EX-SITU CONSERVATION STRATEGIES IN SOUTH AFRICAN INDIGENOUS GOAT GENETIC RESOURCES

CHOKOE TLOU CASWELL

A RESEARCH THESIS
submitted in fulfilment of the requirements for the degree of
DOCTOR OF PHILOSOPHY (ANIMAL PRODUCTION)

in the

FACULTY OF SCIENCE AND AGRICULTURE
(School of Agricultural and Environmental Sciences)
at the UNIVERSITY OF LIMPOPO

PROMOTER: PROF BJ MTILENI (TUT)
CO-PROMOTER: PROF O TADA

2025

DECLARATION

I declare that *EX SITU* CONSERVATION STRATEGIES IN SOUTH AFRICAN INDIGENOUS GOAT GENETIC RESOURCES is my own work and that all the sources that I have used or quoted have been indicated and acknowledged by means of complete references and that this work has not been submitted before for any other degree at any institution.

___________________ 01 March 2025

Chokoe, T.C (Mr) Date

ACKNOWLEDGMENT

I want to thank the following people for their respective contributions to the completion of this thesis:

- The study promoters, Prof. BJ Mtileni and Prof. O Tada for familiarizing me with population genetics, their support and advice. The senior scientific researchers for the guidance throughout the study. The gates that you have opened for me can only better the young scientist in me.

- What could this study amount to be, had it not been you the goat farmers? You who allowed us to use your goats for this study and welcomed a team of scientists to your farms and households expecting no reward. I really appreciate it.

- A special thank you to the Agricultural Research Council: Biotechnology Platform for making goat genotype data (Boer, Kalahari Red, Savanna) available for this study.

- Many thanks to Dr. Noluthando Netnou-Nkoana, the Director: Genetic Resources of the Department of Agriculture, Land Reform and Rural Development for all the support that was provided to me during this study.

- Thanks, are also owed to advisory services workforces of Departments of Agriculture (Limpopo, Gauteng, Free State and North West provinces) for their co-operation during sample collection.

- The Agricultural Research Council Animal Production Institute and the Agricultural Research Council Biotechnology Platform are acknowledged for the human resources and infrastructure support of this study.

- I would like to express my gratitude to my lab team members, Mr. Tumudi Mphahlele, for his dedication to my study during the sampling phase. Acknowledgement goes to Mr. Nick Mokotoane for his support with genotyping and data analysis; the staff of the Agricultural

Research Council: Biotechnology Platform for sharing their skills and hours in the laboratory with me.

- To Seoka Chokoe, Phenyo Letuboko Chokoe and Tlou Junior Chokoe my sons, for your smiling faces that warms my heart; Phuti and Mahlatse Chokoe, my daughters, your inquisitive attitude on my studies and visits to the laboratories gave daddy more strength.

- My brothers Freddy “Moshe” Ngobeni-Chokoe, and Lesiba “Chokoechokoe” Chokoe for being there as my hands, eyes and ears during this study. A Big thank you.

- My best friend Motsumi Solomon AKA “General Kwaak” Sethosa for believing in all that I initiated in our lives and being there by my side. Thank you, General Kwaak.

- To my late father, Mmaphuti “Seoka” Solomon Chokoe and my late mother, Elizabeth Chokoe, you have always wanted me to explore the Agricultural Industry and to study harder. I did it as you have requested Papa and Mmane.

- To God and Badimo baga Chokoe le baga Malakalaka; baga Kgopa le baga Seleka.

DEDICATION

This thesis is dedicated to my best friend, confidant and pillar of strength, throughout my entire life, my late grandmother "Koko Ngwana-Seleka" Mmachoene Maria Chokoe who took care of me in my secondry school years until I matriculated. It is also dedicated to my children; Phuti Chokoe, Mahlatse Chokoe, Seoka Chokoe, Phenyo Chokoe and Tlou Junior Chokoe who are my great cheerleaders.

