

A genetic profile of the Kalahari Red goat breed from southern Africa

A. Kotze^{1#}, H. Swart¹, J.P. Grobler² and A. Nemaangani¹

¹ARC Animal Improvement Institute, Private Bag X2, Irene 0062, South Africa

²Biodiversity, School of Molecular & Life Sciences, University of the North, Private Bag X1106, Sovenga 0727, South Africa

Abstract

The erosion of the Kalahari Red with red Boer goats is a major concern among breeders. Little empiric information is available with no comprehensive system of monitoring special characteristics. Eighteen microsatellite markers were applied to investigate the genetic diversity of the breed and to set up a molecular inventory. The results provide genetic characterization information, which forms the bases for future management of the Kalahari Red.

Keywords: Kalahari Red, indigenous, microsatellite markers, heterozygosity

[#]Corresponding author. E-mail: akotze@idpi.agric.za

^{1#}Present address: Plant Science Genetics, University of the Free State, P.O. Box 339, Bloemfontein 9300, South Africa

Introduction

The Kalahari Red is regarded as an indigenous goat breed originating from southern Africa. Records indicate that the goats have been selected from lop-eared animals that migrated with tribes to the southern part of Africa more than 2000 years ago (Epstein, 1971). Breeders from the Northern Cape Province in South Africa and the southern part of Namibia, specifically the Kalahari Desert area, selected animals slightly smaller than the red and white improved Boer goat, but with uniform red pigmentation. The Kalahari Red was recognized as a landrace breed in 1998 with the establishment of a breeder's organization. Today this goat breed is an important meat-producing breed in South Africa with characteristics such as adaptation to arid and semi arid savannah, good foraging abilities and excellent mothering abilities. It is regarded as a "minimum care / maximum profit" breed (Ramsay *et al.*, 2001).

The purpose of this study was to optimize microsatellite markers for goats at the ARC Irene laboratory; to use the Kalahari Red goat as an example to investigate the genetic diversity of markers within a population; and to commence with a molecular inventory describing the distinctiveness of the Kalahari Red goat breed.

Materials and Methods

A total of 214 hair samples was collected from goats of six breeders identified by the breeders association from different geographical regions: the Northern Cape Province (Kuruman 61, Prieska 75, Douglas 22) and Limpopo Province (Tshipise 34) in South Africa; and from Namibia (Maltahohe 15).

DNA was extracted from the hair roots using a modified Proteinase K digestion method (Higuchi *et al.*, 1988). Microsatellite loci were selected for exploratory screening based on the degree of polymorphism and genome coverage of these loci (Arevalo *et al.*, 1994; Bhebhe *et al.*, 1994; Barker *et al.*, 2001). These microsatellite markers are listed on the FAO and ISAG recommended list and adhere to international standards.

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.

Results and Discussion

Eighteen microsatellite markers were optimised for PCR and successfully divided into four multiplexes based on their product size and dye label (Table 1). The difference in size between two adjacent markers was at least 20 bp to allow for the identification of new alleles outside the known fragment ranges. Not all the criteria have been fulfilled in the case of each marker, primarily in an effort to tie this list in with existing screening efforts. In some cases more than one marker have been selected from one chromosome. This was not foreseen as problematic in population genetic studies if there is no linkage.

Table 1 Standardization of selected microsatellite markers and plexus

Multiplex:	Microsatellite loci:
PLEX 1	SRCRSP24, SRCRSP5, SRCRSP8
PLEX 2	MCM527, INRA2, BM1329, OARFCB20, CSRD247, ILST87, SRCRSP23
PLEX 3	OARFCB11, ILST002, RM004, INRA63
PLEX 4	INRA006, BM1818, MAF65, CSSM36, BM1258

The mean number of alleles and the expected heterozygosities detected are good indicators of the genetic polymorphism within the breed. Generally the mean number of alleles is highly dependent on the sample size because of the presence of unique alleles in populations, which occur in low frequencies and also because the number of observed alleles tends to increase with increases in population size. The number of alleles scored for each marker is an invaluable indicator of the future usefulness of the marker for genetic screening.

Table 2 Variability of the microsatellite markers used

	Pooled populations:	Individual populations:
Mean number of alleles	7.77	3.83 - 6.89
Average heterozygosity	0.63	0.56 - 0.68

The average number of 7.77 alleles per locus, with even the most monomorphic locus having 3.83, is promising for future application of these markers (Luikart *et al.*, 1999). It should be noted that the number of 7.77 is the mean across 18 loci, and specific loci provided up to 12 alleles per locus.

The genetic relationships between the different populations within the Kalahari Red breed were measured by determining the genetic distance (Nei, 1978) between populations. Genetic distance values were small and ranged from 0.072 to 0.171. A dendrogram based on these genetic distances revealed no specific link with geographic distance.

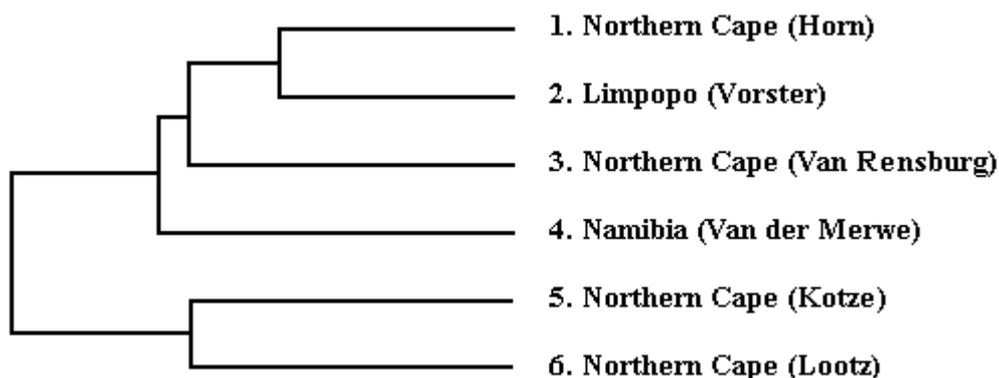


Figure 1 Dendrogram depicting the relationships between six Kalahari Red populations

The results indicate no differentiation between the different populations that can be linked to geographical separation. Note that various populations of Northern Cape origin fall into two distinct

clusters, overlapping divergence between these groups and populations from the Limpopo Province and Namibia. This indicates uniformity within the breed. The limited differences that do exist among populations may suggest local selection / adaptation, and the presence of such possible ecotypes in distinct environments should be further investigated (Tunon *et al.*, 1989; Saitbekova *et al.*, 1999; Yang *et al.*, 1999; Watts *et al.*, 2001). Possible ecotypes should not be forfeited but should be used to their full potential to benefit livestock production in their respective areas. Crossbreeding with other breeds should be done with discrimination as to preserve this important farm animal genetic resource.

Conclusion

Microsatellite DNA is currently the most useful marker of choice for a wide range of molecular genetic studies such as population structure, population differentiation and reconstruction of phylogenetic relationships among populations. The criteria for the markers were that a common PCR program could amplify them, have a minimum of five alleles and were easily scored for PCR products. The primers evaluated and optimised in this study met the criteria set, and can now contribute to standardization for genetic characterization studies of Kalahari Red populations within the SADC region, and be used for parentage determination and for forensic analyses.

The results provide characterization information that forms the basis for future management of the Kalahari Red goat breed. This study has also provided a DNA repository for the Kalahari Red breed and detailed genetic data applicable to future research and development. Establishing the profile of the Kalahari Red breed through survey, monitoring population status and descriptive qualities is the essential first step in better understanding, developing and utilizing this animal genetic resource.

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