distances observed were those among the different UDB populations from Ceará. The population from the Middle-Eastern meso-region was genetically differentiated from goats from other meso-regions in the State of Ceará.

UDB goats from Ceará were more closely related to Haute Roya and Rove goats (Continental European populations) than goats from Drâa, Zagora, Sardinia, Sakhar, Sicily and Macedonia (North African, Insular and Balkan populations). The consensual tree of 16 populations was more accurate than that with 18 populations (more taxons, fewer characters). However, the latter allowed the inclusion of the Northern Spanish and Rove goats. The proximity relations of the trees should be interpreted as relationship since the phenetic method chosen itself presupposes a common affiliation.

DISCUSSION

The differences observed among goats from the interior of the State of Ceará are probably due to different degrees of crossbreeding in each meso-region. The genetic distance existing between UDB goats from Ceará and goats from northern Spain is greater than that between UDB goats

Table I - Gene frequencies used in calculating genetic distances (Nei, 1972) of the goat populations.

Population	Loci, number of animals (N) and alleles															
	A		EL		Ho		Wa		Br		Rn		B		HL	
	N	a	N	+	N	+	N	+	N	b	N	+	N	b	N	+
Sakhar	103	0.704	103	1.000	103	0.900	103	0.975	103	0.980	103	0.995	103	0	103	0
Macedonia	62	0.475	72	0.967	72	0.976	72	0.979	72	0.833	72	1.000	70	0	72	0
Haute Roya	57	0.737	62	0.975	62	0.851	62	0.793	62	0.880	57	0.991	53	0	62	0.766
Rove	70	0.414	70	1.000	70	1.000	70	0.786	70	0.358	70	0.971	-	-	70	0.963
Corsica	90	0.527	94	1.000	94	0.995	104	0.679	94	1.000	90	0.888	81	0.567	94	0.103
N. Spain	1168	0.438	1643	0.830	1607	0.580	1604	0.780	1607	0.450	272	0.290	-	-	1603	0.670
Basilicato	291	0.718	300	1.000	300	0.786	300	0.779	300	0.913	291	0.812	246	0.451	300	0.362
Calabria	130	0.541	136	0.989	136	0.862	129	0.737	133	0.761	136	0.818	109	0.287	136	0.309
Sicily	806	0.564	813	0.966	813	0.787	813	0.705	813	0.848	806	0.870	595	0.179	813	0.012
Malta	332	0.618	445	0.998	445	0.445	445	0.657	433	0.462	332	0.751	139	0.509	445	0.558
Sardinia	92	0.387	145	1.000	145	0.017	145	0.797	145	0	129	0.747	126	0.311	145	0.346
Drâa	56	0.327	102	1.000	102	0.804	102	0.939	82	0.506	99	0.302	84	0.267	102	0
Rhâali	181	0.895	189	1.000	189	0.987	189	0.973	167	0.982	187	0.599	187	0.103	189	0.987
Zagora	19	0.688	34	1.000	34	0.748	34	0.924	34	0.485	33	0.174	30	0.183	34	0.955
UDB N CE	199	0.496	203	1.000	203	0.939	203	0.973	163	0.559	199	0.911	194	0.176	203	0.726
UDB M-E CE	92	0.521	92	1.000	92	0.828	92	0.978	81	0.369	92	0.801	90	0.105	92	0.676
UDB S CE	134	0.414	139	1.000	139	0.873	139	0.971	112	0.535	136	0.920	134	0.122	139	0.796
UDB CE	438	0.484	447	1.000	447	0.892	447	0.967	367	0.517	440	0.894	430	0.145	447	0.742

Table II - Matrix of genetic distances for the 18 goat populations, according to Nei (1972).

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	0																	
2	0.1070	0																
3	0.1801	0.4315	0															
4	0.1801	0.3870	0.0130	0														
5	0.0962	0.4168	0.1117	0.1300	0													
6	0.0802	0.1942	0.3089	0.2809	0.1933	0												
7	0.1182	0.3272	0.2764	0.2287	0.0831	0.1596	0											
8	0.0842	0.3534	0.3300	0.0527	0.0389	0.1712	0.1697	0										
9	0.0774	0.3031	0.0383	0.0322	0.0579	0.1491	0.1312	0.0131	0									
10	0.1275	0.3301	0.0198	0.0213	0.1258	0.2395	0.2585	0.0319	0.0207	0								
11	0.1720	0.4709	0.0240	0.0244	0.1030	0.2697	0.2358	0.0305	0.0206	0.0135	0							
12	0.0868	0.3002	0.1359	0.1180	0.0401	0.1287	0.0267	0.0761	0.0575	0.1426	0.1306	0						
13	0.0608	0.2050	0.1684	0.1383	0.0769	0.0891	0.0347	0.1004	0.0742	0.1609	0.1724	0.0120	0					
14	0.0852	0.2768	0.1696	0.1382	0.0503	0.1223	0.0204	0.0979	0.0753	0.1700	0.1597	0.0032	0.0132	0				
15	0.0772	0.2714	0.1500	0.1237	0.0459	0.1166	0.0236	0.0838	0.0636	0.1520	0.1450	0.0080	0.0078	0.0017	0			
16	0.1825	0.2623	0.1567	0.1191	0.3048	0.1232	0.3162	0.1556	0.1084	0.1123	0.1458	0.1995	0.1628	0.2189	0.1985	0		
17	0.1827	0.6055	0.2083	0.2454	0.0489	0.1755	0.1436	0.0978	0.1393	0.2475	0.2015	0.0892	0.1236	0.1042	0.0961	0.3370	0	
18	0.1459	0.3560	0.3858	0.3868	0.1841	0.0450	0.1620	0.2104	0.2181	0.3613	0.3609	0.1385	0.1084	0.1388	0.1296	0.2288	0.0941	0