TABLE OF CONTENTS

Contents

CHAPTER 3: STUDY ONE

CHAPTER 4: STUDY TWO

CHAPTER 5: STUDY THREE

CHAPTER 6: STUDY FOUR

LIST OF TABLES

LIST OF FIGURES

LIST OF ABBREVIATION

AFLP	Amplified Fragment Length Polymorphisms
AIA	Animal Improvement Act
AII	Animal Improvement Institute
AIP	Animal Improvement Policy
AMOVA	Analysis of molecular variance
AnGR	Animal Genetic Resources
AREC	Animal Research Ethics Committee
ARC	Agricultural Research Council
AU	African Union
AU-IBAR	African Union – InterAfrican Bureau for Animal Resources
BL	Body length
CI	Confidence interval
DAD-IS	Domestic Animal Diversity Information System
DAFF	Department of Agriculture Forestry and Fisheries
DAGRIS	Domestic Animal Genetic Resources Information System
DALRRD	Department of Agriculture, Land Reform and Rural Development
DEA	Department of Environmental Affairs
DNA	Deoxyribonucleic acid
DRSM	Dr. Ruth Segomotsi Mompati
E_{HOM}	The number of expected homozygous genotypes
EC	Eastern Cape
EL	Ear length
EO	Ear orientation
FACT	Farm Animal Conservation Trust
FAnGR	Farm Animal Genetic Resources
FAO	Food and Agriculture Organisation
F_{HOM}	numbers of homozygous genotypes
F_{ROH}	Genomic inbreeding coefficient based on ROH
F	inbreeding

F_{IS}	Within-population inbreeding coefficients
FS	Free State
F_{ST}	Pairwise Fixation Index
GP	Gauteng Province
GPA	Global Plan of Action
GPS	Global Positioning System
$\mathrm{H_E}$	Expected Heterozygosity
HG	Heart girth
HL	Head length
$\mathrm{H_O}$	Observed Heterozygosity
HW	Head width
HWE	Hardy–Weinberg equilibrium
IBD	identical-by descent
ICAR	International council for animal Recording
IGGC	International Goat Genome Consortium
ILRI	International Livestock Research Institute
INTERGIS	Integrated Recording and Genetic Information System
KEGG	Kyoto Encyclopaedia of Genes and Genomes
KZN	KwaZulu-Natal
L_{AUTO}	Total length of the autosomes
L_{ROH}	Total length of ROH on autosomes
LD	Linkage disequilibrium
LP	Limpopo
LSD	Least Significant Difference
MAF	Minor allele frequency
mtDNA	Mitochondrial Deoxyribonucleic acid
$\mathrm{MN_{ROH}}$	mean number of Runs of homozygosity per individual
n	Population size
NC	Neck circumference
Ne	Effective population
NLDS	National Livestock development Strategy

NSAP	National Strategies and Action Plan
NW	North West
O_{HOM}	The number of observed homozygous genotypes
PROC-GLM	General Linear Model procedure
PC	plot of the first
PCA	Principal component analysis
QTL	Quantitative trait locus
SADC	Southern African Development Committee
SAS	Statistical Analysis System
SNP	Single nucleotide polymorphism
RH	Rump height
RL	Rump length
ROH	Runs of homozygosity
RW	Rump width
Thabo Mofutsa	Thabo Mofutsanyane
TD	Thorax depth
TL	Tail length
TSEs	Transmissible spongiform encephalopathies
UL	University of Limpopo
Vet	Veterinary
vs	Versus
WH	Wither height

ABSTRACT

The study was undertaken to investigate the genetic adaptation in South African communal indigenous goat populations using the socio-economic status, phenotypic traits, Illumina SNP50K data, and conservation strategies approaches. Proper conservation strategies become important for endangered breeds/populations and those that are not properly utilized. *Ex Situ* conservation objectives include avoiding extinction, maintaining genetic diversity and incorporating the cultural and socio-economic merit of breeds/populations.

