



Microsatellite analysis of the Rousse de Maradi (Red Sokoto) goat of Burkina Faso

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ABSTRACT

A total of 33 reproductive individuals of the Rousse de Maradi (Red Sokoto) goat breed of Burkina Faso were genotyped for 19 microsatellites and compared with 154 samples from four different populations of Burkinabé Sahelian and Djallonké goat. The between-populations molecular coancestry for the Rousse de Maradi-pairs varied from 0.420 (with the Northern Sahelian population) to 0.459 (with the Eastern Djallonké population). The between-populations genetic differentiation assessed using F_{ST} varied from 0.018 for the pair formed by the two Sahelian populations to 0.050 for the pairs formed between the Rousse de Maradi population and each of the Djallonké populations. Both correspondence and STRUCTURE analyses showed that the Rousse de Maradi breed: (a) has a particular genetic background; and (b) it is genetically nearer to the Sahelian goat. Overall, the present analysis characterise the Rousse de Maradi breed as a part the goat metapopulation exploited in the Sahel area rather than a population derived from the West African Dwarf goat. Implementation of strategies to further characterise production and reproduction performance of the Burkinabé Rousse de Maradi goat breed can be advised.

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1. Introduction

There is an increasing interest in the characterisation of the African domestic small ruminant populations using morphological (Dossa et al., 2007; Traoré et al., 2008a,b), microsatellite (Álvarez et al., 2009, in press; Traoré et al., 2009; Peters et al., 2010) and mitochondrial (Royo et al., 2008) markers. The Burkina Faso goat population is mainly formed by three breeds (Traoré et al., 2008a, 2009): (a) the Northern Sahelian breed is the Burkina Faso representative of the long-legged goat group, spread throughout the Sahel region of West Africa; (b) the Djallonké breed, located in the Southern Burkinabé Sudan area, is a short-eared and small-horned goat belonging to the West African Dwarf

goat population; and (c) the Mossi breed, a transition population between the Sahel and the Djallonké goat breeds, which is kept in the Central Sudan-Sahel area of Burkina Faso. Morphological and microsatellite analyses suggested that the Mossi breed is closely related with the Djallonké breed (Traoré et al., 2008a, 2009) and differences between the Mossi and the Djallonké breeds are likely to be due to an ancient and sustained introgression southwards of the Sahelian goat favoured by nomadic pastoralism and the increase of the duration of the dry seasons in West Africa since the 1970s.

Moreover, in the last decades the Rousse de Maradi (Red Sokoto) goat breed introgressed from Niger into Burkina Faso and is becoming increasingly popular in the Sahel area of the country. The Rousse de Maradi breed is a representative of the Savannah goat group (DAGRIS, 2007), a relatively small-sized goat owned principally by Hausa-speaking agricultural tribes. The Rousse de Maradi goat

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is kept mainly in the Sokoto and Kano States of Nigeria and in the Maradi and Tessoua Departments of Niger. Although morphological differences between Red Sokoto and Dwarf goat are significant and allow a clear differentiation between them (Yakubu et al., 2010, 2011), the relatively small size and relatively high prolificacy of the Rousse de Maradi individuals led to hypothesise an intense crossing with Dwarf goats during the formation of the breed (Wilson, 1991).

The aim of this note is to start with the characterisation of the Rousse de Maradi goat in Burkina Faso. A representative sample of this breed will be genotyped with a set of 19 microsatellites. The obtained results will be compared with different populations of the Sahelian and Djallonké goat breeds of Burkina Faso to ascertain their genetic relationships and differentiation with the Rousse de Maradi population.

2. Materials and methods

2.1. Sampling and genotyping

Blood samples were obtained from a total of 33 reproductive individuals (10 bucks and 23 does) belonging to the Rousse de Maradi goat breed (Fig. 1). Samples were obtained in different flocks around Dori (Northern Burkina Faso) and from an experimental flock managed at INERA in Ouagadougou. Also, 82 samples from Sahelian goat and 72 samples from Djallonké goat were obtained in different flocks of Yakouta (22), Dori (11), Yalga (26), Kaya (23), Orodara (28) Gaoua (21) and Kampti (23). Samples were pooled according to geography to form four different reference populations. The samples from Yakouta and Dori were pooled to form the so called 'Northern Sahelian' population and those from Yalga and Kaya were pooled to form the 'Southern Sahelian' population. The individuals sampled in Orodara were considered representative of the 'Eastern Djallonké' population while those sampled in Gaoua and Kampti were pooled to form the 'Western Djallonké' population. Within each location, from 3 to 10 different flocks were sampled. When possible, sampling within a flock included the 2 older does and the younger buck.

