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Genetic characterization of commercial goat populations in South Africa

by

Anèlle Pieters

Submitted in partial fulfillment of the requirements for the degree Msc.(Animal Science)

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August 2007

I declare that the thesis/dissertation, which I hereby submit for the degree Msc. Animal Science at the University of Pretoria, is my own work and has not previously been submitted by me for a degree at any other tertiary institution.

Signature: ……..

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Abstract

A genetic study of four commercial goat breeds in South Africa was performed using microsatellite markers. The commercial breeds included the Boer goat, Savanna, Kalahari Red and the Angora goat. Indigenous goat populations from Delftzijl and Groblersdal were also included in this study. Seventeen microsatellite markers were tested to determine the genetic variation. Genetic variation within the breeds were relatively high with heterozygosity values ranging from 57% for the Boer goat, 68% for the Kalahari Red, 69% for the Savanna goats and 70% for the Angora goats. Fst values indicated that the Savanna and Boer goat are genetically the closest (0.114), while the Kalahari Red and Boer goat are the least related (0.237). Phenotypic measurements included height, length, depth, heart girth, pelvic length and width for a phenotypic description. Significant differences were observed in the phenotypic measurements among all the breeds. The genetic and phenotypic differences indicate that these goats can be distinguished as different breeds. Results of this study contribute genotypic information of the commercial goats in South Africa.

Samevatting

Genetiese karakterisering van vier kommersiële bokrasse van Suid Afrika is uitgevoer met behulp van mikrosatelliet merkers. Die Boerbok, Savanna, Kalahari Red en die Angora bok is as kommersiële populasies ingesluit. Twee addisionele inheemse populasies, van Delftzijl en Groblersdal het ook deel gevorm van hierdie studie. Sewentien mikrosatelliet merkers is getoets om data te verkry vir beraming van genetiese variasie. Relatiewe hoë heterosigositeit waardes is waargeneem. Die laagste heterosigositeit was by die Boerbok (57%), opgevolg deur 68% vir die Kalahari Red, 69% vir die Savanna en die hoogste heterosigositeit vir die Angora bokke (70%). Die Boer bok en Savanna bokke toon die hoogste verwantskap terwyl die die verhouding tussen die Boer bok en Kalahari Red die kleinste is. Hoogte, lengte, diepte, bors omtrek, bekken lengte en breedte het deel gevorm van die fenotipiese metings vir ras beskrywing. Betekenisvolle verskille is tussen die rasse waargeneem by die fenotipiese mates. Die genetiese en fenotipiese verskille dui aan dat hierdie bokke as verskillende rasse onderskei kan word. Resultate van hierdie studie dra by die genetiese karakterisering van kommersiële bokke in Suid Afrika.

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Abbreviations

AFLP	Amplified Fragment Polymorphic DNA
AGPTS	Angora goat performance testing scheme
ARC – AII	Animal Improvement Institute – IRENE
bp	Base pairs
DNA	Deoxyribonucleic Acid
D*A*	Modified Cavali-Sforza genetic distance
Ds	Nei's Standard Genetic Distance
FAO	Food and Agricultural Organization of the United Nations
FCA	Factorial correspondence analyses
Fst	Standardized variance in Allele frequencies among Populations
He	Expected Heterozygosity
Ho	Observed Heterozygosity
HWE	Hardy Weinberg Equilibrium
ISAG	International Society for Animal Genetics
JEF	Jansenville Angora goat Experimental farm
NJ	Neighbour Joining topology tree
PCR	Polymerase Chain Reaction
PIC	Polymorphic Information Content
RAPD	Random Amplified polymerase DNA
RFLP	Random Fragment length polymorphisms

Chapter 1

Introduction

The lifestyles of humans were dramatically improved since the domestication of animals and plants. It enabled people to consolidate food resources which were the key to civilization, making people more independent from environmental fluctuations (Vila *et al.*, 2005). Goats have been kept since ancient times for meat, milk, hide and fibre (cashmere and mohair) production, control of bush encroachment, as well as for cultural and religious purposes in a large number of countries (De Villiers *et al.*, 1999; Boyazoglu *et al.*, 2005). Today different goat breeds inhabit diverse environments throughout the world with body weights ranging from nine to 13 kg for small tropical breeds to 100 kg for the European Dairy breeds and the Boer goat (Mason, 1981).

The origin of the domestic goat (*Capra hircus)* is not confirmed. Archaeological evidence suggests that domestication of the goat took place approximately 8 000 to 7 000 BC when hunter-gatherers began to change their way of life (Mason, 1981; Boyazoglu *et al.*, 2005). Goats spread all over the continents from the slopes of the Zagros Mountains on the border of Iran and Iraq and inhabit all climatic zones. By 5 000 BC they were in Syria and from there they migrated to the west and the south. In Europe, only Crete and other Greek Islands had wild goats followed by domesticated goats migrating to Europe from Southwest Asia. The wild species of *Capra* which are believed to have contributed to the domestic goat include the Ibex (*C. Ibex)* and the Bezoar (*C. hircus)*. Studies on horn cores suggest that domestic goats are closer related to the Bezoar than the Ibex (Maree & Plug, 1993).

Goats were probably introduced to South Africa via southern migration of nomadic tribes. There is evidence of goat remains in South Africa, dated to the early 300 AD. Rock paintings of goats are found in many regions of Africa (Maree & Plug, 1993). According to some authors it is not always possible to distinguish between goats and sheep remains (Mason, 1981).

Demand for goat meat exceeds supplies in many parts of the world, especially in the tropics and subtropics where the majority of the world's goat meat is produced (Van Niekerk & Casey, 1988). Cultural and traditional background and the socio-economic status of the community

dictate consumer preferences for goat meat and mutton to a large extent. In a society where sheep and cattle are the dominant sources of red meat, prejudices against goat meat arise. Mutton enjoys premium prices in South Africa while goat meat consumption is limited to specific cultural groups (Van Niekerk & Casey, 1988).

In South Africa research regarding meat qualities primarily focus on sheep and cattle with the result that standards for growth rate and carcass evaluation are very limited for goats. There are three commercial meat type goats in South Africa namely the Boer goat, Savanna goat and the Kalahari Red. The Boer goat is the primary breed for meat production followed by the Savanna and Kalahari Red. These meat types developed from indigenous goats have been established over many years. The majority of the Boer goats are found in the Northern Cape and Angora goats in the Eastern Cape. These breeds have gained popularity and have also been exported to Europe and the USA. The South African Angora goat dominates the mohair industry in South Africa and contributes 62% to mohair production in the world, which is exported to 18 countries (Snyman, 2002; Donkin *et al*., 2006).

European breeds such as the Saanen and the Toggenburg were imported from Europe and are the main dairy goat breeds in South Africa. The majority of the other goats beside the breeds mentioned are indigenous or local types kept in the rural areas (de Villiers *et al.*, 1999). Very little production information is available for this unimproved goat breeds and is often characterized on phenotype and or the specific geographic area they inhabit. Unimproved indigenous goats are found in almost all provinces of South Africa with the highest concentration in the Eastern Cape, Northern Cape and Kwa-Zulu Natal.

Research in South Africa on goat breeding and genetics have been limited to quantitative studies on South African Boer goats and Angora goats. Genetic parameters have been estimated for early growth traits in Boer goats (Schoeman *et al*., 1997) and body weight, fleece weight and fibre diameter in Angora goats (Snyman & Olivier, 1996; Snyman & Olivier, 1999; Snyman, 2002). Several scientific papers have been published concerning general aspects of goat production in South Africa (Malan, 2000; Erasmus, 2000). Research papers in South Africa focus mainly on reproduction (Els, 1995; van Niekerk, 1997; Mahanjana, 1999), growth traits (Els, 1995; Casey & van Niekerk, 1988; Tshabalala *et al*, 2003) and nutrition (Sheridan *et al.*, 2003; van Niekerk & Casey, 1988).

Aims of study

The commercial meat type goats in this study originated from local goat types found in South Africa. They have been subjected to artificial selection for improved production and growth and three meat type breeds have been established. Although a positive development, the question arises if specific genetic characteristics could be compromised by continuous selection for improvement of growth and meat characteristics. Often these breeds and our indigenous types are marketed as having special adaptive characteristics; local types often survive tick borne diseases better than commercial types (Malan, 2000; Erasmus, 2000). This has not been confirmed and genetic data is lacking for South African commercial and indigenous populations.

The commercial goats, including the Angora have a history of being bred from indigenous or local types. These breeds, especially the Savanna, Boer goat and Kalahari Red are well adapted to the South African climate and have found to be popular elsewhere in the world (www.cals.ncsu.edu/an_sci/extentsion/animal/meatgoat/ahgoats_index.html). Commercial goat production is an important part of the South African livestock industry, especially in a small farming context. Therefore, both genetic and phenotypic information would make a valuable contribution to the long term survival and utilization of these goats.

Goat breeds have been studied phenotypically in various studies (Campbell, 2003; Malan, 2000; van Niekerk, 1997; Els, 1995) and a National Performance Testing scheme exists, but participation by the breeders are very limited (Els *et al.*, 2004, Visser *et al.*, 2004). The development of DNA-technology and genome mapping of various farm animals made it possible to perform genetic characterization of breeds and gain useful information on genetic diversity and assist with breed differentiation. To date only two studies have been reported for genetic diversity in goats representing Namibia and South Africa (Els *et al.*, 2004, Visser *et al.*, 2004).

The breeds in this study originate from indigenous goat types. Therefore is there merit in gaining information on their genetic diversity, which could assist in breed differentiation and conservation as true South African breeds.

The aim of the study was therefore to perform a genetic characterization of the commercial goat breeds of South African using microsatellite markers. The Angora goat was included as mohair makes a significant contribution to export of agricultural commodities.

In order to perform the genetic characterization the following objectives were set:

- Selection of breeds and the collection of representative blood samples from unrelated individuals;
- Using a microsatellite marker panel for genotyping;
- Determine the genetic variation and distances using different statistical programmes;
- Compile a genetic and phenotypic description of each breed.

Chapter 2

Literature review

2.1 Conservation

Goal of conservation

The Food and Agricultural Organization of the United Nations (FAO) defines conservation as "the maintenance of live populations of animals in their adaptive environment or as close to it as practically possible" (FAO, 2002). Four reasons for conservation of unprofitable breeds are presented by Mendelsohn (2003) namely "genetic stock value, environmental/landscape effects, maintaining traditional lifestyles and existence value". Various authors have expressed serious concerns about the continuing reduction in the overall pool of domestic breeds of livestock genetic resources (Signorello & Pappalardo, 2003; Shrestha, 2004). Although indigenous breeds' performances are lower than highly selected animals, they are often better adapted to their local environment compared to commercial breeds, which could lead to more efficient use of natural resources (Martens *et al.*, 2003). Commercial livestock over the world is bred from a relatively narrow genetic base and due to the emphasis placed on maximum production; these breeds are replacing most of the indigenous breeds. An indigenous breed might not be economically viable due to low productivity, but they might contain special characteristics that will be useful for future breed development. Mendelsohn (2003) stated that for conservation to be efficient; the program should prioritize conserving species that best protect the genetic basis of the breed. Iamartino *et al.*, (2005) remarked that the first step for exploitation of domestic animal biodiversity and conservation is "a comprehensive knowledge of the existing genetic variability and the partitioning of this variability among breeds".

It is inevitable that selection, inbreeding and various crossbreeding systems may lead to the loss of valuable genetic resources. It may become necessary to keep conservation populations of certain breeds where they may contribute to the possible discovery of previously unknown or unrecognised genes, which could enhance the productivity of existing breeds. Conservation populations provide a safeguard against a possible genetic variation loss, preserve cultural heritage and create opportunities for education and tourism (Martens *et al.*, 2003).

Current estimates indicate a total loss of general species (including "lower species groups") of approximately 27 000 per year, or one species every 20 minutes (Martens et al., 2003). Shrestha & Fahmy (2005) reported that nearly 800 farm animal genetic resources have been lost through the past and about 30 percent of the remaining is associated with some degree of risk. The FAO predicts that 28 percent of livestock breeds are at risk of extinction, the current loss rate is estimated at one breed per week, and more than half of these breeds are likely to be found in developing countries (FAO, 2004).

Conservation strategies

Three general aspects of selection were considered by the FAO in developing conservation strategies. First, where inbreeding might be a problem in small populations, no selection must be practised until the population numbers have been increased. Secondly, selection may be imposed on males, whilst maintaining the influence of the founders through the females. Breeding programmes usually involve the use of more females than males. And thirdly, selection should be carried out in the native environment of the breed, in order that the environment does not restrict the performance and characterization of the breed (FAO, 2002).