The first objective of the study was to characterize the socio-economic factors influencing indigenous goat value and production constraints in selected rural areas of South Africa. Individual interviews were conducted in 241 households using semi-structured questionnaires from four randomly selected provinces of South Africa; namely Free State (FS), Gauteng (GP), Limpopo (LP) and North West (NW) respectively. Data were analysed using Statistical Package for Social Science (SPSS 26.1 for Windows) for multifactorial analysis of variance and covariance. The major constraints to indigenous goat production were unavailability of feed (85 %) followed by low indigenous goat sales (72 %) and their value by the indigenous farmer (60 % of the households). Odds ratios for selling goats were high for the following predictors: age of the head of household, farm size, production system, mating system, external parasite control, belong to union and source of breeding bucks. To effectively address production constraints faced by indigenous goat farmers, it is therefore, fundamental to consider their socioeconomic profiles.

The second objective of the study was to determine the phenotypic diversity of South African indigenous goat population in selected rural areas. Appearance of indigenous goat phenotypes and their typical features were observed from 297 individual goats. There was a significant ($P<0.05$) difference in all phenotypic measurements, with higher ($P<0.05$) values for body length (48.23 cm), body weight (26.86 kg) and wither height (64.61cm) observed in indigenous goats of Dr. Ruth Segomotsi Mompati (DRSM) region. The indigenous goats of the Thabo Mofutsanyana region had the highest ($P<0.05$) value for rump length (17.52 cm), however, have the shortest tail length (7.17 cm) compared to those at other regions. Results from the study show considerable phenotypic heterogeneity in qualitative traits of the indigenous goat population and their distributions in different regions.

The third objective was to determine genetic diversity of South African Communal indigenous goat population using genome-wide SNP data. Communal indigenous goat populations were genotyped using the Illumina Goats SNP50 BeadChip. Analysis of molecular variance revealed variations of 3.39% ($P< 0.0001$) and 90.64% among and within populations, respectively. The first two PCAs, and revealed a unique Limpopo population separated from GP, FS and NW Communal indigenous goat populations with high levels of admixture with commercial goat populations. Population differentiation tests (PCAdapt) revealed PC2 as optimal and 5 outlier SNPs were detected on chromosomes 10, 15, 20 and 21. The study revealed that the SNPs identified by the first two principal components show high F_{ST} values in LP Communal goat population and allowed to identify candidate genes which can be used in the development of breed selection programs to improve this unique LP population and other Communal goat population of FS, GP and NW and find genetic factors contributing to the adaptation to harsh environments.

Lastly, conservation status and historical relatedness of South African indigenous goat populations using genome-wide SNP marker was determined as part of the fourth objective of the study. Across populations, the current N_e of Gauteng was the lowest at 371 animals, while the historical N_e across populations suggests that the ancestor N_e has decreased by 53.86%, 44.58%, 42.16% and 41.16% in Free State (FS), North West (NW), Limpopo (LP) and Gauteng (GP), respectively, over the last 971 generations. Genomic inbreeding levels related to ancient kinship (F_{ROH} >5Mb) was highest in FS (0.08±0.09) and lowest for Eastern Cape (EC) (0.02±0.02). The genomes of KZN and LP shared an origin but have substantial admixture from the EC and NW populations. The use of Illumina goat SNP50K BeadChip shows that there was a migration route of communal indigenous goat populations from the northern part (LP) of South Africa to the eastern areas of the KZN, that confirmed their historical relatedness and which coincide with the migration periods of the Bantu nation.

Key words: *households, production system, socioeconomic, body length, characterisation, coat colour, single nucleotide polymorphism (SNPs).*

CHAPTER 1

GENERAL INTRODUCTION

1.1 Background

Goat populations of the world comprise approximately 861 million, of which 94% are found in developing countries (FAO, 2021a). In South Africa, the goat population is estimated at between 6.6 and 6.8 million (Donkin *et al.*, 2006; Mdladla *et al*, 2016a; DALRRD, 2018). Goats in developing countries are considered one of the most important farm animal genetic resources and thus play an important socio-economic role in resource-poor farmers of Africa (Peacock *et al*., 2005; Muema *et al*., 2009). Communal indigenous goat populations in developing areas are mainly kept for ceremonial purposes as well as for investment and they are commonly kept for their meat, milk, skins as well as for controlling bush encroachment. South Africa has several indigenous goat populations with limited genetic population data, and they are associated with different geographical areas (Visser, 2016).

