

Genetic Diversity and Relationships Of Sheep Breeds Of Kenya: Preliminary Results And Evidence of Dilution Of the Indigenous Red Maasai

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Introduction

Indigenous sheep are an important resource especially to pastoralists and resource-poor people of Kenya, providing them with meat, milk, manure and are also a quick source of income during emergencies (Rege *et al.*, 1996). The sheep of Kenya can be classified as either fat-tailed (e.g. Red Maasai and East African Fat-tailed), or fat-rumped (e.g. Somali Blackhead Persian) (Rege *et al.*, 1996). These sheep breeds are faced with major challenges that include persistent droughts, diseases, conflicts and poor nutrition (Kosgey *et al.*, 2008). Their ability to walk long distances in search of pasture and adaptability to the harsh environmental conditions of the Arid and Semi-Arid Lands and resistance to gastrointestinal nematodes increase their importance to resource-poor farmers and pastoralists (Baker *et al.*, 2002; Owen *et al.*, 2005).

Material and methods

Population studied and molecular analysis. Nine sheep populations (Table 1) were sampled from, the West of the Rift Valley (Migori, Homa Bay/Kendu Bay, Transmara and Kakamega) and the East of the Rift Valley (Kajiado, Naivasha/Olmagogo, Mutara, Laikipia East and Laikipia West) of Kenya. DNA was extracted from blood and PCR amplified using 15 microsatellite markers (*OARFCB20*, *TGLA53*, *MCM42*, *OARVH72*, *BM8125*, *ILSTS11*, *OARJMP29*, *OARFCB11*, *ILSTS005*, *MAF209*, *SRCRSP5*, *DYMS1*, *SRCRSP9*, *MAF214*, *OARFCB226*) (Muigai *et al.*, 2009). PCR products were separated using an ABI 3730 DNA analyzer. The data were collected by GeneMapper® software (version 3.7, Applied Biosystems). The third order least squares method was used for size calling.

Genetic diversity, population structure and phylogenetic analysis. Each populations genetic diversity was assessed by calculating the mean number of alleles, the expected heterozygosity and its standard errors using DISPAN (Ota, 1993). The genetic relationships between the sheep breeds were calculated using Nei's genetic distances (D_a) (Nei *et al.*, 1983) and a neighbor-joining tree was constructed using the DISPAN program (Ota, 1983). Population structure analysis was performed using a Bayesian clustering approach using the

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STRUCTURE programme (Pritchard *et al.*, 2000) and Principal component analyses were performed using the XLSTAT ver. 4.2 program (<http://www.xlstat.com>).

Table 1: Breed type, sampling location, number of individuals, expected heterozygosity (H_e) and mean number of alleles (MNA) per locus of the populations studied

Breeds/Sampling Location	Type	Number	H_e (s.e)	MNA*
<i>West of Rift Valley</i>				
Migori	East African Fat – tailed	30	0.662 ± 0.033	6.16
Homabay/KenduBay	East African Fat – tailed	32	0.644 ± 0.033	5.61
Kakamega	East African Fat – tailed	30	0.697 ± 0.026	6.65
Transmara	East African Fat – tailed	40	0.702 ± 0.030	6.4
<i>East of Rift Valley</i>				
Red Maasai - Mutara	Fat – tailed	48	0.700 ± 0.025	6.16
Red Maasai - Olmagogo	Fat – tailed	47	0.661 ± 0.030	5.88
Dorper - Laikipia East	Thin– tailed	30	0.713 ± 0.025	6.37
Dorper - Laikipia West	Thin– tailed	30	0.706 ± 0.032	6.59
Red Maasai - Kajiado	Thin – tailed	47	0.675 ± 0.036	5.69
Mean		334	0.680 ± 0.030	6.17

*After 99 replicate re-sampling of 20 individuals with replacement

Results and discussion

The genetic relationships between the breeds are illustrated in Figure 1. The neighbour-joining tree shows two main groups. One group comprised two Red Maasai populations from the Rift Valley, the Olmagogo and Mutara, and the East African fat-tailed sheep, Kakamega, Migori and Transmara, with the latter showing a closer clustering pattern. However the Red Maasai population from Kajiado clustered in the same group as the two Dorper populations from Laikipia East and West respectively. This result is supported by the Principal Component (Figure 2). Population admixture analyses (Figure 3) show grouping patterns of the sheep populations for $K=2$ to $K=5$. At $K=2$ the two Dorper populations clustered with the two Red Maasai populations sampled in Kajiado and Mutara giving an indication that these populations are highly introgressed by the Dorper. At $K=3$ the Olmagogo population was realized, while at $K=4$ the East African fat-tailed populations were realized.