Conservation can be done through *ex situ* conservation where a biological sample such as semen, ova, and embryo's, frozen blood (DNA extraction) and somatic cells are collected and stored. Conservation of live domestic animals through selection and breeding in their natural environment is also an option. It has the apparent advantage that a live population genetically adapts to changing conditions (Groeneveld, 2005; Simianer, 2005).

Conservation can be distinguished between that of breeds vs. the conservation of genes. To conserve a breed it is necessary for the populations to be large or that special strategies are employed to avoid gene loss. Genes can be conserved in cross-bred populations, in gene pools or new composite breeds as well as in existing breeds (Quarterman, 1991); especially genes that affect obvious morphological features, which can be easily identified (FAO, 2002). Quantitative genetic principles have made it possible to improve livestock genetically through the crossbreeding of established breeds with indigenous breeds for specific objectives (Shrestha & Fahmy, 2005). This promote the conservation of the inherent potential in some rare breeds with considerable genetic merit and to ensure their utilization this composite population should be

established with as broad as possible genetic base to ensure a greater initial heterozygosity in the newly formed population. This should enhance response to selection and represent higher performances (Shrestha & Fahmy, 2005).

There are a number of disadvantages with gene pool conservation. The expression of specific characteristics is not predictable in a crossbred population as it is in purebred breeds. It may be impossible to identify animals carrying a specific gene within a crossbred, because other alleles from the other breed or breeds might influence the expression of that gene. Through the interaction of these different genes, economic important characteristics might come forward. Breeders might select for such complementary genes that could cause the disappearance of the valued characteristic within the crossbred (for example some parasite resistance). A large number of pre-existing genes can be lost over time through genetic drift, since these crossbred populations might be considerably smaller than the original size of the indigenous breeds kept independently (FAO, 2002).

Before sampling can begin, it must be established to whether the programme is to conserve unique genes within the population or the breed itself. If only a few animals are left for conservation, as many animals as possible must be included, since diversity is limited to the initial sample. The FAO (2002) recommend 25 males and 50 females as a minimum for a live conservation programme to result of less than 1% of the possible genetic variation present in the original population. Three different methods of sampling are recommended by the FAO; random sampling must be taken by dividing a population into strata, or form groups of similar animals and if the pedigree is known, it is possible to create a sample which represents the largest possible number of ancestral or founder animals.

In addition to conservation strategies, molecular techniques provide ways to perform genetic characterization of populations. Therefore the storage of DNA in biological banks has become an important method for the conservation of the resources. DNA studies can provide information which can be used in estimating and monitoring the effective population size needed for conservation (FAO, 2005).

Conservation of goats

It appears that the conservation of goat genetic resources is of less concern than that of other domestic species and wildlife. Of the world goat numbers, 96 percent are harboured in developing countries, where intensive breeding schemes using modern technology have not yet made much impact on the number of local breeds or on gene loss from local populations (Quarteman, 1991). There are little stratification of local goats into well defined breeds in South Africa and other developing countries, since they are named according to their geographical location. Phenotypic and genetic conservation of local goat types could contribute to make information available for the decision making for improvement and development of breeding programmes (Wollny, 2003).

Reports indicate that livestock policies in Africa are aimed at introducing exotic breeds via centralised provision of exotic with local F1 animals (Wollny, 2003). Results from crossbred goats in an upgrading program in Ethiopia showed no increased benefits compared to indigenous goats under improved management (FAO, 2002). It seems that the emphasis is on the improvement of local breeds, rather than on the conservation of the breeds.

Conservation in South Africa

True indigenous breeds in South Africa have been virtually bred to extinction due to the development of the Boer goat and the "upgrading" of indigenous goats with Angora goats (Campbell, 1995). Some researchers and farmers believe that the pure "unimproved" indigenous goats possess important economic traits, which should not be disregarded. These traits are viability, good mothering ability, disease resistance and resistance against ticks (Campbell, 1995). Private breeders and government research institutes established and maintained nucleus flocks from these indigenous goats, referred to as the Khosa goats (The Savanna white goat, speckled goats, Loskop south indigenous goats from the Eastern Cape, Kwazulu Natal goats, Delftzyl goats and Damara goats). The Speckled goats are kept by few private breeders as well as the Ovambos and Damaras in Namibia. Since the Khosa goats of the Ciskei and Transkei are in danger of extinction, a limited number of goats from the Ciskei were obtained from 1988 to 1991 and transferred to the Loskop-South Research Station near Groblersdal where they are kept as a purebred breed (Campbell, 1995). A herd of Zulu goats, also known as the Nguni goats, are kept at the Bartlow Combine Research Station. At Delftzijl, a decent flocks of goats were collected by

the Department of Development to preserve these goats and teaching farmers improved animal husbandry techniques (Campbell, 1995).

2.2 Goat statistics

Due to goat farming systems and communal practises under which goats are kept, it is difficult to sustain accurate data. There are approximately 570 goat breeds in the world, of which 89 (16%) are found in Africa, 146 (26%) in Asia and the Pacific region and 187 (33%) in Europe (Shrestha & Fahmy, 2005). In table 2.1 the goat numbers for 2001 to 2005 are summarised. As shown according to the FAO (http://www.faostat.org), China has the highest number of goats and the country with the lowest number of goats is Gambia. In general there is a positive growth in the number of goats kept all over the world.

Gall (1981) reported that the number of goats kept per capita do not necessary reflects the importance of goat milk or meat in the various countries of the world and that the impact of the different goats and their products should be assessed per country. The majority of goats in South Africa are unimproved indigenous types and are mainly used for meat, milk and skin, for controlling bush encroachment and ceremonial purposes (De Villiers *et al.*, 1999). In 2005, 35% of production animals were slaughtered, but of the total goat populations only 0.55% are slaughtered and consumed by the formal sector through abattoirs each year. It can be assumed that most of these are slaughtered in the informal sector (Donkin *et al.*, 2006).

Table 2.1 Major goat producing countries in the world (FAOSTAT)

Country	2001	2002	2003	2004	2005	Average growth 2001 – 2005
Algeria	3,129,400	3,200,000	3,200,200	3,200,000	3,200,000	9,881
Angola	2,150,000	2,050,000	2,050,000	2,050, 000	2,050,000	3,571
Benin	1,250,000	1,270,000	1,300,000	1,350,000	1,380,000	14,579
Botswana	2,250,000	2,250,000	2,250,000	2,250,000	2,250,000	7,143
Cameroon	4,400,000	4,400,000	4,400,000	4,400,000	4,400,000	42,857
Chad	5,303,536	5,500,000	5,500,000	5,716,800	5,842,600	56,054
Ethiopia	9,620,890	9,622,088	9,623,000	9,626,000	9,626,000	5,834
Gambia	228,404	261,965	262,000	265,000	270,000	8,600
Ghana	3,200,000	3,410,000	3,450,000	3,595,600	3,631,600	50,043
Kenya	10,979,680	10,959,676	11,000,000	12,000,000	12,000,000	73,763
Lesotho	650,000	650,000	650,000	650,000	650,000	-5,681
Malawi	1,669,669	1,700,000	1,700,000	1,900,000	1,900,000	33,776
Mali	8,690,510	8,850,000	8,850,000	12,036,000	12,050,000	190,788
Morocco	5,133,300	5,090,400	5,100,000	5,358,600	5,358,600	46,729
Mozambique	392,000	392,000	392,000	392,000	392,000	143
Namibia	1,469,060	1,769,060	1,774,560	2,100,000	2,100,000	29,302
Niger	6,900,000	6,900,000	6,900,000	6,900,000	6,900,000	24,286
Nigeria	26,500,000	27,000,000	27,000,000	28,000,000	28,000,000	142,857
South Africa	**6,550,000**	**6,849,000**	**6,850,000**	**6,372,000**	**6,407,000**	**-3,576**
Sudan	39,952,200	40,000,000	40,000,000	42,000,000	42,000,000	332,429
Swaziland	422,000	422,000	422,000	274,000	274,000	-4,209
Uganda	6,620,000	6,600,000	6,600,000	7,700,000	7,700,000	108,571
Zambia	1,270,000	1,270,000	1,270,000	1,270,000	1,270,000	14,357
Zimbabwe	2,968,275	2,970,000	2,970,000	2,970,000	2,970,000	4,295
Mexico	8,701,860	9,600,000	9,500,000	8,991,752	8,991,752	-5,477
Argentina	3,386,600	4,000,000	4,200,000	4,200,000	4,200,000	56,950
Peru	1,997,870	1,937,070	1,950,000	1,950,000	2,000,000	-4,876
Bangladesh	34,400,000	34,400,000	34,500,000	36,900,000	36,900,000	221,429
China	157,361,497	161,492,200	172,957,208	183,363,073	195,758,954	3,843,038
India	123,500,000	124,000,000	124,500,000	120,000,000	120,000,000	-180,714
Indonesia	12,463,889	13,044,938	12,450,000	12,781,000	13,182,100	34,338
Iran	25,757,000	25,757,000	26,000,000	26,300,000	26,500,000	53,071
Mongolia	10,269,800	9,591,300	8,858,000	10,652,900	12,238,000	84,007
Pakistan	49,100,000	50,900,000	52,800,000	54,700,000	56,700,000	778,571
Saudi Arabia	3,995,000	2,500,000	2,700,000	2,200,000	2,200,000	-12,022
Europe						
Greece	5,180,000	5,023,000	5,000,000	5,362,000	5,400,000	-15,323

http://faostat.fao.org\faostat\

2.3 Goat breeds of the world and Southern Africa

In general, goat breeds are classified into six types (Table 2.2). The goats in Southern Africa are classified as small short-eared, large lop-eared or developed breeds. In central East Africa all goats have short erect ears. Lop-eared goats appear again in South Africa but the lop- and short-eared are often mixed together – as among the Boer goats (Mason, 1981).

Table 2.2 Goat breeds of the world (Mason, 1981)

Group	Characteristics	Example
1. Short eared goats with small/sabre horns or none	Resemble the wild bezoar, short hair, prick ears, straight facial profile	Saanan (Switzerland), Malaga (Spain), Creole (West Indies), African Pygmy (West Africa), Small East African (Kenya, Uganda, Tanzania)
2. Short eared goats with twisted (*prisca*) horns	Horns were selected into a loose spiral to give the prica horns	Valais Blackneck (Switzerland), Pyrenean (France), Garganica (Italy), Maradi (Nigeria)
3. Pashmina or Cashmere goats	Horns are heteronymous twisted; ears are intermediate between short and drooping	Morghose (Iran), Vatani (Afghanistan), Kaghani (Pakistan), White Himalayan (India), Chungwei (China, Mongolia)
4. Angora goats	Mohiar goats with lop ears and spiral horns	Angora goats (Turkey)
5. Lop-eared goats	Larger goats with lop ears; frequently spiral horns	Nubian (Sudan), Benadir (Somalia), Boer goat (South Africa), Bikaneri (India)
6. Long-eared hornless dairy goats	Goats are kept under intensive conditions	Maltese (Malta), Damascus (Syria), Zaraibi (Egypt)

The goats typically belong to the group characterized by small-ears and with small horns group have been subjected to selection against the original colour of the wild goat and the horns have often been reduced in size or eliminated (Mason, 1981). The present day goats of this type tend to be dwarf, it is believed to be the results of natural selection on thermoregulation under the unfavourable humid and hot climate. The distribution of this goat type extends southwards through central Africa as far as Zaire, Angola and the north of Namibia (Mason, 1981). The Landim from Mozambique and the Zimbabwe goat are two breeds of this group which are found in Southern Africa (http://dagris.irlri.cgiar.org).

The lop-eared goats are the main group in Southern Africa, which are characterized by their long drooping ears. These types of goats are heavily represented in the atlas region of North Africa, western Mediterranean region as well as in Syria, Iraq and India. The Damara Goat, Kalahari Red, Tswana, Savanna, Nguni, Swazi and Zulu goats from Southern Africa belongs to this group. (http://dagris.irlri.cgiar.org). The Pafuri is a developed goat breed that resulted from

crossbreeding the indigenous Landim females with imported Boer males (introduced in 1928 from South Africa). This breed is restricted to a small area in Southwest Mozambique (http: dagris.irlri.cgiar.org).

On the borders of the Eastern Cape farmers acquired shorthaired lop-eared goats from local inhabitants of Southern Africa (Masson, 1981; Malan, 2000; Campbell, 2003). They used these goats to open up thorn-bush country for Angora goats, woollen sheep and mutton sheep and even for cattle farming (Campbell, 2003). Epstein (1971) claimed that the goats of the "Southern Bantu" furnished the foundation stock not only of the Hottentot goats but also of the Boer goat. During the twentieth century farmers started improving the indigenous goats with European, Angora and Indian goats (http://www.ansi.okstate.edm/breeds). By means of selection farmers have eliminated throat tassels, speckled colour, dappled colour and the piebald markings of the indigenous goats in the modern improved Boer goat (Campbell, 1995). Figure 2.1 show the approximate place of origin of the Boer goat compared to other indigenous breeds of Southern Africa.