Total DNA was isolated from blood samples following standard procedures (Sambrook et al., 1989). A microsatellite set, including 19 markers (BM6526, BM757, BMS2626, BMS356, CSSM66, McM53, RBP3, BM8125,

BMS2461, BMS975, CSRD2111, CSSM31, ILSTS005, INRA26, McM527, OarHH64, SPS115, TGLA53 and LSCV29), was analysed on all the individuals. The microsatellites used were selected from those previously used in diversity analyses of goat (Traoré et al., 2009) and sheep (Álvarez et al., 2009, in press). Genotyping was performed on an Automatic Sequencer ABI 310 (Applied Biosystems, Barcelona).

2.2. Statistical analyses

The following parameters were computed using the program MolKin 3.0 (Gutiérrez et al., 2005): number of observed alleles, expected heterozygosity (H_e), Wright's F -statistics and raw (A) and rarefacted (A_g) average number of alleles per locus (allelic richness). Here, g was fitted to 38, which is twice the minimum number of individuals within a population with genotype known for all the microsatellites. See Gutiérrez et al. (2005) and the User's Guide of the program MolKin (freely available at http://www.ucm.es/info/prodanim/html/JP_Web.htm) for a detailed description of the methodologies used. The statistical significance of the obtained values was estimated by bootstrapping using 1000 replications. To avoid bias because of unequal sample sizes, statistical significance of the obtained values the bootstrapping method recommended by Simianer, 2002; Simianer (2002; Baumung et al., 2006) was applied using 1000 samples with exactly 30 individuals per sampled population.

Individual multilocus genotypes were also investigated carrying out a canonical discriminant analysis using the Proc CORRESP of SAS/STAT (1999) to obtain an unbiased test of population structure. Correspondence analysis dimensions were plotted using Microsoft Excel™.

The program STRUCTURE (Pritchard et al., 2000) was used to ascertain cryptic genetic structure in the analysed dataset. The program gives Bayesian estimates of the natural logarithm of the probability that a given genotype X is part of a given population K ($\ln \Pr(X|K)$). As the implemented algorithm uncovers 'hidden structure' without using a priori knowledge about the number of clusters (populations or breeds) present in a dataset, we identified the most likely K -value in our data set according to Evanno et al. (2005) using the website STRUCTURE HARVESTER v0.6.8 (Dent and Bridgett, 2011). We set K to vary between 1 and 10, and for each K -value we performed 10 simulations with different starting points. All runs used a burn-in period of 100,000 iterations and a period of data collection of 100,000 iterations. The program was run under the admixture model, considering correlated allele frequencies.

Finally, presence of first generation migrants was detected using the program GENECLASS 2.0 (Piry et al., 2004). This program implements the methodology proposed by Paetkau et al. (2004) which seeks the maximisation of the ratio of the likelihood computed from the population where

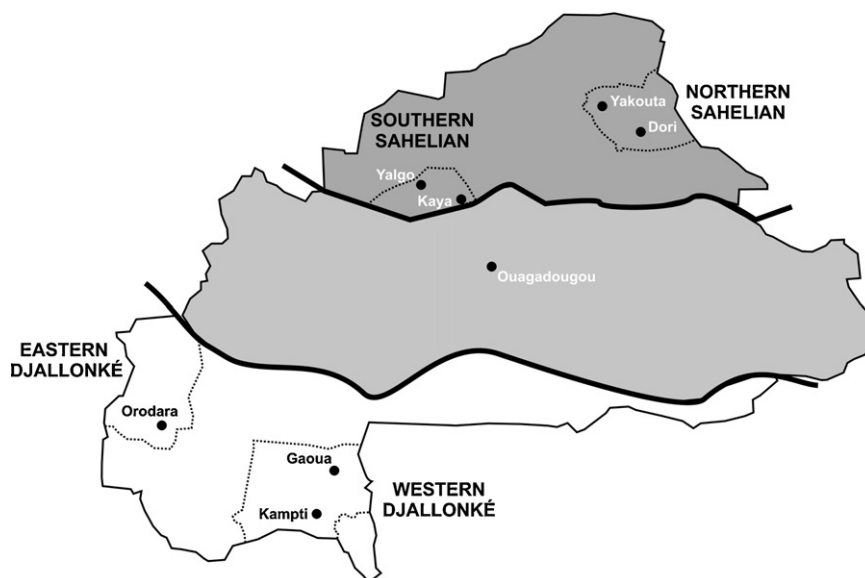


Fig. 1. Map illustrating the limits of the Northern Sahelian and Southern Sudan environmental areas of Burkina Faso. The main locations and the areas in which the sampling was carried out are also given.

