

## Genetic diversity of indigenous goats in Namibia using microsatellite markers: preliminary results

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### Abstract

Four different goat ecotypes are recognized in Namibia. These ecotypes represent a unique genetic resource due to their adaptation to the different environmental conditions. Sufficient phenotypic characteristics exist that distinguish between the ecotypes. This study is a first attempt to genetically characterize the different ecotypes for the efficient conservation and management of this resource. In this study we report on preliminary results on the genetic diversity and relationships of the four goat ecotypes of Namibia using 18 microsatellite loci. Within-breed genetic diversity was estimated by the average number of alleles per locus (ranged from 4.67 to 6.00) and the average observed heterozygosity, ranged from 60 (Kunene) to 71% (Kavango). Genetic differences between the ecotypes were estimated by Nei's (1978) standard genetic distance, which ranged between 0.12 (Kunene and Ovambo) to 0.44 (Caprivi and Kalahari Red). The four ecotypes cluster in two groups (Kalahari Red, Kavango and Ovambo, Kunene and Caprivi). The relationships among the ecotypes reflect partly the morphological classification.

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### Introduction

Namibia has a rich diversity of indigenous breeds of livestock. These livestock have a unique cultural value in maintaining the traditional lifestyles. However, the conservation of the genetic resource in the traditional livestock sector has not been given due importance. Animals in this sector have remained uncharacterized and face the risk of genetic dilution due to indiscriminate crossbreeding, breed replacement and neglect. This is largely because indigenous breeds were regarded as being inferior to exotic breeds for years.

One of the major objectives of the FAO is the assessment of extent of biodiversity of the farm animals in the SADC region. One species that is most important to this region is goats, and this study is therefore a first attempt to determine the genetic variation within and among the goat populations of Namibia. Goats are primarily found in the northern and northeastern parts of the country. Four distinct ecotypes based on phenotypic characteristics are recognized that have evolved in different areas and are specially adapted to their environment. These ecotypes are the Ovambo, Caprivi, Kunene and Kavango (Els, 2001). In accordance with the FAO's Global Strategy for the Management of Farm Animal Genetic Resources this study was conducted as part of the global research project for the Measurement of Domestic Animal Diversity where molecular techniques are used to establish the genetic diversity within species by quantifying the genetic distance between breeds based on differences in their genetic make-up. The main objective of this study was to genetically characterize the four identified ecotypes and to make preliminary assessment of the extent of genetic differentiation among them.

### Material and Methods

Hair samples were collected from 40 pure, unrelated animals (10 male and 30 female) from each of the four goat ecotypes: Ovambo (North Central Namibia), Kavango (North East Namibia), Kunene (North West Namibia) and Caprivi (Caprivi region). Owners were questioned on the purity and relatedness of the goats. Animals were also sampled from different populations within the regions to ensure unrelatedness. Where animals from Government Stations were sampled, the records were checked to ensure that the animals were not related. The Kalahari Red goat breed was sampled as the reference group. It is regarded as being indigenous to Southern Africa. It is well known that breeders from the Northern Cape Province and the southern part of Namibia selected animal slightly smaller than the improved Boer goat, but with uniform red pigmentation.

DNA was extracted from the hair roots using a modified Proteinase K digestion method (Higuchi & Bradley, 1988). Microsatellite loci were selected based on the degree of polymorphism and genome coverage (Barker *et al.*, 2001) and in accordance with the FAO and ISAG recommended list to adhere to international standards. The 18 primers included *SRCRSP5*, *SRCRSP8*, *SRCRSP24*, *MCM27*, *INRA23*, *BM1329*, *OARFCB20*, *CSRD247*, *ILSTS87*, *SRCRSP23*, *OSRFCB11*, *ILSTS002*, *RM004*, *INRA63*, *INRA006*, *BM1818*, *MAF65* and *BM1258*.

PCR reactions were performed in a Perkin Elmer Thermal Cycler. Genotyping was carried out on an automated ABI 377 DNA sequencer (Perkin Elmer, Foster City, USA), with fragments separated using 0.5% polyacrylamide gels. The data was captured using GeneScan 2.1 Software and initial data analysis was carried out using Genotyper 2.0 to determine the fragment sizes in base pairs. Data were then analysed using POPGENE software to determine the heterogeneity of the markers used and the extent of genetic differentiation among populations, the genetic distance and phylogenetic analysis to construct a phylogenetic tree.

## Results and Discussion

The mean number of observed alleles per locus was 5.17, 4.67, 5.11 and 6.00 for the Ovambo, Caprivi, Kunene and Kavango populations respectively (Table 1). The Kavango population thus had on average the most alleles per locus and the Caprivi population had the least. The Kavango indicated the highest average heterozygosity (71.0%) while the Caprivi population had the least average heterozygosity (57%). All the populations indicated relatively high levels of heterozygosity when compared to the study by Barker *et al.* (2001) where values ranged from 31 to 48% using 25 microsatellite loci among Asian goat populations. On the other hand the estimates compared favourable with values reported by Li *et al.* (2002) which ranged from 61 to 78% using 26 microsatellite loci among Chinese indigenous goat populations. The heterozygosity estimates indicated that the Kavango ecotype had the largest genetic variability. A possible explanation is that the Kavango ecotype has a larger number of individuals and a broader distribution area. Possible mixing with other goat populations can also result in higher heterozygosity levels. This is highly unlikely in this case as the farmers confirmed the purity of the animals sampled.