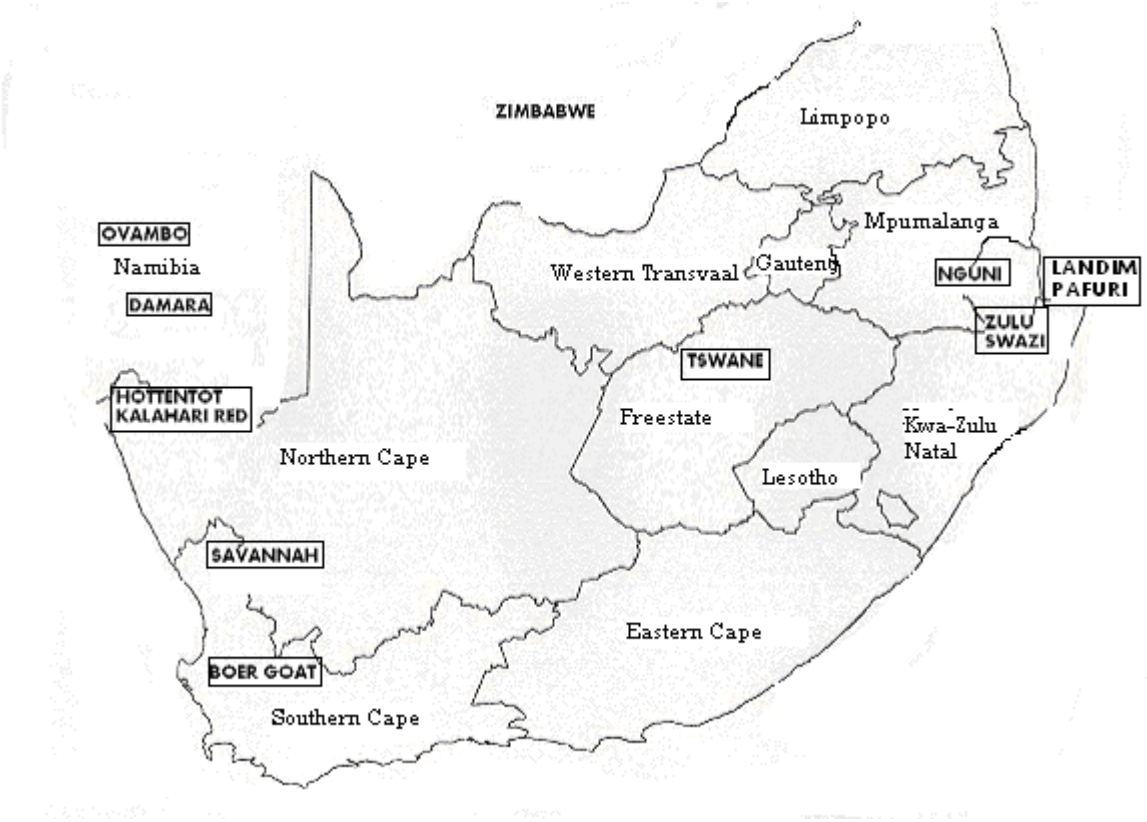

Figure 2.1 Origin of Southern African goats

2.3.1 The Angora goat

The Angora goat originated from the Himalayan region, but modern development of the breed dates from the middle of the 16th century in the Angora region of Turkey. One female and 12 bucks were the first Angora goats imported to South Africa in 1838. Other importations followed until 1896, where after the Angora became a well established goat breed in South Africa (http: dagris.irlri.cgiar.org).

Breed standards for the Angora goat focus mainly on the production of mohair. The Angora goat is pure white with long silky, curly hair, a slightly concave nose line and medium-length to long lop ears (Fig 2.2). The males have corkscrew-shaped horns, curving back and out, the sickle-shaped horns of the females are considerably shorter (Sambraus, 1992). Angora goats have deep wide chests, a good body capacity and spring of rib. The back of the Angora goats is straight with a slightly sloped croup. The belly and chin is full-covered and the legs to the knees. The mohair consist of distinct, well formed locks, which is uniform in style, character, length and fineness, with only a light sprinkle of kemp in the topline or britch (www.cagba.orgg/standards.html).

Figure 2.2 Angora goats

Table 2.3 illustrates the production traits of the Angora in South Africa. They are sensitive to the cold, only 80% of the female's kid and only 1% of births are twins. It is known that males can be placid in the mating season and the females are considered as poor mothers (Sambraus, 1992).

Table 2.3 Production traits of the Angora goats of South Africa

	Ewes
Body weight, (kg)	33.6 ± 0.3
Fleece weight (kg per year)	3.39 ± 0.04
Clean yield (%)	79.6 ± 0.1
Clean fleece weight (kg per year)	2.66 ± 0.03
Fibre diameter (µm)	36.0 ± 0.1
Staple length (cm per 4 month clip	10.4 ± 0.05
Fleece weight as percentage of body weight	10.7 ± 0.13
Kids born per 100 does mated (%)	84.3
Kids survival rate (%)	78.5
Kids weaned per 100 does mated (%)	65.1
Total weight of kids weaned per doe per year (kg)	7.1 ± 0.7

Source: Snyman, 2004

Various studies were done in the last decade in South Africa on the selection for mohair production (Snyman & Olivier 1996; Herselman *et al.*, 1998; Snyman & Olivier, 1999; Snyman, 2002; Snyman, 2004). Fibre diameter is the single most important price-determining variable in mohair production. Other economic important traits for Angora goats are the length of the mohair, style and character, kemp, coloured fibres and contamination. Productive efficiency and clean yield is of major importance, since the income of an individual animal depends on the mass of high quality mohair produced. Although growth rate is less important in Angora goats, it is still of economic importance since it is related to the adaptation of the animals.

Repeatability and heritability estimates are illustrated in Table 2.4 for AGPTS (Angora goat performance testing scheme) and JEF (Jansenville Angora goat Experimental farm) traits of economic importance. It appears that economic important traits for Angora goats are low to moderately heritable. Genetic selection has a major influence on fibre production in the long term. Changes to fibre production through breeding is slow, the achieved gains are continuously interacting with the various non-genetic factors (Sumner & Bigam, 1993). It is evident that maternal genetic effects have to be taken in consideration, when estimating (co)variance components (Snyman & Olivier, 1996).

Table 2.4 Repeatability (SE) and heritablilty (SE) estimates for body weights and fleece traits

Trait	Repeatability		Heritability	
	*AGPTS	**JEF	*AGPTS	**JEF
Body weight	0.53 (0.12)	0.63 (0.06)	0.35 (0.05)	0.47 (0.01)
Fleece weight	0.41 (0.13)	0.27 (0.04)	0.22 (0.04)	0.22 (0.04)
Fibre diameter	0.68 (0.14)	0.35 (0.03)	0.30 (0.05)	0.29 (0.05)
Softness	0.32 (0.14)	0.31 (0.06)	0.07 (0.15)	0.33 (0.07)
Face cover	0.37 (0.11)	0.60 (0.07)	0.33 (0.12)	0.66 (0.11)
Pigmentation	0.62 (0.13)	0.62 (0.08)	0.43 (0.14)	0.49 (0.10)
Neck cover	0.26 (0.06)	0.39 (0.06)	0.13 (0.06)	0.33 (0.07)
Style	0.24 (0.06)	0.17 (0.05)	0.13 (0.06)	0.23 (0.06)
Character	0.35 (0.08)	0.39 (0.07)	0.14 (0.08)	0.34 (0.09)
Evenness	0.23 (0.09)	0.13 (0.04)	0.26 (0.10)	0.16 (0.05)
Kemp	0.29 (0.05)	0.25 (0.06)	0.01 (0.04)	0.32 (0.08)
Bellies and points	0.22 (0.09)	0.12 (0.04)	0.30 (0.10)	0.30 (0.04)

* AGPTS (Angora goat performance testing scheme)

** FEF (Jansenville Angora goat Experimental farm)

Repeated by Snyman & Olivier, 1999

2.3.2 The Boer goat

Boer goats are large, long-legged goats with short, soft hair and long lop ears. They are white with reddish-brown heads, ears and necks. The Boer goat's head is powerful with a compressed nose and strong horns with a gradual backward curve (Fig 2.3). The neck of the Boer goat is of moderate length, full and well fleshed. They have fleshy, well-developed broad briskets, well-sprung ribs, broad backs and muscular legs (Sambraus, 1992). The Boer goat has a broad rump with a slight incline, well fleshed buttocks and thighs. The mature Boer goat ram weighs between 110 – 135 kg and ewes between 90 and 100 kg (Malan, 2000).

Figure 2.3 Boer goats

The Boer goat has good mothering ability and can kid every seven to eight months. It is a meat goat with a carcass yield of about 50%. Boer goats have an exceptional ability to withstand and resist diseases such as blue tongue, prussic acid poisoning and, to a lesser extent, enterotoxaemia (Malan, 2000; Erasmus, 2000). Malan (2000) reported that the South African Boer goat is regarded as the best meat goat in the world and that its meat is a good alternative for red meat for the health conscious consumers.

2.3.2 The Kalahari Red

The Kalahari Red is believed to have originated from two lines consisting of a line of red-head Boer Goats and another from "unimproved" local goats in South Africa (Campbell, 2003). The Kalahari Red today, have a distinct red colour and is often used in crossbreeding to result in goats with a uniform, solid, red colour. They are fully pigmented and are able to endure heat and strong sunshine (Fig 2.4). Their dark coats and long ears provide good heat resistance (http: studbook.co.za). The breed has excellent walking ability and good mothering ability and they will kid three times in two years. Kalahari Reds are believed to be less susceptible to diseases and require less vaccinations compared to other goat breeds.

Figure 2.4 Kalahari Red Goats

2.3.4 The Savanna goat

The white Savanna goat, also known as the white Boer Goat, was developed from indigenous goats of Southern Africa for the past few decades (Campbell, 2003). The breed standards allow a limited amount of red, blue and black hair (www.ourfarmsite.com). The Savanna goat has a lively appearance and symmetrical confirmation. They have short kempy white hair with a black skin, horns, nose, and udder and during the winter the goats develop extra fluffy cashmere hair for protection. The Savanna goat has a fairly long slightly curved head with big, oval shaped ears. The goats have strong jaws and strong long lasting well-developed teeth. The neck is well muscled and reasonably long so that the goat can easily reach as high as possible to browse on branches and pods. The forequarter is well muscled and of medium width (Fig 2.5). The hindquarter should be wide with a reasonable slope. Ewes have very good mothering traits and are very protective as far as their kids are concerned. About 22 percent twins and triplets are born under extensive conditions (http:/www.ourfarmsite.com web goat's goatsavanna breedstandards.html).

Figure 2.5 Savanna Goats

2.3.5 Research on South African meat goats.

Most of the research done in South Africa regarding meat producing goats was on the Boer goat. Studies directly related to the South African Boer goat include selection for reproduction (Els, 1995; van Niekerk, 1997; Mahanjana, 1999), growth (Els, 1995; van Niekerk, 1997; Schoeman *et al.*, 1997) and meat characteristics (Naude & Hofmeyr, 1981; van Niekerk & Casey, 1988; Tshabalala *et al.*, 2003).

Reproductive performance is a major characteristic in selection for increased production in meat goats. Table 2.5 illustrate the results of a study done by Mahanjana (1999) for the reproductive performance of the Boer goat and South African indigenous goats and in Table 2.6 the heritability estimates for growth traits are summarized.

Table 2.5 Reproductive estimates for goats

Breed	Kidding percentage	Fecundity	Pre-weaned mortality %	Source
Improved Boer	119	1.8	19	Mahanjana, 1999
Indigenous Honeydale South Africa	142	1.66	6	Mahanjana, 1999
Indigenous Delftzyl South Africa	111	1.36	4	Mahanjana, 1999

Table 2.6 Heritability estimates for pre-weaning growth traits

Breed	Birth weight	Weaning weight	ADG	Source
Improved Boer	0.187	0.191	0.189	Van Niekerk, 1997
Improved Boer	0.36	0.6		Els, 1995
Boer (Adelaide)	0.327	0.273	0.257	Schoeman *et al*., 1997
Boer (Omatjenne)	0.357	0.602		Schoeman *et al*., 1997

In addition to growth, selection for meat production has also received attention. There is very little data available on the heritability estimates for dressing percentage although differences between breeds have been recorded. Van Niekerk and Casey, (1988) reported a dressing percentage of 48.3 percent for the Boer goat. In a study done on South African indigenous goats, Boer goats and two breeds of sheep, Tshabalala *et al.,* (2003) reported that dressing out percentage of goats are less than those of sheep, because of the goat carcasses containing significantly less fat. In a study on the acceptability of meat goat the Boer goat patties had a stronger "goatty" aroma than indigenous goats (Tshabalala *et al.*, 2003). It was also found that the Boer goat has a higher fat percentage than indigenous goats, the aroma compounds are more soluble in fat and tend to remain for longer in the fat matrix (Tshabalala *et al.*, 2003).

