South African Journal of Animal Science 2004, 34 (Supplement 1)

Peer-reviewed paper: 8th International Conference on Goats

Genetic variation of three commercial and three indigenous goat populations in South Africa

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Abstract

Three commercial and three indigenous goat populations from South Africa were studied for genetic variation using ten microsatellite markers. Heterozygosity values of between 0.62 and 0.69 were obtained for the populations, except for the SA Boer Goat, which had the lowest variation (0.49). Genetic differentiation using FST values indicated a clear genetic differentiation between the SA Boer Goat and the Kalahari Red population (0.283), while only moderate genetic differentiation was observed among the other populations. This data forms part of an extensive study on the genetic characterization of South African goat populations and additional makers are being tested on more samples to determine phylogenetic relationships.

Keywords: Indigenous, commercial goats, microsatellite markers, genetic diversity
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Introduction

Primarily three commercial breeds, the South African Boer Goat, Kalahari Red and Savanna goat, dominate the meat-producing goat industry in South Africa. These breeds are believed to originate from indigenous goat types found in South Africa (Ramsey *et al*., 2000). Although these breeds as well as the local goat populations have been classified as separate breeds on phenotypic traits, allelic diversity and genetic relationships are unknown. Over the last thirty years, genetic improvement of agricultural species has accelerated at a staggering rate. As the profitability of these improved breeds become apparent, the traditional ways of farming are abandoned as too risky (Wollny, 2003). The replacement and uncontrolled crossbreeding of indigenous animals with "improved" breeds may lead to the replacement of indigenous populations and the subsequent loss of their unique genetic traits. South Africa has several indigenous goat populations associated with different geographical areas and genetic data on these populations are non-existent. A project was established in collaboration with the ARC AII (Irene) to study the genetic biodiversity of goat populations in South Africa. This is the first attempt to study genetic variation of both commercial and indigenous goats of South Africa, using DNA marker technology.

Materials and Methods

For this paper data of three commercial breeds (SA Boer Goat, Kalahari Red and Savanna) as well as three indigenous populations representing three different climatic regions (the Eastern Cape, Mpumalanga and Limpopo Provinces) in South Africa were included. The SA Boer Goat, which is the main meat producing goat, originates from indigenous goats kept by farmers during the 1920's in the Eastern Cape. These goats were selected for adaptability, carcass quality, excellent conformation and distinctive red head and white body (http://www.dnafrica.co.za/boergoat.htm). The Savanna goat developed from the indigenous white goat stud of Messrs Cilliers and Sons, which was started in 1957 from a mixture of coloured indigenous ewes and a white ram (http://www.dnafrica.co.za/savanna). South African and Namibian farmers have collected red goats for the past 25 to 30 years and have specifically selected for the red colour, which resulted in a new breed known as the Kalahari Red. The breed was developed from mainly African types of red and speckled goats (http://www.dnafrica.co.za/k-red). The goats are evenly pigmented, and have a natural resistance against heat and the sun. The indigenous goat populations in South Africa exhibit quite distinct phenotypic variation in their size, and other conformation traits such as horns and ears. Breeds are not defined and are usually associated with specific areas, i.e. Venda and Lebowa goats. The indigenous populations included in this paper are firstly a population kept at Fort Hare University in the Eastern Cape,

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consisting of local, unimproved Boer Goat types. A second population kept at Delftzyl farm (a former experimental unit in the Limpopo Province) consists of local types, while a third population from Groblersdal (Mpumalanga) represents goats from local communities.

Blood samples were collected from between 30 and 100 non-related animals per population. For the purpose of this study, 30 individuals per population were analyzed. After collection, the blood samples were frozen in Eppendorf tubes and kept at –70 °C until extraction was done using a Qiagen DNAeasy Tissue Kit. The DNA was quantitated by spectrophotometry and diluted to a final concentration of 50 ng/μL.

A total of 10 microsatellite markers was selected, based on the degree of polymorphism and genome coverage. Markers were selected from the ISAG and FAO recommended lists in order to compare results with global goat diversity studies. Microsatellite markers were optimised for PCR, multiplexed and PCR products analyzed on an ABI 377 sequencer and Genescan version 2.0 and Genotyper for MacIntosch were used to determine the fragment sizes. Statistical analyses were performed using Genepop (Raymond & Rousset, 1995), Arlequin (http://lgb.unige.ch/arlequin/) and Genetix (Belkhir *et al.*, 1996).

Results and Discussion

All ten microsatellite markers were found to be highly polymorphic, with the number of different alleles per marker varying from seven to 14 over all the populations studied. The heterozygosity (Hz) values per population are indicated in Table 1. Except for the Boer goats (0.49), which showed the lowest Hz, the other populations were fairly similar, ranging from 0.63 to 0.69. Similar Hz values using microsatellite markers in diversity studies in goats have been reported (Barker *et al.*, 2001; Li *et al.*, 2002; Kott *et al.*, 2003).