Table 1
Number of individuals analysed (N), within-population expected heterozygosity (H_e), heterozygote deficiency within population (F_{IS}), average number of alleles per locus (A) and average number of alleles per locus rarefacted to 38 copies ($A_{(38)}$) per analysed population and for the whole dataset. The between-populations molecular coancestry (above diagonal) and F_{ST} (below diagonal) matrices are also given. Standard deviations of the estimates are in brackets.

Breed	N	Within-population parameters					Between-populations parameters				
		H_e	F_{IS}	A	$A_{(38)}$	1	2	3	4	5	
1. Rousse de Maradi	33	0.483 (0.021)	0.032 (0.040)	5.1	4.5		0.420 (0.011)	0.441 (0.012)	0.459 (0.015)	0.454 (0.013)	
2. Northern Sahelian	33	0.601 (0.009)	0.036 (0.023)	7.3	6.3	0.034 (0.006)		0.392 (0.009)	0.403 (0.010)	0.401 (0.009)	
3. Southern Sahelian	49	0.573 (0.014)	0.060 (0.029)	7.4	6.0	0.029 (0.005)	0.018 (0.003)		0.403 (0.010)	0.401 (0.009)	
4. Eastern Djallonké	28	0.496 (0.018)	0.103 (0.037)	5.7	5.3	0.050 (0.007)	0.042 (0.006)	0.041 (0.005)		0.462 (0.013)	
5. Western Djallonké	44	0.505 (0.014)	0.114 (0.034)	6.0	5.2	0.050 (0.007)	0.040 (0.005)	0.035 (0.005)	0.037 (0.005)		
Totals	187	0.565 (0.007)	0.068 (0.014)	9.9	6.2						

the individual was sampled over the highest likelihood value among all population samples including the population where the individual was sampled.

3. Results

F -statistics computed for the whole population were 0.068, 0.058 and 0.122 for, respectively, F_{IS} , F_{ST} and F_{IT} . Parameters characterising genetic variability of the analysed goat populations are given in Table 1. The Sahelian goat populations had the higher expected heterozygosity and rarefacted average number of alleles per locus values in the dataset while the Rousse de Maradi had the lowest values ($H_e = 0.483$ and $A_{(38)} = 4.5$). The Djallonké populations had also low expected heterozygosity values (roughly 0.5) and rarefacted allelic richness (5.3 and 5.2 for the Eastern and Western Djallonké populations, respectively). All the analysed populations had positive F_{IS} values, with the Djallonké populations having marked heterozygote deficiency (0.103 and 0.114 for the Eastern and Western Djallonké populations, respectively).

The between-populations molecular coancestry (f_{ij}) and F_{ST} matrices are also given in Table 1. The lowest paired molecular coancestry value (0.392) was computed between the two Sahelian goat populations while the highest was computed between the two Djallonké populations (0.462). The Rousse de Maradi population showed high genetic identity with the other analysed populations, varying from 0.420 (pair with the Northern Sahelian population) to 0.459 (with the Eastern Djallonké population). The between-populations genetic differentiation assessed using F_{ST} varied from 0.018 for the pair formed by the two Sahelian populations to 0.050 for the pairs formed between the Rousse de Maradi population and each of the Djallonké populations.

Fig. 2 shows the between-populations (Plot A) and between-individuals (Plot B) genetic relationships assessed using correspondence analysis. The Djallonké populations and individuals are separated from the others on Dimension 1 (X -axis) while Dimension 2 (Y -axis) allows differentiating between the Rousse de Maradi and the Sahelian goat. However, between-individuals differentiation is not as clear as that assessed for the populations. As expected, the Sahelian (on the left of Dimension 1) and the Djallonké individuals (on the right of Dimension 1) tend to overlap regardless the populations to which they are assigned. However, this overlap also exists with the Rousse de Maradi individuals.

Population structure and degree of admixture were assessed using the program STRUCTURE. The most likely number of clusters (K) present in the dataset according to Evanno et al. (2005) was 4 (Fig. S1). Table 2 gives the membership (in percentage) of each of the analysed goat breeds in each of the 4 most likely clusters inferred. Clusters 2, 3 and 4 included most Sahelian, Rousse de Maradi and Djallonké individuals, respectively. However, the analysed populations showed a high degree of admixture. A significant proportion of Sahelian and, particularly, Eastern Djallonké individuals clustered in the inferred group 1.