The National Goat Performance Testing scheme was started in 1970, but interest was low and participation was limited. It is an animal recording scheme that assists farmers and breeders in assessment of production performance of their herds, the following phases are available for participation (Tshabalala *et al.*, 2003; www.arc.agric.za/home.asp?pid=2753):

- Phase A: The dam's mothering characteristics and milk production is determined, as well as the growth rate of the kid or kids up to weaning.
- Phase B: This phase determine the post weaning growth of the kid at various ages.

- Phase C: The efficiency of feed conversion and the growth rate of male kids are determined under controlled and standardised conditions at a local ram testing station.
- Phase D: In this phase the post-weaning growth rate of male kids under standardised conditions on the farm under the supervision and direction of the Animal and Dairy Science Research Institute of Irene is measured.
- Phase E: The qualitative and quantitative carcass composition of a sire progeny is determined.

Figures for the average 100-day masses (corrected for age and multiple births and rearing affects) are illustrated in Table 2.7. It was collected by the National Mutton Sheep and Goat Performance Testing Scheme.

Table 2.7 Average 100-day weights of performance tested Boer goat kids.

Year	Male kids	Female kids
1970	24.0	21.9
1972	26.3	24.1
1975	23.6	21.7
1979	36.5	29.2
1982	32.3	27.8
1984	23.6	19.0
1986	26.9	23.4
1988	25.36	22.3

Repeated by Cambell, 2003

A relative large number of indigenous goats are found in almost all provinces in South Africa. These types are currently only characterised by their phenotypic characteristics, such as coat colour, ears and tails. It is believed that South African indigenous goats are more resistant to disease than the improved Boer goat (Mahanjana, 1999), but there is no specific evidence up to date. There is a lack of production information available for these goats and they are mainly use for meat and milk in cultural and rural communities. Research done were on the origin (Campbell, 1998), cashmere production (de Villiers *et al.*, 1999), and meat characteristics (Tshabalala *et al.*, 2003).

2.4 Assessment of genetic diversity in goats

Both biochemical markers and DNA markers can be used to estimate genetic variation (Table 2.8). Due to the availability and reliability of various markers, DNA markers have become the preferred method for genome mapping. Deoxyribonucleic acid (DNA) based markers have a number of favourable characteristics compared with phenotypic and quantitative traits as they are not influenced by environmental effects, heterogeneity, pleiotropy and complex gene interactions (Ajmone-Marsan *et al.*, 2001). DNA markers are generally considered neutral with little or no adaptive and selective value. In table 2.8 a summary is provided of studies of genetic diversity between various breeds were estimated using biochemical markers.

Table 2.8 Genetic diversity using biochemical markers

Goat Breeds	Aim of study	Reference
Tinerfeño; Majorero; Palmero	Erythrocytes	Garcia-Casass et al., (1992)
German Improved Fawn; Boer goats	Polymorphisms of five biochemical systems	Menrad et al., (1994)
Creole goats from Argentina	Protein polymorphisms	Deza et al., (2000)
Changthangi pashmina; Bakerwali goat breeds	Blood protein polymorphisms	Menrad et al., (2002)
Eight Mongolian native goat populations	Blood protein polymorphisms	Nyamsamba et al., (2003)

Genomic development led to several DNA markers mapped for several species, including goats. DNA markers are generally classified into single and multi-locus markers (Crawford *et al.*, 2000). Multi locus markers include random amplified polymorphic DNA (RAPD) and Amplified Fragment length polymorphism (AFLP). AFLP markers are the multilocus marker of choice, being more reproducible than RAPD. Both these markers are easily generated and have the disadvantage of being dominant (Crawford *et al.*, 2000). AFLP markers have been used to assess the genetic diversity within and between seven Italian goat populations (Ajomone - Marsen *et al*., 2001).

Single locus markers include RFLP (restriction fragment length polymorphism), microsatellites and SNP's (single nucleotide polymorphism). These markers have the advantage of being codominant and have a high reproducibility. RFLP markers refer to differences in banding patterns from DNA fragments, require large amounts of DNA and are technical demanding. Microsatellite markers require only a small amount of template DNA and are easy to find and

characterize (Crawford *et al.*, 2000). Microsatellites are two- to six-nucleotide repeats throughout the genome. They are highly polymorphic and abundant. Microsatellites have a high mutation rate and there is often large numbers of alleles that vary in size at a single locus. Microsatellite-derived markers represent a powerful way of mapping genes because of the easily detected length variation using unique flanking primer sequences (Beuzen *et al.*, 2000).

Cattle, sheep and goats have markers in common and these markers can be amplified with the same primer pairs (Jandurová *et al.*, 2003). In Table 2.9 some studies on the genetic diversity of goats using microsatellite loci are summarised.

Table 2.9 Studies on goats using microsatellite markers

Goat Breeds	Aim	References
Chinese indigenous goats	Microsatellite variation	Yang *et al.*, (1999)
Moroccan breeds, Alpine, Saanen, Poitevine and Pyrénéene)	Diversity using microsatellite markers and polymorphic milk protein gene encoding alpha-casein	Tadlaoui *et al.*, (2002)
Swiss breeds, Creole, Ibex and Bezoar	Genetic diversity using PCR amplification	Saitbekova *et al.*, (1999)
11 Asian goat breeds and Australian feral population	Genetic variation within and relationship among populations using 25 microsatellites and 59 protein coding loci	Barker *et a*l., (2001)
White Short-Haired and Brown Short-Haired.	Variation	Jandurová *et al.*, (2003)
6 Italian goat breeds and 2 composite breeds	15 microsatellites to evaluate genetic diversity	Iamartino *et al.*, (2005)
Jamanapuri goats	Genetic structure using 23 microsatellite loci	Gour *et al.*, (2005)
Canary goat	Genetic structure using 27 microsatellites	Martinez *et al.*, (2006)
Boer, Kalahari –Red, Savanna goats and indigenous populations of South Africa	Genetic variation using microsatellites	Visser *et al.*, (2004)

Genetic characterization is an important tool to assess genetic diversity of a population. Phenotypic traits are usually limited to colour of recognition and place of origin and assist in qualitative selection if measurements are included. According to Scherf (2000) a breed can be classified as “a subspecific” group of domestic livestock with definable and identifiable external characteristics which result in separate groups by visual appraisal compared to other similarly defined groups within the same species. Groups are also distinguished according to geographical

and/or cultural separation from phenotypically similar group and this has led to acceptance of its separate identity" (Scherf, 2000).

The South African commercial goat breeds are relatively well described in terms of phenotype and can be distinguished as breeds according to the definition of Scherf (2000). Research up to date has been primarily on quantitative studies. In order to characterize South African goat breeds both genotypic and phenotypic information is required. In this study the phenotypic traits measured have been added to describe and assist in breed standards. Microsatellites were applied for estimation of genetic variation and diversity to contribute to long term conservation and utilization of the goat breeds studied.

Chapter 3

Material and Methods

3.1 Genetic variation

Selection of goats for sampling

In this study three meat type breeds and one fibre producing breed were included. The samples included were collected to be representative of the different breeds. The commercial breeds are the Kalahari Red, Savanna and Boer goat and Angora goats. Two unimproved populations of Boer goats from the Eastern Cape (Fort Hare University, Research farm) and the Limpopo province (Mara Research station), respectively were included in the study. Additional data of indigenous goats from the Limpopo (Delftzyl experimental farm) and Mpumalanga (Groblersdal) provinces were obtained from the Department of Animal and Wildlife Sciences at the University of Pretoria. The largest number of the meat type breeds is primarily from the Northern Cape Province and care was taken to include as many breeders as possible to ensure unrelated samples. Angora samples were obtained from Jansenville Research Station and breeders from the Eastern Cape (Table 3.1). Blood samples were collected over a period of two years. Approximately 60 unrelated animals were sampled from each breed. Boer goats are spread over the country and samples were taken from three different areas, while the Savanna and Kalahari Red breeders are mainly situated in the Northern Cape.

Table 3.1 Number of blood samples collected for the study

Breed	Province	Farm	Number of samples
Boer goat	Northern Cape (G)	A	37
	Eastern Cape (J)	B	38
	Limpopo (M)	C	17
Kalahari Red (KR)	Northern Cape	D	13
	Northern Cape	E	10
	Northern Cape	F	10
	Northern Cape	G	7
	Northern Cape	H	10
	Northern Cape	I	10
Savanna (S)	Northern Cape	J	59
Angora goat (A)	Eastern Cape	K	60

DNA extraction

The blood samples were transferred to eppendorf tubes and frozen at -40˚C for storage. DNA was extracted using the GFX Genomix Blood DNA Purification Kit (Amersham Biosciences) with RBC Lysis. 900µl RBC lysis was mixed with 300µl whole blood and incubated for five minutes at room temperature after which it was centrifuged for 20 seconds at 10 000 rpm. The supernatant was removed without disturbing the pellet, which was resuspend by vortexing and 500µl extraction solution was added, vortex and incubated for five minutes at room temperature. The solution was transferred to a GFX column and centrifuged for one minute at 8 000 rpm, the flow-through discarded and an empty collection tube used to add another 500µl extraction solution and centrifuged once more. After the flow-through was discarded, 500µl wash solution was added (new collection tube) and centrifuged for three minutes at 10 000 rpm, the collection tube was then discarded. Buffer (200µl) was added and preheated in a waterbath at 70°C; centrifuged for 1 min at 8 000 rpm, GFX column discarded and the DNA remained in the eppendorf tube.

Microsatellite markers

Nineteen polymorphic microsatellites were selected from a panel of markers recommended by the International Society for Animal Genetics (ISAG) for application in diversity studies. Two of these markers (BM1818 and CSSM36) did not amplify well as part of a multiplex and were excluded in the final analysis. The characteristics of these microsatellites according to Econogene are summarised in table 3.2 (http://lasig.eplf.ch/projects/econogene/list_of_msmarkers.html; http://dga.jouy.inra.fr).

Table 3.2 Microsatellite marker information applied in this study

Microsatellite Marker	Chromosome Number	Fluorescent Lable	Product Size Range	Sequence
PLEX 1				
SRCRSP24	*Unknown*	*Fam*	162 – 174	F 5'– AGC AAG AAG TGT CCA CTG ACA G-3'
				R 5' –TCT AGG TCC ATC TGT GTT ATT GC-3'
SRCRSP5	*21*	*Tet*	171 -183	F 5' –GGA CTC TAC CAA CTG AGC TAC AAG- 3'
				R 5 –TGA AAT GAA GCT AAA GCA ATG C-3'
SRCRSP8	*Unknown*	*Tet*	210 – 260	F 5' –TGC GGT CTG GTT CTG ATT TCA C-3'
				R 5' –CCT GCA TGA GAA AGT CGA TGC TTA G- 3'
PLEX 2				
MCM527	*5*	*Hex*	155 – 173	F 5' –GTC CAT TGC CTC AAA TCA ATT C- 3'
				R 5' –AAA CCA CTT GAC TAC TCC CCA A- 3'
INRA 23	*3*	*Tet*	208 – 214	F 5' –GAG TAG AGC TAC AAG ATAA AAC TTC- 3'
				R 5' –TAA CTA CAG GGT GTT AGA TGA ACT CA- 3'
BM1329	*6 (sheep)*	*Tet*	168 – 182	F 5' –TTG TTT AGG CAA GTC CAA AGT C- 3'
				R 5' – AAC ACC GCA GCT TCA TCC- 3'
OARFCB20	*2*	*Tet*	99 – 125	F 5' – AAA TGT GTT TAA GAT TCC ATA CAG TG- 3'
				R 5' – GGA AAA CCC CCA TAT ATA CCT ATA C- 3'
CRSRD247	*14*	*Fam*	236 – 244	F 5' – GGA CTT GCC AGA ACT CTA CAA T- 3'
				R 5' –CAC TGT GGT TTG TAT TCA GG- 3'
ILST087	*28*	*Fam*	145 – 165	F 5' – AGC AGA CAT GAT GAC TCA GC- 3'
				R 5' –CTG CCT CTT TTC TTG AGA GC- 3'
SRCRSP23	*Unknown*	*Fam*	83 – 111	F 5' – TGA ACG GGT AAA GAT GTG -3'
				R 5' –TGT TTT TAA TGG CTG AGT AG- 3'
PLEX 3				