Table 1 Heterozygosity (Hz) values (Unbiased and observed), with standard deviations (s.d.) for the six goat populations typed with 10 loci

	Loci typed	Unbiased Hz		Observed Hz	
Population	n	Mean	s.d.	Mean	s.d.
A (Groblersdal	10	0.6400	0.0466	0.6731	0.0272
BB (Boer goat)	10	0.4924	0.0602	0.4661	0.0295
D (Delftzyl)	9	0.6993	0.0451	0.6311	0.0304
J (Fort Hare)	10	0.6981	0.0341	0.6448	0.0281
S (Savanna)	10	0.6238	0.0376	0.5838	0.0301
G (Kalahari Red)	10	0.6394	0.0452	0.6247	0.0245

Genetic differentiation was described using FST values (table not shown), which indicated a clear genetic differentiation between the SA Boer Goat and the Kalahari Red population (0.283). Moderate genetic differentiation occurred between populations A and J (0.11), D and J (0.098), A and S (0.095), D and S (0.12), J and S (0.14), with the least differentiation between populations A and D (0.085). The Kalahari Red (G) showed genetic differentiation with all other populations. Figure 1 is a graphical representation of the factorial correspondence analysis using GENETIX (Belkhir *et al.*, 1996), which also illustrates the genetic differentiation between the populations in the study, as well as a clear genetic differentiation of the G population from the other populations.

The results indicate a relatively high genetic variation in the different populations sampled, except for the SA Boer Goat. This is expected as the SA Boer Goat is the oldest of all the breeds and has been subjected to artificial selection for various traits since the late fifties. Genetic differentiation among these populations described by both FST values (Hartl, 1998) and factorial correspondence analyses (Belkhir *et al.*, 1996) indicate that the Boer Goat, Savanna and the Fort Hare population, which mainly consists of Boer Goat populations, have genetic similarities, while the Kalahari Red goats are the most different in genetic composition compared to the other populations. Although the Savanna goat is defined as a breed with specific characteristics, it seems that they are genetically closer to the Boer goat than previously thought. The Delftzyl was an experimental population with indigenous types and shows some differentiation. The Kalahari

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Reds were developed from Namibian and South African indigenous types and seem to be quite different from the others with the markers tested.

Conclusion

Microsatellite markers were found useful and informative for studying genetic diversity in goats. There is sufficient genetic variation within the populations, with a distinct genetic differentiation between the Kalahari Red and other populations tested. Additional markers are being tested in order to complete the genetic characterization and determine phylogenetic relationships.

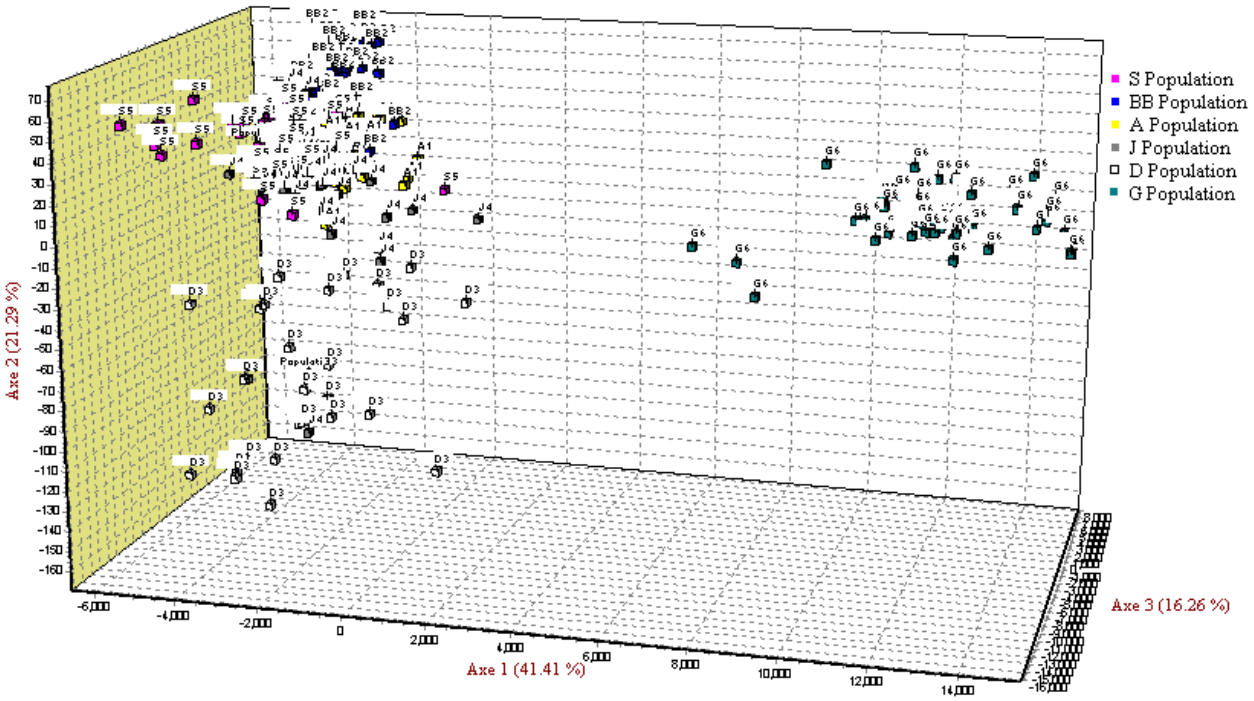

Figure 1 Factorial correspondence analysis of all the individuals in the study

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