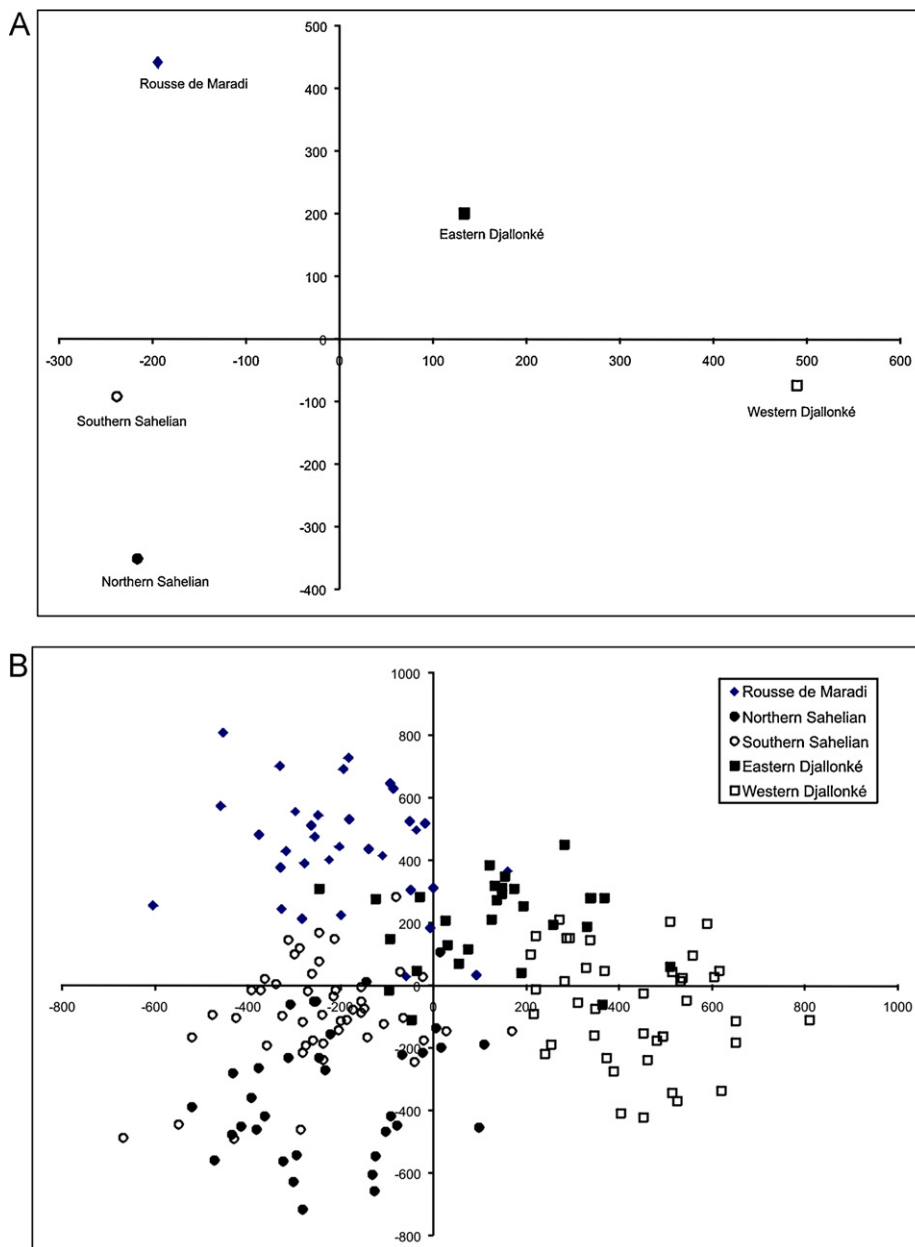


Fig. 2. Distribution of the analysed goat population (Plot A) and the individual multilocus genotypes (Plot B) on the bidimensional space formed by the two dimensions computed via a canonical discriminant analysis. Dimension 1 is on the X-axis while Dimension 2 is on the Y-axis.

Table 2

Number of individuals per breed (*N*) and proportion (in percentage) of membership of each sampled population in each of the four clusters inferred in the most likely run using the program STRUCTURE. Proportions of membership higher than 0.2 are in bold.

