

## GENETIC CHARACTERIZATION OF WEST AFRICAN DJALLONKE SHEEP USING MICROSATELLITE MARKERS

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### Summary

Genetic diversity of 11 Djallonke sheep populations from Guinea, Mali, Senegal and The Gambia and three reference populations from Mali, Nigeria and Portugal was estimated using 15 microsatellites. Djallonke sheep in Mali, Gambia and eastern Guinea have higher genetic diversity compared to those in Senegal and southern and western Guinea. Close genetic relationships was observed between the Djallonke sheep from Senegal and The Gambia.

### Keywords

West Africa, sheep, genetic diversity, trypanosomosis, resistance

### Contribution

African tsetse fly-transmitted trypanosomosis affects a wide range of wild and domesticated animal species. Sheep breeds e.g. Djallonke with the trypanotolerant trait are a dependable asset to the local farmers in West Africa. These breeds which are relatively small in body size have proven to be productive under difficult conditions [1]. However, their genetic characteristics are poorly documented.

In this study, 11 Djallonke sheep populations were collected from four West African countries: 147 blood samples from five sites in Guinea; 103 samples three sites in Mali; 62 samples from two sites in Senegal and 57 samples from The Gambia. Fifteen microsatellite markers were used to genotype these 369 individuals together with 124 samples from three reference populations from Mali, Nigeria and Portugal (Table 1).

Observed ( $H_O$ ) and expected ( $H_E$ ) heterozygosity values and mean number of alleles ( $MNA$ ) across the 15 loci for the 14 populations were calculated with Microsatellite Toolkit [2] (Table 1). An adjusted  $MNA$  estimate based on sample size [3] was carried out using 250 replicates of re-sampling of 24 individuals with replacement for all but one of the Guinea populations sampled in site 1, which had only 24 individuals. Nei's  $D_S$  [4] genetic distances between pairs of populations were calculated using the program DISPAN [5] and an UPGMA phylogenetic tree was constructed (Fig. 1).

A total of 205 alleles were observed in 493 individuals. Malian, Gambian and eastern Guinean (G3 and G4) Djallonke sheep populations have higher genetic diversity with  $H_E$  ranging between 0.678 and 0.706 and adjusted  $MNA$  between 6.49 and 7.35 compared to the Senegalese and southern and western Guinean (G1, G2 and G5) populations with  $H_E$  varying from 0.657 to 0.671 and adjusted  $MNA$  from 5.76 to 6.80 (Table 1).

Table 1.  $H_E$ ,  $H_O$ ,  $MNA$  and the adjusted  $MNA$  in the 14 sheep populations studied.

**THE ROLE OF BIOTECHNOLOGY**  
Villa Gualino, Turin, Italy – 5-7 March, 2005

Country	Breed	Sampling site	No.	$H_E \pm SD$	$H_O \pm SD$	$MNA \pm SD$ (all animals)	$MNA$ (24 animals)
Guinea	Djallonke	G1	24	0.671 ± 0.041	0.630 ± 0.026	6.80 ± 2.60	6.80
		G2	27	0.656 ± 0.041	0.646 ± 0.024	5.93 ± 2.05	5.80
		G3	31	0.706 ± 0.046	0.670 ± 0.022	7.27 ± 2.05	6.87
		G4	34	0.687 ± 0.042	0.659 ± 0.021	7.07 ± 2.46	6.62
		G5	31	0.656 ± 0.047	0.641 ± 0.023	6.07 ± 1.79	5.76
Mali		M1	35	0.700 ± 0.048	0.671 ± 0.021	7.40 ± 2.16	6.78
		M2	29	0.678 ± 0.040	0.703 ± 0.022	6.80 ± 2.24	6.49
		M3	39	0.705 ± 0.032	0.631 ± 0.020	8.33 ± 2.66	7.35
Senegal		S1	27	0.657 ± 0.043	0.644 ± 0.024	6.20 ± 1.66	6.07
		S2	35	0.663 ± 0.040	0.662 ± 0.021	6.73 ± 2.09	6.23
The Gambia		TG	57	0.690 ± 0.037	0.657 ± 0.016	8.33 ± 2.61	7.01
Mali	Macina	Macina	42	0.751 ± 0.028	0.659 ± 0.019	9.13 ± 2.80	8.08
Nigeria	Uda Black	Nigeria	40	0.745 ± 0.027	0.653 ± 0.021	8.73 ± 2.55	7.67
Portugal	Merino	Portugal (PBM)	42	0.754 ± 0.020	0.759 ± 0.017	7.73 ± 2.49	6.98

Note: G1 samples were collected from Koundara, Gaoual, Boke and Telimele; G2 from Dinguiraye and Tougue; G3 from Mandiana and Siguiri; G4 from Beyla and Kerouane; G5 from Faranah and Mamou; M1 from Sagabory, M2 from Tousséguéla; M3 from Manankoro; S1 from Kafesse and Mangoulene Dioga; S2 from Sédhiou; TG from Keneba, Mamut and Pachonki.

Phylogenetic analysis clearly separates the Djallonke from the non-Djallonke sheep populations (Fig. 1). Senegalese and Gambian Djallonke sheep populations form a relatively close cluster (supported by 95% of the bootstrap values) joined by the southern and western Guinean populations (85%). Malian and eastern Guinean Djallonke sheep populations group together into another cluster (89%) except the M3 population which may have been heavily introgressed with non-Djallonke sheep.

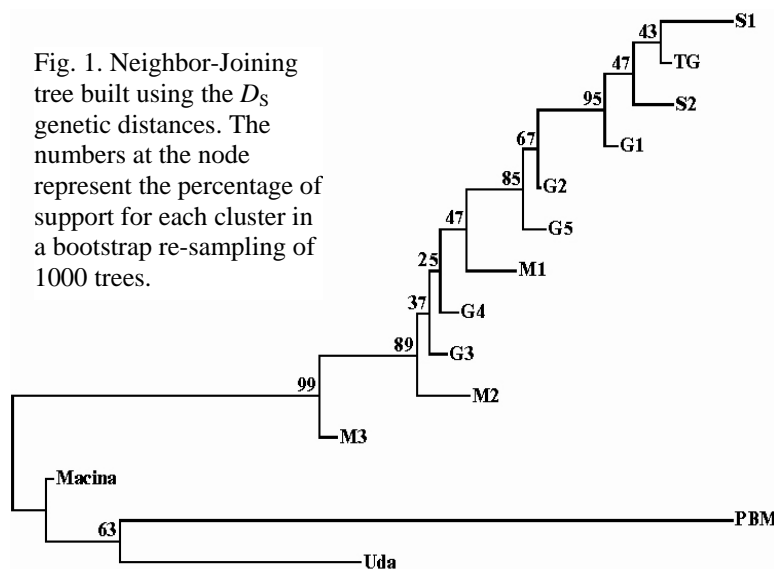


Fig. 1. Neighbor-Joining tree built using the  $D_S$  genetic distances. The numbers at the node represent the percentage of support for each cluster in a bootstrap re-sampling of 1000 trees.

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