In a developing country like South Africa, some animals may belong to (relatively) homogenous groups distinguishable from neighbouring populations on the basis of identifiable, even though parts of the "non-descript" populations are known to be multiple crosses of recognized breeds, and stable phenotypic characteristics (among which may be unique and valuable attributes) that warrant their being distinguished as separate breeds (Visser, 2019). Levels of genetic diversity to sustain genetic improvement was sufficiently indicated by characterisation studies on these populations (Mdladla, 2017; Magoro *et al*., 2022). It is believed that some extent reasonable economic indicators are provided by various breed characteristics. Basic knowledge of genetic variations that can be effectively measured within and between populations is required for breed characterization.

Diversity erosion of farm animal genetic resources (FAnGR) has become a major concern worldwide (Hammond & Leitch, 1996; FAO, 2007a). According to the recently published State of the World's Animal Genetic Resources for Food and Agriculture (FAO, 2007b; FAO, 2015b), in the past century, approximately 10% of farm animal breeds have become extinct and an additional 15% are considered rare or endangered. Moreover, the situation is presently unknown for 34% of the breeds, most of which are reared in developing countries. Assessing the diversity of FAnGR is made more difficult by the existence of many animal populations that are not assigned to any recognized breed. The replacement and uncontrolled crossbreeding of indigenous animals with “improved” breeds may lead to the replacement of indigenous populations and the subsequent loss of their unique genetic traits.

1.2 Problem statement

Conservation of communal indigenous goat populations has long been divided into two main objectives: those which have immediate applicability plus future value and those that seek to conserve for the future (Oldenbroek, 2007). The erosion and loss of animal genetic resources (AnGR) would compromise the flexibility of future breeding measures (Berthouly-Salazar *et al*., 2012; FAO, 2015a). Goats' genetic resources are endangered and under-conserved, and it is estimated that about 33 % of the world’s goats’ breeds being endangered (FAO, 2015b). The South African experience is that the indigenous goat genes are in danger of extinction (Kotze, 2014; Mdladla, 2017; Zhang *et al*., 2021). South African communal indigenous goat populations are open to different natural selection pressures from different production and environmental conditions. The study posits that the variance of different goat populations reflects the diverse selection pressures emanating from environmental factors. These highly valuable genetic resources should be conserved for their adaptive features, traits of scientific and economic interest, cultural-historical values, strong links to regional traditions, and their ability to generate income for poor communities. This study sought to investigate the genetic adaptation in South African communal indigenous goat populations using the Illumina SNP50K data for better implementation of conservation strategies.

1.3 Rationale of the study

Characterisation of genetic resources serves as an essential prerequisite for the identification, effective management and utilization of farm animal genetic resources which facilitates their conservation. For many years, breed characterisation has accordingly been recognized as the first approach to the sustainable use of the animal genetic resource (Onzima *et al*., 2017). The essential ingredient of the programs for rational conservation and improvement is the analysis of the genetic variability of the breed or population (FAO, 2021b).

The characterisation data of the South African indigenous goats is gaining scientific research momentum because earlier studies based on morphological and biochemical markers present an insight research knowledge on their relationships. The populations are exposed to extreme climatic conditions and disease pathogens. The level of local adaptation is well defined by forces of evolution such as founder effects, genetic isolation, and drift, the different environmental factors, diseases, and disease pathogen impose diverse natural selection pressures that influence the population genetic structure and distribution of genotypes (Mdladla, 2018). Communal indigenous goat populations and other livestock species are considered to be generally highly adapted to local environmental conditions contrary to exotic breeds (Harper and Penzhorn 1999; Mdladla *et al*., 2016b; Onzima *et al*., 2017). Communal indigenous goat populations in South Africa, are known to survive and produce optimally even under harsh environmental and production conditions (Gwaze *et al*., 2009).