Population	Inferred clusters				<i>N</i>
	1	2	3	4	
Rousse de Maradi	0.132	0.138	0.652	0.077	33
Northern Sahelian	0.210	0.607	0.081	0.102	33
Southern Sahelian	0.255	0.494	0.164	0.087	49
Eastern Djallonké	0.547	0.165	0.068	0.220	28
Western Djallonké	0.092	0.106	0.047	0.755	44

This admixture scenario was confirmed using the program GENECLASS. One Rousse de Maradi, 4 Northern Sahelian, 1 Eastern Djallonké and 2 Western Djallonké individuals were classified as migrants from the Southern Sahelian population. In turn, the Southern Sahelian population received 2 migrants from the Northern Sahelian population. The Rousse de Maradi population received one migrant from the Western Djallonké population.

4. Discussion

Overall differentiation assessed is higher than that reported in Burkina Faso goat ($F_{ST} = 0.035$; Traoré et al., 2009) and consistent with the scenario recently described by Missohou et al. (2011). The latter study analysed 9 goat populations from 8 West African countries and concluded that genetic differentiation in West African goat is more likely due to geographic distance rather than to a different origin of the livestock populations. The current study and that by Traoré et al. (2009) are not directly comparable with the present analysis due to differences in sampling. The study by Traoré et al. (2009) included a significant number of Mossi goat, which is a transition population sharing many genetic features with both the Sahel and the Djallonké breeds, therefore erasing overall genetic differentiation. Also, these discrepancies are likely to be explained by the differences between the microsatellite sets used.

In any case, as previously reported, the overall genetic differentiation assessed in the dataset is moderate due to a wide gene flow all over Burkina Faso (Traoré et al., 2009). This is reflected in the relatively high between-populations genetic identity (molecular coancestry) and low differentiation between populations (F_{ST} ; Table 1). The Sahelian goat populations showed both the lowest genetic identity and differentiation showing that these populations belonging to the same breed share similar alleles set with unbalanced allele frequencies. Higher between-populations genetic identity and low differentiation were found for the Djallonké goat, associated to the higher F_{IS} values computed. The Djallonké goat was reported to gather less genetic diversity than Sahelian goat in Burkina Faso (Traoré et al., 2009). The present analysis, using additional Djallonké samples (those from Orodara), confirms this fact.

The main goal of this note is the study of the Burkinabé Rousse de Maradi goat. In this respect, the analyses carried out characterise this breed as a 'non-Djallonké' goat. Both the between-populations F_{ST} 's assessed and the correspondence analysis clearly separate the Rousse de Maradi goat from the Djallonké populations of Burkina Faso. Although the Rousse de Maradi breed has a particular genetic background, as reflected in the STRUCTURE analysis, it is genetically nearer to the Sahelian goat (Fig. 2). In any case, the Rousse de Maradi population has received genetic influence from the other Burkinabé goat populations, as reflected by the GENECLASS analysis. The Rousse de Maradi goat of Burkina Faso is mainly spread in the Sahel area around Dori, which is the major livestock market place of this part of the country, therefore leading to extensive commercial trade and favouring genetic exchanges. This would

explain the identifications of Djallonké migrants into the Rousse de Maradi population (Fig. 2B).

In any case, the influence of the Djallonké (Dwarf) goat on the Rousse de Maradi population of Burkina Faso is limited. In this respect, the present analysis does not support the hypothesis suggesting that the formation of the breed was highly influenced by the West African Dwarf goat (Wilson, 1991). On the contrary to that previously did for the Mossi goat breed of Burkina Faso (Traoré et al., 2008a, 2009), the Rousse de Maradi cannot be defined as a transition population between the Sahel and the Dwarf Djallonké populations. Although some body traits, such as body length and withers height of the Mossi and the Rousse de Maradi goat may be similar (Traoré et al., 2008a; DAGRIS, 2007), at the microsatellite level the Mossi breed had lower genetic distance with the Sahelian and the Djallonké breeds than that assessed between the two parent populations (Traoré et al., 2009). This scenario could not be observed in the present analysis. Differentiation (F_{ST}) between the Sahelian and the Djallonké populations varied from 0.035 to 0.042 while differentiation between the Rousse de Maradi and the Sahelian and the Djallonké goat populations of Burkina Faso are, respectively, below and above these bounds.

In summary, although definition of livestock breeds in Africa is difficult due to lack of selection and high between-populations gene flow (Traoré et al., 2008a, 2009; Missohou et al., 2011), the Rousse de Maradi goat can be considered as a population with particular genetic background in Burkina Faso. This genetic background is a part of the goat metapopulation exploited in the Sahel area rather than that of the West African Dwarf goat. Implementation of strategies to further characterise production and reproduction performance of the Burkinabé Rousse de Maradi goat breed can be advised.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.smallrumres.2012.01.012.

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