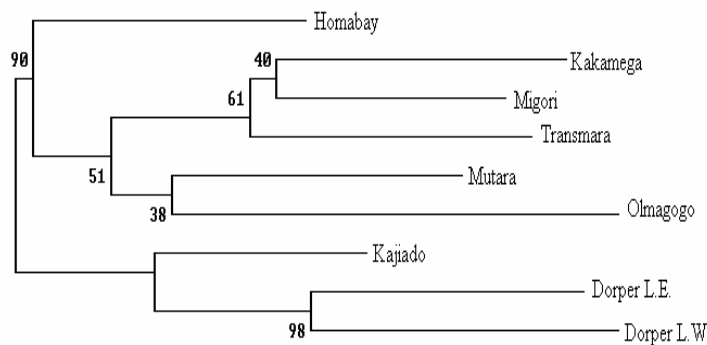


Figure 1 D_A Phylogenetic tree representing the genetic relationship between the Kenyan Sheep: KEY: Dorper L.E. = Laikipia East Dorper; Dorper L.W. = Laikipia West Dorper

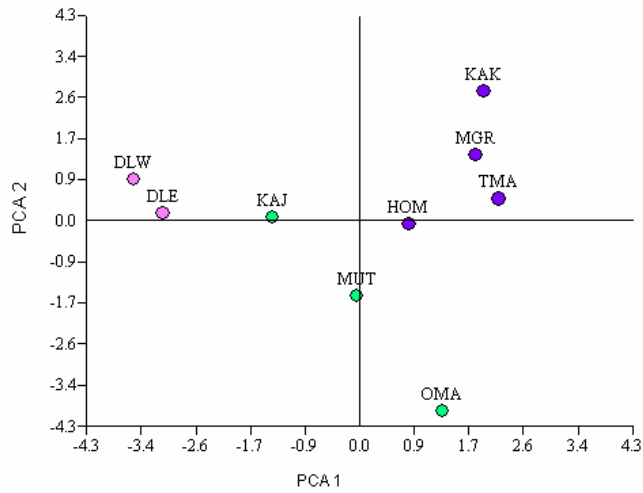


Figure 2 Principal Component Analysis (PC1 vs PC2) among populations based on allele frequencies from 15 microsatellite loci: MUT - Mutara, OMA - Olmagogo, KAK - Kakamega, TMA - Transmara, MGR - Migori, DLE - Laikipia East Dorper, DLW - Laikipia West Dorper, HOM - Homabay, KAJ – Kajiado

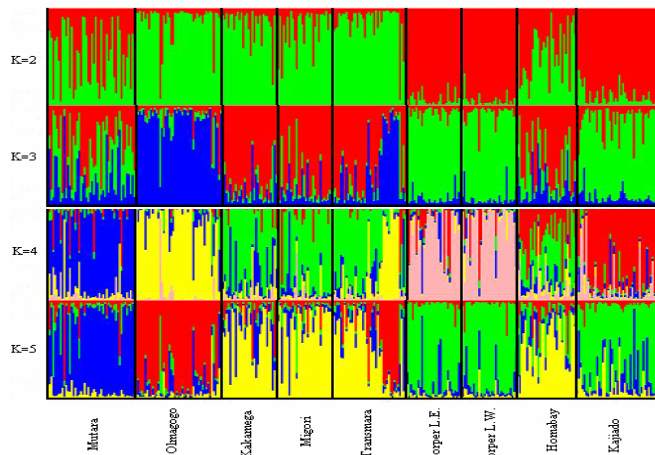


Figure 3 Population admixture analyses using allele frequency data from 15 microsatellite loci typed in 9 Sheep populations

Conclusion

These results clearly show that indigenous Red Maasai population from Kajiado has been systematically cross bred with the Dorper resulting in introgression of Dorper genes into the Red Maasai. This has resulted into the direct replacing of this indigenous genotype. The Red Maasai population from Olmagogo clustered with the Mutara, suggesting a common ancestry. This is not surprising since the later population originated from Naivasha. However of the two populations the Olmagogo shows the highest degree of purity while the Mutara population shows some degree of introgression by the Dorper. Of the East African fat-tailed populations the Homabay population showed the greatest genetic distinction. These results call for rapid intervention measures to stop the genetic erosion of this important small ruminant genetic resource.

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