1. Malta, 2. Sardinia, 3. Sakhar, 4. Macedonia, 5. Haute Roya, 6. N. Spain, 7. Rove, 8. Basilicato, 9. Calabria, 10. Sicily, 11. Corsica, 12. UDB N CE, 13. UDB M-E CE, 14. UDB S CE, 15. UDB CE, 16. Drâa, 17. Rhâali, 18. Zagora.

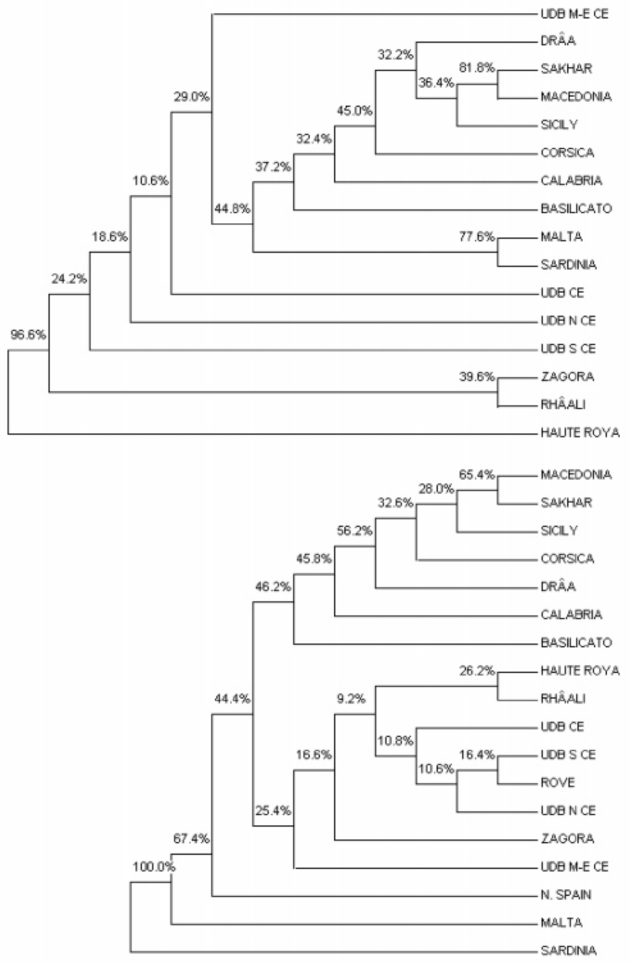

Figure 1 - Consensus taxonomic trees designed using Philip (1993), with 16 and 18 goat populations, respectively.

from Ceará and goats from southern France. This is probably explained by the locus ear length. The allele which determines short ears is normally rare, but it appears at a frequency of 0.17 in the Spanish goat population. In other words, 2.9% of all goats in northern Spain have reduced ears.

The number of times branches appeared at the same position on 500 trees, taken randomly, was occasionally superior to 80%. This happened, on the first tree, between Haute Roya goats and other populations and between Sakhar and Macedonia goats. On the second tree it happened between Sardinia goats and other populations. It would be necessary to increase the number of traits examined to increase reliability. It is suggested that future studies include the loci *Spotting* and *Frosting* as well as certain quantitative traits such as facial profile (convexity), and biochemical and molecular markers.

In conclusion, the Brazilian UDB goats are more closely related to Continental and Western European populations than to North African, Balkan or Insular Mediterranean populations.

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RESUMO

Foram comparadas cabras do tipo Sem Raça Definida ou UDB do Ceará (N = 447), nordeste do Brasil, cabras mediterrâneas européias (N = 3847) e mediterrâneas africanas (N = 325) visando o estabelecimento de distâncias genéticas e de árvores taxonômicas. Foram utilizadas as freqüências alélicas em cada população para a presença ou ausência dos caracteres cornos, orelhas reduzidas, pêlos longos, brincos, barba, pelagem ruão, eumelanina de coloração castanha e padrão pigmentar eumelânico. As distâncias genéticas segundo o método de Nei (1972) são: as menores entre as cabras de diferentes mesorregiões do Ceará (0,0008 a 0,0120); pequenas entre o conjunto das UDB do Ceará e as cabras francesas do Rove e do Alto Roya (0,0236 e 0,0459); grande entre o conjunto das cabras UDB do Ceará e as cabras do norte da Espanha (0,1166); as maiores entre o conjunto das cabras UDB do Ceará e as cabras norte-africanas (marroquinas do Drâa, Rhâali e Zagora), balcânicas (Sakhar da Bulgária e Macedônia da Grécia) e algumas populações insulares (Córsega, Sicília, Sardenha) mediterrâneas (0,1237 a 0,2714). As cabras brasileiras UDB estão mais aparentadas com as populações européias do oeste do continente do que com as populações caprinas norte-africanas, balcânicas ou mediterrâneas insulares.

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