OARFCB11	*2*	*Hex*	142 – 150	F 5' –GGC CTG AAC TCA CAA GTT GAT ATA TCT ATC AC- 3'
				R 5' –GCA AGC AGG TTC TTT ACC ACT AGC ACC- 3'
ILST002	*Unknown*	*Hex*	118 – 127	F 5' –TCT ATA CAC ATG TGC TGT GC- 3'
				R 5' –CTT AGG GGT GAA GTG ACA CG- 3'
RM004	*15*	*Tet*	138 – 146	F 5' –AG CAA AAT ATC AGC AAA CCT- 3'
				R 5' –CCA CCT GGG AAG GCC TTT A- 3'
INRA63	*18*	*Fam*	174 – 190	F 5' –ATT TGC ACA AGC TAA ATC TAA CC- 3'
				R 5' –CCA CCT GGG AAG GCC TTT A- 3'
PLEX 4				
INRA006	*3*	*Hex*	109 – 123	F 5' –AGG AAT ATC TGT ATC AAC CTC AGT C- 3'
				R 5' –CTG AGC TGG GGT GGG AGC TAT AAA TA- 3'
MAF65	*15*	*Tet*	117 – 127	F 5' – AAA GGC CAG AGT ATG CAA TTA GGA G- 3'
				R 5' – CCA CTC CTC TGA GAA TAT AAC ATG- 3'
BM1258	*23*	*Fam*	102 – 106	F 5' –GTA TGT ATT TTT CCC ACC CTG C- 3'
				R 5' – GAG TCA GAC ATG ACT GAG CCT G(AT)- 3'

Dye colour of fluorescent label Fam = blue; Tet = green and Hex = yellow

PCR conditions and gel analyses

Microsatellite markers were divided into three plexes according to differences in size and fluorescent labels namely HEX (yellow), FAM (blue) and TET (green) (Table 3.2) (Kotze *et al*, 2004). The total volume of the Polymerase chain reaction (PCR) was 8.2µl, containing 1.74 units Taq, 50ng/µl target DNA, 4.54 pmoles of each primer and 3.48 nMoles dNTP's which consist out of 10µl ATP, CTP, GTP, TTP each and 60µl sterilized water. After the preparation of the samples, they were transferred in the Perkin Elmar Thermal Cycler using the following programme: 12 minutes at 94 °C followed by 33 cycles of 45 sec at 94 °C, 80 sec at 60 °C, 60 sec at 72 °C and an extension step of 60 minutes at 72 °C.

Before automated resolution of amplificated fragments in the automated analysis, using ABI PRISM 377, the microsatellite amplicons were tested on agarose gel for a clear product (Perkin Elmer, Foster City, USA). Polyacrylamide gels (PAGE) were used for the automated analysis. The 5 % polyacrylamide gel consist of 2.5 ml acrylamide, 12,5 ml sterilised water, 2,5 ml TBE Buffer and 9 g urea mixed, filtered and set for 5 minutes in a sonification bath. It was mixed with 17,5 ml Temed and 125 µl ammoniumpersulfate to polymeryze the gel which was poured into clean glass plates and left for 2 hours to set.

The PCR product were diluted with 110 µl sterilised water, 1 µl of the diluted PCR mixture mixed with Blue Juice (3µl Formamide, 0.35 µl Rox and 1.3 µl loading Buffer containing the GENESCAN-350 TAMRA internal standard mixed together. The product were denatured at 95°C for three minutes and transferred onto ice. Samples were loaded onto each lane of the polyacrylamide sequencing gel using the ABI PRISM 377 automated sequencer.

Statistical analyses

The DNA fragments were determined using Genescan version 3.1 and Genotyper 2 for MacIntosh for determining of fragment sizes. Data was then edited, cross checked and converted to applicable formats to perform statistical analysis.

Different software programs designed for analyses of molecular data were applied to estimate heterozygosity, Polymorphic Information Content (PIC) and genetic distances among the populations.

Hardy Weinberg Equilibrium (HWE), heterozygosity and effective number of alleles were calculated using POPGENE 32 software. Heterozygosity was estimated according to Nei (1987):

$$H1 = [2n/2n\text{-}1][1 - iQ^{ml} (pl_i^2)]$$

Where: n = the number of individual goats per population,

ml = the number of alleles at locus 1

pl_i = the frequency of the Ith allele at locus 1

PIC of the 17 microsatellites was calculated according to Bostein et al, (1980) using SAS.

$$PIC = 1 - (\sum_{i=1}^{n-1} p_i^2) - \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} 2\, p_i^2\, p_j^2$$

Where: n = number of different alleles for the specific locus

P_i^2 and p_j^2 = the population of the ith and jth allele

Genetic distances were calculated using the POPGENE32 program according to Nei (1978), unbiased standard genetic distance Ds:

$$Ds = (1 - J_{xy}) - \tfrac{1}{2} \{(1 - J_x) + (1 - J_y)\}$$

$$Ds = \ln(J_{xy}/\sqrt{J_x J_y})$$

Where: $J_x = (2n_x \sum x^2_i - 1) / (2n_x - 1)$

$J_y = (2n_y \sum y^2_i - 1) / (2n_y - 1)$

$J_{xy} = \sum xy$

n = population size (number of individuals in sample)

$x_i y_i$ = allele frequencies for xth allele in population x and y

A factorial correspondence analysis (FAC) was performed to illustrate the relationship among the breeds using Genetix 4.03 software (Belkhir *et al.,* 1996). FCA is an indication of how well the individual goat group to its specific breed. Arlequin Vers. 3.0. was applied to calculate pairwise Fst to estimate for the South African breeds. An analysis of variance was performed to indicate differentiation within and between breeds using Arlequin301 (cmpg.unibe.ch/software/arlequin3/arlequin301.pdf).

NJ (Neighbour Joining) tree was constructed using DISPAN (Ota, Institute of Molecular Evolutionary Genetics, Pennsylvania State University PA, USA), generated from allele frequencies resampled with 1 000 bootstrap replicates.

3.2 Phenotypic traits

A number of linear traits were measured for a total of 67 Angora, 42 Boer goats, 47 Kalahari Reds and 49 Savanna goats. These animals were all kept under extensive grazing systems (Table 3.3). The animals were on average 12 months old. A tape measure and measuring-rod were used to obtain various body measurements (in cm) and the animals were in an upright position during measurements.

Table 3.3 Origin and number of goats measured in this study

Population	Origin	Number of animals
Angora goats	Eastern Cape (Jansenville)	67
Boer goats	Gauteng (Hammanskraal)	31
Boer goats	Limpopo (Warmbad)	11
Kalahari Red	Northern Cape (de Aar)	47
Savanna	Northern Cape (de Aar)	49

The goats were also classified according to qualitative characteristics, including beardedness (absence or presence of beard), incidence of horns (horned or polled) and coat colour. Descriptive statistics were calculated using SAS.

Table 3.4 Descriptions of measurements

Measurement	Description
Height (H)	Vertical distance to the ground, measured behind the whithers
Length (L)	From the anterior shoulder point to the posterior extremity of the pin bone
Loin width (LW)	Measured just before the haunches *(os coxea)*
Depth (D)	Between *Corpus Sterni* and the point between the shoulder blades
Heart girth (HG)	Measured just behind the shoulder
Hock length (HL)	From the front to back margin
Head width (HW)	Distance between eyes
Head length (HL)	Length of head
Neck circumference (N)	Circumference
Tail length (TL)	From the tail base to tip
Pelvic width (PW),	Between pelvis bones
Pelvic length (PL)	From pelvic bone to os coxea

Chapter 4
Results

4.1 Genetic variation

DNA extraction & Microsatellite markers

Although samples of low quality were discarded, good quality DNA were extracted from frozen blood samples using the Amersham Kit. The PCR was conducted at the ARC Animal Production institute's Animal Genetics Laboratory. The equipment at this laboratory is regularly calibrated, since it is ISAG standardized. A panel of 17 markers were analyzed within a multiplex which is a more cost effective way of handling a large number of samples. All the markers analyzed were found to be highly polymorphic.

Allele frequencies

Allele frequencies were calculated and are summarized in Appendix 1. The number of alleles observed across microsatellite markers varied between two (RM004) for the M Boer Goats and 14 (BM1258) for the Angora Goats as illustrated in Table 4.1. Allele sizes ranged from a six bp difference (143 – 149) for locus OARFCB11, to a 40 bp difference (85 – 125) for locus OARFCB20.

Table 4.1 Number of alleles observed in each marker within the South African Goat breeds

Marker	G Boer Goat	J Boer Goat	M Boer Goat	Kalahari Red	Savanna Goat	Angora Goat	Groblers-dal	Delftzijl
SRCRSP24	3	7	8	8	4	9	3	7
SRCRSP5	4	7	3	7	8	9	4	7
SRCRSP8	6	8	6	8	5	11	5	5
MCM527	4	6	5	6	4	7	6	9
INRA23	6	9	8	9	10	7	7	
BM1329	3	5	6	5	4	7	5	6
OARFCB20	5	6	6	8	7	5	6	8
CSRD247	3	5	7	9	5	8	3	9
ILSTS87	3	5	3	7	5	8	5	6
SRCRSP23	4	7	7	8	9	9	7	6
OARFCB11	3	4	3	4	4	4		
ILSTS002	5	5	5	6	5	5		
RM004	4	5	2	5	4	5		
INRA63	5	6	4	6	5	5		
INRA006	8	2		7	7	11		
MAF 65	11	7		7	7	12		
BM1258	8	6		10	7	14		
MEAN	5	6	5	7	6	8	5	6

The average effective number of alleles ranged from 1.4 for ILst087 in the M Boer goats to eight for BM1258 in the Angora goats (Table 4.2). The Boer goats sampled represented three areas of South Africa and a difference in the mean effective number of alleles can be observed among these three populations (Table 4.2). The average effective number of alleles for the Fort-Hare Boer goats was higher than the commercial Boer goat population for the majority of the microsatellites markers.

Table 4.2 Number of samples per population for different microsatellite markers analyzed

Microsattelites	G boergoat		J Boergoat		M Boergoat		Kalahari Red		Savanna		Angora	
	n	ne*	n	Ne*	n	ne*	n	ne*	n	ne*	N	ne*
SRCRSP 24	29	2.7	29	2.7	17	4.7	60	3.1	58	2.2	56	3.8
SRCRSP5	28	2.1	27	2.4	17	1.9	60	3.2	58	4.5	56	4.5
SRCRSP8	28	3.7	27	3.4	17	2	60	3.5	58	2.8	56	3.8
MCM527	29	2.9	29	4.1	17	3.2	60	3	49	2.3	54	3.8
INRA023	28	2.4	29	4.6	17	3.7	60	3.2	56	4.3	53	2.5
BM1329	29	2.8	29	3.9	17	4.7	60	2.6	58	2.5	53	4
OarFcb20	36	2.1	36	4.9	17	4.3	60	4.2	56	5	54	3.3
CsRd247	29	2	29	2.3	17	4.6	60	2.7	58	2.1	53	4.7
ILst087	29	1.7	29	3.4	17	1.4	60	1.6	58	2.8	54	2.7
SrCRSP23	28	2.1	27	3.4	17	3.5	60	3	58	5.7	51	5.4
OARFCB11	29	2.1	29	2.4	17	1.9	60	2.5	58	2.8	57	2
ILSTS002	36	3	36	2	17	2.2	60	4.1	56	4.3	57	2.2
RM004	37	2.1	36	3	17	1.9	60	2.8	56	2.8	57	1.6
INRA63	37	3.3	36	3.1	17	3.3	60	3.8	56	2.1	57	3.4
INRA006	27	3.1	33	1.5			60	4.1	38	2.5	53	7
MAF65	33	7.1	31	6.2			60	4.9	51	5.5	56	4.2
BM1258	30	4.1	34	3.8			59	4.3	53	4.3	55	8
Mean	30.7	2.9	31	3.3	17	3.1	60	3.3	55	3.4	55	3.9

*ne = effective number of alleles

A number of specific alleles were observed in the different breeds for the markers tested. The highest number were observed for the Angora goats (19), followed by the Kalahari Red (10) and Boer goat (M) (5), Savanna goat and Boer goat G (2) and the lowest number in the Boer goats (J) (one) (Table 4.3). These alleles were investigated before it was accepted as true alleles and statistical analyses done.

Additional data of two indigenous groups with ten markers each were obtained from the Department of Animal and Wildlife Sciences at the University of Pretoria. The ten markers corresponded with the markers tested in the commercial breeds. For four of the markers additional alleles were observed for the Delftzyl and Groblersdal goat populations, compared to the commercial breeds (Table 4.3).