**Table 1** Genetic variability at 18 loci in all populations

Population	Observed number of alleles/locus (Na)	Effective number of alleles/locus (Ne)	Mean Heterozygosity (H%)
Ovambo	5.17	2.94	61
Caprivi	4.67	2.57	57
Kunene	5.11	2.64	60
Kavango	6.00	3.79	71

The mean  $F_{IS}$  estimate of 0.04, indicating the differentiation within the different types, was low and not significant different from zero. This low estimate corresponds to most studies of livestock populations where it is generally not significant from zero, even for rare breeds (Tunon *et al.*, 1989). The mean genetic differentiation ( $F_{ST}$ ) value (0.11) demonstrates that only about 11% of the total genetic variation is accounted for by a population difference, while the remaining 89% corresponds to differences among individuals within populations. The result found in this study is lower than that found to distinguish between eight Swiss goat breeds (Saitbekova *et al.*, 1999). These preliminary statistical results confirm four ecotypes with some differences.

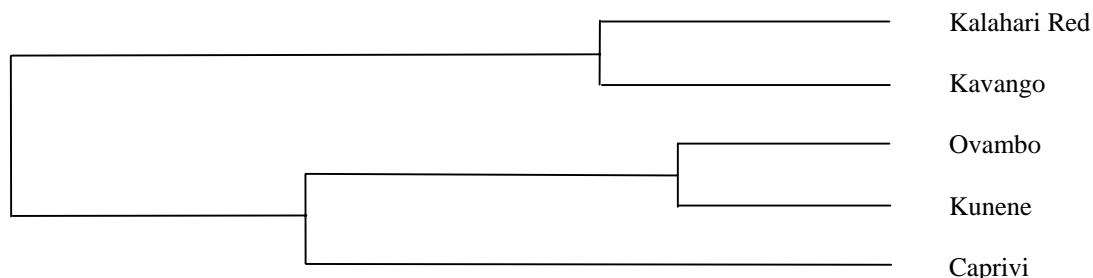
**Table 2** Matrix of genetic similarity and/or distance coefficients

Population	Kalahari Red	Ovambo	Kavango	Caprivi	Kunene
Kalahari Red	*****	0.6476	0.8497	0.6412	0.6479
Ovambo	0.4345	*****	0.7938	0.7427	0.8826
Kavango	0.1629	0.2310	*****	0.7367	0.7860
Caprivi	0.4445	0.2975	0.3056	*****	0.7673
Kunene	0.4341	0.1248	0.2408	0.2649	*****

Genetic identity (above diagonal) and genetic distance (below diagonal) (Nei, 1978).

Table 2 illustrates that the Kalahari Red, which was presumed to be unrelated to the indigenous goats of Namibia, shares a large number of ancestral genes. This matrix further indicates that some of the populations are perhaps far enough removed from each other, to be grouped as separate populations. This result is also supported by the low genetic differentiation ( $F_{ST}$  value) between the four ecotypes.

The phylogenetic tree (Figure 1) summarizes the genetic relationships between the different ecotypes. Two distinct clusters are observed. The Kavango clusters with the Kalahari Red while the Ovambo, Kunene and Caprivi cluster together, with the Ovambo and the Kunene as a sub-cluster. The closest related ecotypes are the Ovambo and Kunene with the largest distance between the Kalahari Red and the Caprivi. It can be concluded that the relationships among the four different ecotypes is consistent with their geographic origins as the four ecotypes have evolved to suit their distinct environments. The clustering of the Kavango with the Kalahari Red is unexpected. This indicates a closer relationship than expected.



**Figure 1** Dendrogram depicting the relationships between four Namibian goat ecotypes

## Conclusion

The present study indicates a low percentage of genetic differentiation (11%) between the different ecotypes. This only partly supports the characteristic phenotypical differences between the four ecotypes. The four ecotypes seem to have evolved to suit their distinct environments, that differs markedly from the arid areas of the north-west to the sub-tropical areas of the Caprivi. The heterozygosity values indicate sufficient genetic variation when compared to results of goat populations from other studies. The adaptive traits of these ecotypes should not be forfeited but should be utilized to their full potential to benefit livestock production in their respective areas. Crossbreeding with exotic breeds should be done with care to preserve this important farm animal genetic resource. The Kalahari Red was used as a supposedly unrelated reference, but demonstrate a surprisingly close relationship with the Kavango. This can indicate the sharing of some ancestral alleles. As this is a preliminary study, further statistical analysis will be performed on the data set and compared with other indigenous goat populations from the region to determine any significant differentiation among the ecotypes and the history.

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