Table 4.3 Specific alleles observed over all the breeds

Marker	G Boer Goat	J Boer Goat	M Boer Goat	Kalahari Red	Savanna Goat	Angora Goat	Groblersdal	Delftzijl
SRCRSP24			146 156 172	150	148			
SRCRSP5					161			
SRCRSP8	248	246				222 240		
MCM527						163		141 145 151 161
INRA23			218	196				
BM1329			186			206		176
OARFCB20				85 109 125		93		
CSRD247				224		230 232		240 250
SRCRSP23				103		79 91	83 109	111
INRA63						170		
INRA006	107			105		103 111 125		
MAF65				117 119		151 153		
BM1258						100 120 122 124		

Polymorphic Information Content (PIC)

PIC values as described by Bostein *et al.* (1980) were calculated using SAS and is presented in table 4.4. The mean PIC value per marker varied from as low as 0.24 for OarFcb20 in the Boer goats to as high as 0.86 for BM1258 in the Angora goat. The highest PIC values were observed for MAF65 and BM1258. ILSTS087 had the lowest PIC value, but not the lowest number of different alleles. The PIC value can be relatively small if one or two alleles dominate (Buchanan *et al.*, 1994).

It was found that allele OARFCB11 and RM004 with only four and five alleles respectively, had a higher PIC value than ILSTS087 that had nine different alleles among the populations due to a common allele in the Boer goat (G) population representing 95% of all alleles. Another allele for the same marker was also common in the Kalahari Reds and Boer goats (M) representing 78% and 85% respectively of the nine different alleles observed for this marker.

Table 4.4 Polymorphic Information Content (PIC) for all the microsatellite markers

Microsatellite	G Boer goat	J Boer goat	M Boer goat	Kalahari Red	Savanna	Angora	Mean
SRCRSP 24	0.58	0.58	0.76	0.62	0.45	0.7	0.62
SRCRSP5	0.52	0.63	0.42	0.63	0.76	0.77	0.62
SRCRSP8	0.58	0.74	0.48	0.66	0.6	0.73	0.63
MCM527	0.57	0.73	0.64	0.62	0.59	0.67	0.64
INRA023	0.36	0.73	0.7	0.65	0.75	0.57	0.63
BM1329	0.43	0.75	0.75	0.54	0.51	0.73	0.62
OarFcb20	0.24	0.71	0.73	0.73	0.75	0.61	0.63
CsRd247	0.39	0.42	0.75	0.57	0.72	0.74	0.6
ILst087	0.1	0.52	0.24	0.35	0.59	0.63	0.4
SrCRSP23	0.55	0.62	0.65	0.63	0.8	0.73	0.66
OARFCB11	0.43	0.55	0.39	0.54	0.52	0.44	0.48
ILSTS002	0.57	0.46	0.5	0.72	0.69	0.48	0.57
RM004	0.46	0.59	0.35	0.58	0.52	0.31	0.47
INRA63	0.66	0.62	0.61	0.68	0.51	0.65	0.62
INRA006	0.77	0.17		0.72	0.61	0.84	0.62
MAF65	0.82	0.78		0.76	0.75	0.73	0.77
BM1258	0.76	0.67		0.74	0.76	0.86	0.76

Heterozygosity

Heterozygosity values estimated for the different breeds are indicated in Table 4.5a. The Boer goat (M) population was tested for 14 microsatellite markers while the rest of the populations were tested for 17 markers. Observed heterozygosity values ranged from 0.57 for the G Boer goat population to 0.70 for the Angora goats. The Boer goat (J) (0.66), Kalahari Red (0.68), Savanna (0.69) and Angora breeds were very similar, and indicate a relative high genetic variation of up to 70%.

Table 4.5a Expected and observed heterozygosity

Population	Hexp & sd	Hobs & SE
G Boer goat	0.57 (0.19)	0.57 (0.05)
J Boer goat	0.65 (0.15)	0.66 (0.03)
M Boer goat	0.62 (0.17)	0.63 (0.04)
Kalahari Red	0.68 (0.10)	0.68 (0.02)
Savanna	0.69 (0.10)	0.69 (0.04)
Angora goat	0.69 (0.14)	0.70 (0.03)

In addition heterozygosity values were calculated using only ten markers, including the two additional indigenous populations (Table 4.5b). Heterozygosity values followed a similar pattern tested with fewer markers. The Boer goat still had the lowest heterozygosity value of 0.49 and the Angora the highest among the commercial breeds. The indigenous populations also had a relative high genetic variation with heterozygosity values of 0.64 and 0.70.

Table 4.5b Expected and observed heterozygosity for ten markers

Population	Hexp (SE)	Hobs (SE)
G Boer goat	0.49 (0.06)	0.47 (0.03)
J Boer goat	0.69 (0.03)	0.64 (0.03)
M Boer goat	0.67 (0.06)	0.63 (0.04)
Kalahari Red	0.65 (0.03)	0.64 (0.02)
Savanna	0.71 (0.03)	0.60 (0.02)
Angora goat	0.73 (0.02)	0.65 (0.02)
Groblersdal	0.64 (0.05)	0.66 (0.03)
Delftzijl	0.70 (0.05)	0.64 (0.03)

Hardy Weinberg Equilibrium (HWE)

Hardy Weinberg Equilibrium (HWE) was analysed using the Popgene 3.4 software. For the Boer Goats, 12 and nine markers were in HWE ($P \leq 0.05$) disequilibrium for the G en J population's respectively and only one marker for the M Boer goat population. Two markers were not in HWE in the Kalahari Red. In the Savanna Goat 11 markers were not in HWE, with P values ranging from 0.000 to 0.044. A total of five markers were not in HWE for the Angora goat (Table 4.6).

Table 4.6 Hardy Weinberg Equilibrium values for South African Goats

Microsatellite Markers	G Boer Goat	J Boer Goat	M Boer Goat	Kalahari Red	Savanna Goat	Angora Goat
SRCRSP24	**0.025**	**0.045**	0.870	0.390	0.953	0.120
SRCRSP5	0.051	0.176	0.172	0.582	**0.000**	0.246
SRCRSP8	**0.001**	0.397	0.951	0.785	0.232	0.346
MCM527	**0.027**	**0.005**	0.064	0.069	**0.003**	0.634
INRA23	**0.000**	**0.006**	0.835	0.639	0.600	0.266
BM1329	**0.000**	0.390	0.850	0.670	**0.003**	0.514
OARFCB20	**0.000**	**0.004**	0.290	0.238	0.164	**0.001**
CSRD247	0.092	**0.000**	0.734	0.942	0.490	0.126
ILSTS87	**0.000**	**0.000**	0.875	0.406	**0.001**	0.537
SRCRSP23	0.870	0.452	0.866	0.594	**0.000**	**0.001**
OARFCB11	**0.005**	0.096	0.654	0.143	**0.000**	**0.001**
ILSTS002	**0.031**	0.320	0.508	0.339	**0.001**	0.112
RM004	**0.006**	0.113	0.654	0.260	**0.000**	**0.002**
INRA63	**0.090**	0.668	**0.020**	**0.001**	0.440	0.836
INRA006	0.252	**0.000**		**0.017**	**0.044**	**0.001**
MAF 65	**0.013**	**0.001**		0.782	**0.000**	0.052
BM1258	0.191	**0.021**		0.986	**0.012**	0.301

Genetic differentiation

The genetic differentiation expressed as Fst values was calculated using Arlequin vers.3.0. software. The results are indicated below the diagonal of table 4.7.

Table 4.7 Fst estimates (below diagonal) determined pairwise between South African Goat breeds

	G Boer Goat	J Boer Goat	M Boer Goat	Kalahari Red	Savanna Goat	Angora Goat
G Boer Goat	-					
J Boer Goat	0.092	-				
M Boer Goat	0.288	0.251	-			
Kalahari Red	0.164	0.188	0.237	-		
Savanna Goat	0.114	0.140	0.206	0.112	-	
Angora Goat	0.206	0.152	0.205	0.176	0.120	-

Fst (fixation index) values indicate the level of inbreeding due to genetic drift. The M Boer goat illustrated high Fst values with G Boer goat, Kalahari-Red Savanna and Angora goat. The Fst value was also high between the Angora goat and G Boer goat.

Analyses of molecular variance (AMOVA)

AMOVA analyses were conducted in order to explain the partitioning of the level of genetic variation of South African goats. Results indicated that 83.8% occurred within populations and 16.12% between populations (Table 4.8).

Table 4.8 AMOVA analyses for the commercial breeds

Source of variaton	d.f	Sum of squares	Variance components	Percentage of variation
Among populations	5	528.6	1.14 Va	16.12
Within populations	534	3161.09	5.92 Vb	83.88
Total	539	3689.69	7.06	

Genetic distances

The genetic distances among the commercial breeds were calculated to evaluate genetic relationships (Table 4.9). The smallest distance was observed between the Savanna goats and the G Boer goats (0.26) and also between G Boer goats and J Boer goats (0.26). The largest distance was observed between the Angora and the G Boer goat populations (0.75) and between the G

Boer goat and M Boer goat (0.71). Distance analyses for the indigenous populations were not included, because of the limited number of markers

Table 4.9 Genetic Identity (above diagonal) and Genetic Distance (below diagonal) for commercial breeds and 17 markers

	G Boer Goat	J Boer Goat	M Boer goat	Kalahari Red	Savanna	Angora
G Boer Goat	0	0.77	0.49	0.69	0.77	0.47
J Boer Goat	0.26	0	0.52	0.58	0.66	0.6
M Boer Goat	0.71	0.65	0	0.63	0.6	0.57
Kalahari Red	0.37	0.54	0.47	0	0.75	0.52
Savanna	0.26	0.42	0.52	0.29	0	0.62
Angora	0.75	0.51	0.56	0.65	0.48	0

*estimations based on Nei (1972)

D*A* distances were applied to construct a neighbour-joining (NJ) topology tree relating to the five populations studied (Figure 4.1). The M Boer goat and the two indigenous populations were not included due to limited sample size and only 10 markers. The numbers at the nodes are values obtained in the NJ topology tree, indicating robustness of the tree is not high. The tendency indicated by the tree however corresponds to the results obtained with the factorial correspondence analyses (FCA) (Figure 4.2). In the NJ diagram, the Angora breed plot separately from the Southern African breeds. The G Boer goat and Kalahari Red clustered together with a bootstrap value of 35%. The node of the J Boer goat had a bootstrap value of 35%.

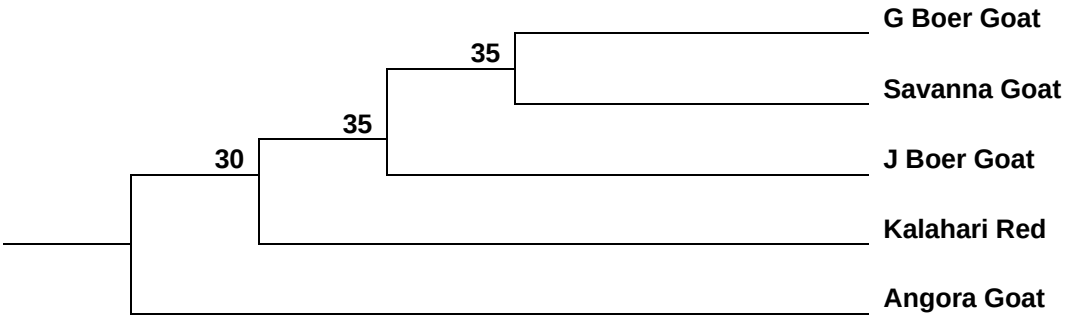

Figure 4.1 Dendogram of relationships between five commercial goat populations using neighbour-joining method.

The Factorial correspondence analyses (FCA) illustrates that the Angora, Kalahari-Red and M Boer goat breeds tended to form distinct groups, while the G Boer goats, M Boer goats and Savanna breeds do not form distinct groups (Figure 4.2).

4.1.2 Phenotypic characterization

Phenotypic description in this study included measurement of body only. All goats recorded in this study were horned. None of the Angora goats were bearded compared for the Boer goat, Kalahari Red and Savanna goats with 13.39, 23.40 and 24.49 % respectively were bearded. Seventy five percent of all the Boer goats had white bodies with red heads, and the remaining 25 percent had either speckled heads or a red spot on the body. The Kalahari-Red was primarily red coated with a white or black spot appearing on the body of 15% of the population. The Angora and Savanna goats were all white.

Body measurements were included for the different breeds in order to describe breed standards and results are presented in Table 4.9. The Angora goats differed ($P<0.0001$) from the other breeds in terms of height, length, depth, heart girth, pelvic width, pelvic length and ear length. The Kalahari Red had the highest depth (27.096 cm), followed by the Boer goat (26.426). The average pelvic length was approximately 19.75cm for the commercial breeds. For all the breeds, the Boer goat had the highest pelvic width (13.817 cm).

Table 4.10 illustrate the minimum and maximum measurements obtained for the four breeds. The greatest variation occurs within breeds and only a small variation can be observed between the breeds.

Figure 4.2 Factorial correspondence of South African breeds

Table 4.9 Minimum and maximum for body measurements for the different breeds

Measurements	Boer goat		Kalahari Red		Savanna		Angora goat	
	min	max	min	max	min	Max	min	max
Height (H)	47.00	67.50	49.30	60.20	47.80	61.90	39.10	55.40
Length (L)	55.00	79.50	60.60	83.20	30.00	71.10	39.00	58.20
Depth (D)	22.20	33.00	23.00	31.80	22.40	29.00	14.10	27.90
Heart girth (HG)	78.00	112.00	65.60	114.00	72.60	100.20	52.00	76.00
Hock length (HL)	16.50	34.00	15.20	36.10	18.10	29.10	15.40	26.30
Head width (HW)	4.80	10.50	4.80	8.90	4.20	7.30	5.50	10.30
Head length (HL)	13.00	21.00	9.80	21.60	13.10	20.00	13.70	19.40
Neck circumference (N)	33.20	57.00	33.70	58.50	30.40	65.40	21.00	34.00
Tail length (TL)	6.00	17.00	10.40	19.20	9.60	19.00	8.50	15.00
Pelvic width (PW),	7.80	21.40	9.00	13.50	8.40	17.70	6.20	11.30
Pelvic length (PL)	13.5	26.50	16.00	24.80	16.70	27.40	9.00	18.60
Ear Length (EL)	14.40	26.00	14.00	18.50	16.30	22.70	15.50	24.00

Table 4.10 Least square means and standard errors for body measurements for the different goat breeds

Measurements	Boer goat	Kalahari Red	Savanna	Angora goat
Height (H)	56.49 +/- 0.50 a	54.05 +/- 0.47 a	55.72 +/- 0.46 a	47.25 +/- 0.39 b
Length (L)	68.22 +/- 0.80 ab	69.84 +/- 0.75 a	64.94 +/- 0.74 b	48.36 +/- 0.63 c
Depth (D)	26.43 +/- 0.314ab	27.10 +/- 0.30 a	24.94 +/- 0.29b	19.15 +/- 0.25 c
Heart girth (HG)	90.32 +/- 1.04 ab	95.32 +/- 0.98 a	86.52 +/- 0.96 b	64.63 +/- 0.82 c
Hock length (HL)	28.31 +/- 0.49 a	27.66 +/- 0.46 a	23.50 +/- 0.45 b	21.72 +/- 0.39 b
Head width (HW)	7.72 +/- 0.18 a	6.57 +/- 0.17 b	5.62 +/- 0.16 c	7.23 +/- 0.14 ab
Head length (HL)	17.16 +/- 0.26 a	15.66 +/- 0.25 b	15.84 +/- 0.24 ab	16.60 +/- 0.21 ab
Neck circumference (N)	48.29 +/- 4.00a	42.46 +/- 3.79 ab	37.67 +/- 3.71 ab	27.94 +/- 3.17 b
Tail length (TL)	12.16 +/- 0.30 ab	13.21 +/- 0.28 a	13.27 +/- 0.28 a	11.03 +/- 0.24 b
Pelvic width (PW),	13.82 +/- 0.28 a	11.08 +/- 0.27 b	11.42 +/- 0.26 b	8.79 +/- 0.23 c
Pelvic length (PL)	19.68 +/- 0.35 a	20.46 +/- 0.33 a	19.13 +/- 0.32 a	13.57 +/- 0.28 b
Ear Length (EL)	21.40 +/- 0.25 a	19.18 +/- 0.24 b	19.49 +/- 0.23 b	15.98 +/- 0.20 c

Variables with different superscripts differ significantly (P<0.0001)

Chapter 5

Discussion

5.1 Genetic characterization

This study was performed to contribute towards the genetic characterization of the South African commercial goat breeds. Four goat breeds and two additional indigenous populations were genotyped at the ARC- II Livestock Laboratory and Department of Animal and Wildlife Sciences, University of Pretoria. A total of 17 microsatellite markers were used to calculate the allele frequencies, PIC values, heterozygosity, HWE equilibrium, genetic differentiation, AMOVA and genetic distances.

Marker polymorphism

The polymorphic information content (PIC) for the markers was illustrated by the PIC values, which takes the number and allele frequency in account per marker at a specific locus (Gourraud *et al.*, 2005). The highest PIC values were observed for the markers MAF65, SRCRSP8 and BM1258 (Table 4.4). It is an indication that all the makers in this study were highly polymorphic. These PIC values are in a similar range compared to other studies which ranged from 0.11 to 0.85 (Luikart *et al*., 1999), 0.11 to 0.78 (Kumar *et al*., 2005), 0.25 to 0.83 (Martinéz *et al*., 2006), 0.75 to 0.80 (Yang *et al*., 1999) and 0.59 to 0.92 (Jandurová *et al*., 2003).

In this study the number alleles observed for the 17 markers ranged from three to 14 (Table 4.2). Li *et al*, (2002) suggested that, for studies of genetic distance, to reduce the standard error of distance estimates, microsatellite loci should have no less than four alleles. The number alleles observed for this study were compared to previous studies (Kumar *et al.*, 2005; Ouafi *et al.*, 2002; Saitbekova *et al.*, 1999) using similar microsatellite markers, and an average tendency was observed for a higher number of alleles per locus in this study. Values by Martínez *et al*, (2006), Jiménez-Gamero *et al*, (2005) and Li *et al*, (2002) reported ten, seven and seven alleles respectively for SRCRSP8, in this study 14 alleles were observed for the marker. Of the seventeen markers, eight presented alleles in the expected range. Microsatellite markers SRCRSP24, BM1329, BM1258 and INRA23 had alleles not within the expected range. SRCRSP8 and MAF65 had four additional alleles, INRA006 three and SRCRSP23 and INRA63

two more alleles than expected. It should however be noted that the number of alleles are dependant on the sample size and therefore the mean number of effective alleles serve as a more appropriate indicator of allelic richness for the markers tested.

Thirteen of the seventeen markers were observed with at least one unique allele over the goat breeds (Table 4.3). Six specific alleles were observed for SRCRSP23 and five for markers the markers SRCRSP24, MCM527, CSRD247 and INRA006. Yang *et al*, (1999) reported OARFCB11 and OARFCB20 with unique alleles among five indigenous goat breeds. No specific alleles were observed in this study for OARFCB11, but four were observed for OARFCB20. These alleles can be useful for the identification of breeds and or populations. This requires further investigation and the ideal would be to test larger sample sizes for all the breeds with the same markers.

The results observed in this study showed that all the markers deviated from HWE in one or more of the breeds (Table 4.6). One and two markers were in disequilibrium respectively for the M Boer goats and Kalahari Red. In contrast, only the Angora goats had higher mean number of observed alleles and heterozygosity than the Kalahari Red. The deviation in the remaining breeds could be attributed to small effective population sizes and the difficulties in collecting enough unrelated pure individuals.

Genetic variation

Heterozygosity was estimated according to Nei(1987) as indication of genetic variation. A Relative high heterozygosity was observed for all the breeds (Table 4.5a). The G Boer goat had the lowest average heterozygosity observed (0.57) compared to the other breeds and the Mara Boer Goats (0.63). The lower variability for the commercial groups is in agreement with their selection as distinct meat goats, while the Mara Boer goat and J Boer goat populations were not subjected to strict selection, therefore the reason for the higher variability observed. Both the Savanna and Kalahari Red have higher heterozygosity values than the Boer goat populations (0.69 and 0.68 respectively). The highest heterozygosity was observed for the Angora goats (0.70). Although selected as a distinct mohair breed, it is a relatively large breed in South Africa compared to the other goat breeds. There may also have been introduction of genes from other goat breeds during early years that ensured a broad genetic base for the Angora in South Africa.

The Heterozygosity values in this study compare well with values reported in previous studies (Martinez *et al*., 2006; Els *et al*., 2004; Martinez *et al*., 2004; Li *et al*., 2002), but higher than reported by Kumar *et al*, (2005) for Marwari goats and Barker *et al*,. (2001) for Asian goat populations and lower than that observed for Southern Italian goat populations and Chinese goats (Iamartino *et al*., 2005; Yang *et al.*, 1999).

Heterozygosity values were also calculated with only ten markers with the inclusion of two additional indigenous populations obtained from the University of Pretoria (Table 4.5b). With fewer markers the heterozygosity is lower for the commercial breeds but in the same order. The heterozygosity of the Delftzijl population is the highest (0.70) and that of the Groblersdal population is also relatively high (0.64). A high genetic variability was observed in these indigenous unimproved goats sampled. It must however be stressed that these were relatively small sample sizes.

An AMOVA analyses were conducted to understand the partitioning of the genetic diversity of the South African goats. Table 4.8 illustrate that 83.88% and 16.12% respectively could be attributed within and among populations. These values are in accordance with the results of Saitbekova *et al*, (1999), but higher than the results of Li *et al*, (2002), who reported a variation of 10.5% between populations and 89.5% within populations.

Breed differentiation

The fixation index (Fst) was calculated to estimate the genetic inbreeding between all the breeds. The value may vary between 0 (no genetic difference) to a 1 (fixation of the allele). Little genetic difference was observed between G and J Boer goat populations (0.093), the Savanna and Kalahari Red (0.112), the Savanna and G Boer goat (0.114) and the Savanna and J Boer goat (0.140). Moderate differences was observed between the rest of the breeds, except for a large difference between the M Boer Goat and the G Boer Goat (0.288) according to the classification of divergence by Hartl (1988)(Table 4.7).

Estimations of the genetic distances are summarized in Table 4.9. With a genetic distance of 0.26 between the G Boer goats and the Savanna goat, they seem to be more related than expected. The largest distance was observed between the Angora and the G Boer goat populations (0.75). Factorial correspondence analysis (Fig 4.2) indicated clusters between the Savanna, G and J Boer

goat populations, while the Angora, Kalahari Red and Boer goat (M) populations formed distinct groups, which corresponds with the distance information observed.

The relationship between the breeds with ten markers did not differ significantly compared to 17 markers (Table 4.8b). The indigenous goats from Delftzijl indicated relatedness with the Savanna goat and G Boer goat, while those from Groblersdal are more closely related to the M Boer goat. These indigenous populations probably had gene introduction from Boer goat over the years.

The NJ-method has been shown to be useful for obtaining correct tree topology in other studies (Oafi A.T *et al*., 2002; Yang L *et al*., 1999; Martínez *et al*., 2006; Iamartino *et al.*, 2005; Li *et al*., 2002). The G Boer goat and Savanna were grouped together first, then with the J Boer goat, while the Kalahari Red and Angora goat formed distinct groups (Fig 4.1).

Considering all the estimations performed on the commercial breeds in this study, results indicate a relative high genetic variation among the breeds and the indigenous populations. Parameters concerned with potential differentiation of the breeds, all tend to group the Boer goats (as expected) together with the Savanna, while the Kalahari Red tend to be a more distinct breed. Results confirm to the uniqueness of the Angora as can be expected and despite selection pressure for fine hair production, has a high genetic variation in the breed.

5.2 Phenotypic characterisation

The goats in this study, except for the Angora goats were developed through the selection and crossing of indigenous goats from South Africa, with some introduction of Indian and European goats. All the breeds have been maintained as separate breeds for at least the past two decades. These breeds have been phenotypically described by breed associations. Breed standards are primarily specified in terms of production traits and to a lesser extent visual phenotypic traits are taken into account for the commercial breeds.

The Boer goats were predominantly white with red heads and ears, only a few animals had either a red spot somewhere on the body or speckled heads. The necks were full and well fleshed with a least square mean circumference of 48.29 cm. The brisket was broad and deep and ribs well fleshed with a depth value of 26.43 cm and heart girth of 90.23 cm. The pelvic was the highest

for the breeds and the goats was of medium height. The South African Boer goat is relatively strict on having a Red head to be classified as a pure Boer goat.

All the Savanna goats in this study were all white. The goats were of medium height and their ears were fairly long. The pelvic width indicated a wide hindquarter and the forequarter was of medium width, depth was 24.94 and heart girth 86.52, much lower than the other meat breeds. They tend to be a smaller breed.

All the goats in the Kalahari Red population were primarily red; a black or white spot appeared on some of their bodies. Their legs were shorter but their bodies longer than the other two meat breeds. The forequarter was broad and well muscled with values for the depth of 27.10 and heart girth 95.32, much higher than the other breeds. The hindquarter of the Kalahari Red was not as broad as that of the Boer goat (pelvic width of 11.08 versus 13.82), but no significant difference appeared for the pelvic length between the meat breeds.

The aim of this study was to perform a genetic characterization of the commercial goat breeds found in South Africa using microsatellite markers. Due to the origin and development of these breeds from indigenous goats, it was important to gain insight on the genetic variation and potential relatedness among the breeds. They have been described on phenotype and have been established as mohair (Angora) and meat type (Boer, Savanna and Kalahari Red) over many years.

This study now confirms that the three commercial goat breeds can be distinguished as different breeds. It will be important for future utilization of the breeds to ensure a broad genetic basis and perform selection in such a way to maintain diversity and uniqueness of the breeds. For utilization conservation of these commercial breeds, both phenotypic information on performance traits and genotypic information should be recorded. Further investigation on unique alleles and special traits should receive attention.

Conclusion

This study was first attempt to contribute genetic information on commercial goat breeds in South Africa. The information obtained will be useful for conserving the genetic basis of the breeds in South Africa and holds potential for "labelling" them as South African bred – "product of South Africa". A total of seventeen microsatellite markers were tested and found to be highly polymorphic and successful for the characterization of the goat breeds. Genetic variation was measured in terms of heterozygosity and genetic distances and found to be relatively high. The study therefore indicates sufficient genetic variation within the breeds, despite artificial selection for improved production. Genetic distances indicate the Boer goat and Savanna breeds are genetically closer related compared to the Kalahari Red and Angora goats which form distinct breeds according to the genetic data observed.

Phenotypic description confirmed that the goats in this study adhere to breed standards for the different breeds. They are selected for meat production and conformation is an important trait to the industry.

In conclusion, genetic variation observed indicates statistical support for the classification of these breeds and therefore should be studied as different breeds managed, selected and conserved for utilization in the diverse South African climate.

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Appendix 1

Allele frequencies

SRCRSP24	Angora	G Boer goat	J Boer goat	M Boer goat	Kalahari-Red	Savanna	Indigenous	Delftzyl
146				8.82				13.79
148						0.86		
150			1.85					
152	0.89				0.83			
154	2.68		7.41	11.76				5.17
156				2.94				3.45
158	7.14			2.94	0.83			
160	3.57		7.41		1.67			5.17
162	26.79	32.14	24.07	38.24	22.50	35.34	53.45	50.00
164	2.68	41.07	55.56	11.76	30.83	6.03	8.62	15.52
166	8.04		1.85		0.83			
168	6.25		1.85		0.83			
170	41.96	26.79		17.65	41.67	57.76	37.93	6.90
172				5.88				

SRCRSP5	Angora	G Boer goat	J Boer goat	M Boer goat	Kalahari-Red	Savanna	Indigenous	Delftzyl
161						8.62		
163	1.79		3.70		6.67	6.90		1.72
165	11.61	8.93			0.83	0.86		3.45
167	0.89	3.57						
169	18.75		3.70			31.03		1.72
171	19.64	50.00	42.59	23.53	40.00	28.45	60.34	44.83
173	32.14		5.56	8.82	0.83		1.72	1.72
175	2.68				0.83			
177			1.85			3.45		3.45
179	10.71		35.19	67.65	15.83	11.21	22.41	43.10
181	1.79	37.50	7.41		35.00	9.48	15.52	

SRCRSP8	Angora	G Boer goat	J Boer goat	M Boer goat	Kalahari-Red	Savanna	Indigenous	Delftzyl
214	8.04	3.57	5.56	2.94		6.90		6.90
222	0.89							
224	18.75			14.71	2.50	2.59	1.72	
226	43.75		25.93	67.65	35.00	48.28	5.17	18.97
228		3.57	20.37		1.67		37.93	58.62
232	1.79			8.82	27.50			
234	3.57	7.14		2.94	29.17	30.17	10.34	6.90
236	0.89	55.36	31.48		0.83		44.83	8.62
238	6.25		1.85		2.50			
240	6.25							
242	7.14		1.85	2.94	0.83	12.07		
244	2.68	23.21	11.11					
246			1.85					
248		7.14						

CsRd247	Angora	G Boer goat	J Boer goat	M Boer goat	Kalahari-Red	Savanna	Indigenous	Delftzyl
222	2.83			17.65	4.17			
224					1.67			12.50
230						17.24		1.79
232						4.31		
234	0.94			2.94	1.67			
236	14.15	36.21	15.52	17.65	37.50	20.69	18.97	
238	25.47			11.76	0.83	29.31		7.14
240								3.57
242	30.19		3.45		2.50			3.57
244	2.83	62.07	72.41	35.29	46.67	28.45	79.31	7.14
246	20.75	1.72	3.45	11.76	2.50			42.86
248	2.83		5.17	2.94	2.50		1.72	17.86
250								3.57

ILStS087	Angora	G Boer goat	J Boer goat	M Boer goat	Kalahari-Red	Savanna	Indigenous	Delftzyl
134					0.83			
141	12.96				2.50			
143	12.04		1.72	2.94	1.67	22.41		1.79
145	53.70			85.29	78.33	42.24	1.72	7.14
147	0.93	94.83	51.72			33.62	63.79	76.79
149	2.78	1.72	36.21		10.83		5.17	
151	2.78			11.76	3.33		25.86	1.79
153	13.89		1.72			0.86		7.14
155	0.93				2.50	0.86		5.36
157		3.45	8.62				3.45	

SrCrsP23	Angora	G Boer goat	J Boer goat	M Boer goat	Kalahari-Red	Savanna	Indigenous	Delftzyl
79	10.78							
81	5.88					15.52		
83							12.07	
85	0.98		1.72	20.59	2.50			
87		25.86	43.10	2.94	12.50	12.93	15.52	
89			1.72	2.94		6.03		
91	6.86							
93	0.98					4.31		
95	40.20					4.31		
97	8.82			8.82	3.33		12.07	
99	21.57		1.72	2.94	7.50	32.76		12.96
101	3.92	13.79	34.48	50.00	20.00	1.72	5.17	20.37
103					0.83			1.85
105		55.17	13.79	11.76	51.67	10.34	41.38	38.89
107		5.17	3.45		1.67	12.07	12.07	7.41
109							1.72	
111								18.52

BM1329	Angora	G Boer goat	J Boer goat	M Boer goat	Kalahari-Red	Savanna	Indigenous	Delftzyl
170	1.89				1.67	3.45	1.72	
172	16.98	36.21	25.86	14.71	32.50	28.45	10.34	26.79
174	29.25	5.17	22.41	14.71	7.50		3.45	16.07
176								1.79
178	21.70		20.69	23.53	5.83	10.34	31.03	23.21
180	2.83	58.62	22.41	32.35	52.50	57.76	53.45	23.21
182	26.42		8.62	11.76				8.93
186				2.94				
206	0.94							

INRA023	AnG Boer goatora	G Boer goat	J Boer goat	M Boer goat	Kalahari-Red	Savanna	Indigenous	Delftzyl
196					0.83			
198	5.66		1.72	11.76	1.67	2.68		
200	49.06		5.17	44.12	5.83	18.75	3.45	
202	1.89	3.57	6.90	2.94	13.33	6.25		
204		5.36	8.62			1.79	13.79	
206	1.89				1.67	8.04		
208	34.91	1.79	3.45	2.94	50.83	37.50	1.72	
210		78.57	44.83	2.94		18.75	18.97	
212	0.94			14.71	8.33	3.57		
214	5.66	5.36	6.90	17.65	16.67	0.89	20.69	
216		5.36	12.07	2.94	0.83	1.79	22.41	
218			10.34				18.97	

OarFcb20	AnG Boer goatora	G Boer goat	J Boer goat	M Boer goat	Kalahari-Red	Savanna	Indigenous	Delftzyl
85					0.83			
93	7.41							
95	50.93	1.72	34.48	11.76		10.34	1.72	12.50
97	17.59	1.72	32.76	8.82	2.50	21.55	24.14	14.29
99	21.30	1.72	6.90	14.71	23.33	27.59	29.31	1.79
101		8.62	5.17	20.59	9.17	25.86	29.31	39.29
103	2.78	86.21	10.34	5.88	38.33	12.07	10.34	8.93
105					13.33	0.86		
107			10.34	38.24		1.72	5.17	19.64
109					9.17			
125					3.33			
162								1.79
164								1.79

MCM527	Angora	G Boer goat	J Boer goat	M Boer goat	Kalahari-Red	Savanna	Indigenous	Delftzyl
141								1.92
145								1.92
151								17.31
155	37.04	8.62	31.03	47.06	1.67	19.39	24.14	25.00
157	35.19	55.17	31.03	11.76	30.00	19.39	41.38	
161								15.38
163	3.70							
165	8.33	20.69	15.52	26.47	45.83	53.06	17.24	17.31
167	0.93		8.62	5.88				9.62
169	11.11				0.83		5.17	3.85
171		15.52	10.34	8.82	14.17	8.16	8.62	7.69
173	3.70		3.45		7.50		3.45	

OARFCB11	Angora	G Boer goat	J Boer goat	M Boer goat	Kalahari-Red	Savanna	Indigenous	Delftzyl
143	68.42	20.83	18.06	64.71	25.83	32.14		
145	11.40	11.11	22.22	32.35	12.50	0.89		
147	1.75		4.17		5.00	13.39		
149	18.42	68.06	55.56	2.94	56.67	53.57		

ILSTS002	Angora	G Boer goat	J Boer goat	M Boer goat	Kalahari-Red	Savanna	Indigenous	Delftzyl
119	22.81	1.39	1.39		12.50	16.96		
121	0.88	41.67	9.72	8.82	37.50	27.68		
123	11.40	5.56	12.50	5.88	21.67	1.79		
125	63.16	41.67	69.44	64.71	18.33	33.93		
127	1.75	9.72	6.94	17.65	9.17	19.64		
129				2.94	0.83			

RM004	Angora	G Boer goat	J Boer goat	M Boer goat	Kalahari-Red	Savanna	Indigenous	Delftzyl
139	3.51	2.70	1.39	64.71	31.67			
141	80.70	20.27	19.44	35.29	11.67	33.04		
143	12.28	10.81	25.00		6.67	0.89		
145	2.63		4.17		49.17	13.39		
147	0.88	66.22	50.00		0.83	52.68		

INRA63	Angora	G Boer goat	J Boer goat	M Boer goat	Kalahari-Red	Savanna	Indigenous	Delftzyl
170	0.88							
172	38.60	6.76	6.94		0.83	18.75		
174	7.02	8.11	16.67	5.88	6.67	4.46		
176	24.56	41.89	26.39	17.65	16.67	63.39		
178	28.95	29.73	47.22	41.18	35.00	6.25		
180		13.51	1.39	35.29	33.33	7.14		
182			1.39		7.50			

INRA006	Angora	G Boer goat	J Boer goat	M Boer goat	Kalahari-Red	Savanna	Indigenous	Delftzyl
103	3.77							
105					0.83			
107		3.70						
109	3.77	27.78			31.67	26.32		
111	4.72							
113	2.83	11.11	10.61					
115	5.66	5.56			9.17	6.58		
117	15.09	3.70			31.67	13.16		
119	14.15	3.70			7.50	1.32		
121	28.30		89.39		2.50	1.32		
123	9.43	27.78			16.67	50.00		
125	8.49							
127	3.77	16.67				1.32		

MAF65	Angora	G Boer goat	J Boer goat	M Boer goat	Kalahari-Red	Savanna	Indigenous	Delftzyl
117					24.17			
119					1.67			
121	6.25	6.06	30.65		5.00	6.86		
123	5.36	16.67	9.68			15.69		
125	4.46	3.03			19.17	4.90		
127	8.93	1.52						
129	46.43	24.24	14.52			17.65		
131	12.50	1.52	9.68		4.17			
133	0.89				20.83			
135	0.89	4.55	3.23		25.00			
137	8.04	21.21	20.97			35.29		
139	2.68	12.12	11.29			18.63		
143		6.06				0.98		
145		3.03						
151	0.89							
153	2.68							

BM1258	Angora	G Boer goat	J Boer goat	M Boer goat	Kalahari-Red	Savanna	Indigenous	Delftzyl
100	6.36							
102	22.73	18.33	45.59		14.41	17.92		
104	15.45	1.67	22.06		6.78	2.83		
106	2.73				3.39			
108	9.09	21.67	7.35		38.14	26.42		
110	16.36	31.67	4.41		22.03	18.87		
112	4.55	13.33	14.71		6.78	26.42		
114	3.64	1.67	5.88		0.85			
116	3.64	8.33			0.85	5.66		
118	0.91	3.33			0.85			
120	6.36							
122	3.64							
124	1.82							
126	2.73				5.93	1.89		