All the issues related to goat resource conservation need to be addressed by the available limited agricultural resources and agricultural policies. The present use of such scarce resources may lead to either economic overutilization or underutilization. As a result, penalties may become irreversible. This requires working towards introducing and attaining an accurate and full information system and building a solid database for the red-meat subsector. Analysis of effective population sizes, inbreeding levels, the effects of natural and artificial selection, as well as population bottleneck events that shaped these populations' current genetic structures will provide valuable information that can be used to manage and conserve these indigenous animal genetic resources (Khanyile, 2015).

Due to their dense distribution over the genome, great variation, codominant inheritance and easy genotyping at the DNA level, molecular markers are found to be accurate and reliable for genetic diversity studies (Koreth, 1996). Investigating the genetic diversity of indigenous communal indigenous goat populations will give insight into genetic mechanisms underlying local adaptation in goats, which is very important for guiding their breed characterisation and conservation strategies.

The genetic mechanism in adaptation is a topic of great concern in recent years and has important implications for understanding adaptation in extreme environments and hypoxia-related diseases (Qiu *et al*., 2012; Yang *et al*., 2016). Whole-genome selective scans have identified positive selection on a set of genes (e.g., *EPAS1, EPO, EGLN1, EGLN2, and EGLN3*) in the HIF-1 (hypoxia-induced factors) pathway associated with hypoxia response (Frede & Fandrey, 2013) in humans (Simonson *et al*., 2010; Wolfson *et al*., 2017) and animals (Miao *et al*., 2017; Zhang *et al*., 2017; Xu *et al*., 2016; Yang *et al*., 2016) living at the high elevations. Goat comprehensive genome coverage and allowance of finer mapping of loci under selection are made possible by the use of genome sequence data and the Illumina goat SNP50K panel. Number of studies in indigenous cattle (Makina *et al*., 2015), goats (Mdladla, 2016; Zhong *et al*., 2023) and sheep (Kim *et al*., 2016) were conducted using different analytical concepts that have provided valuable evidence on signals of selection on a genome-wide scale which can be used to simplify the investigation of adaptive genomic divergence at a genome-wide coverage. According to Mdladla (2016), genome-wide SNPs can be useful in identifying loci under selection for a breed or population that can be modelled to understand the genetic adaptation of populations.

1.4 Aim

The aim of the study was to investigate the *ex-situ* conservation strategies in South African goat populations using the socio-economic status, phenotypic traits, Illumina SNP50K data and landscape genomic approaches.

The specific objectives of the study were:

(i) To characterise the socio-economic factors influencing indigenous goat value and production constraints in selected rural areas of South Africa.

(ii) To determine the phenotypic diversity of South African indigenous goat population in selected rural areas.

(iii) To determine the genetic diversity of South African indigenous goat population using genome-wide SNP data.

(iv) To determine the conservation status and historical relatedness of South African indigenous goat populations using genome-wide SNP marker.

1.5 Hypothesis

(i) The Socio-economic factors influencing indigenous goat value and production constraints in selected rural areas of South Africa are different.

(ii) Indigenous goat populations in selected rural areas of South Africa exhibit a high degree of phenotypic diversity.

(iii) The diversity of indigenous goat populations can be determined by using genome-wide SNP marker.

(iv) Conservation status and historical relatedness of South African indigenous goat populations can be determined using genome-wide SNP marker.

CHAPTER 2

LITERATURE REVIEW

2.1 Introduction

Goats as Animal Genetic Resources (AnGR) are widely recorded as one of the first farm animals to be domesticated. Goats have been for long associated with man in a symbiotic relationship for up to 10,000 years as indicated by the archaeological evidence (Ensminger & Parker, 1986). The wild Bezoar (*Capra aegagragus*) has added to the genetic pool of the majority of today's domestic goat (*Capra hircus*) including the South African communal indigenous goat populations (Ncube, 2016; Mdladla *et al*., 2017). It has been shown that many South African communal indigenous goats are non-descript and raised in variable production systems across the country. According to Campbell (2003), the initial domestication of goats (*Capra hircus*) in Southern African countries was primarily for cultural and religious purposes. Indigenous goats are generally kept for their meat, milk, skins, controlling bush encroachment and in developing areas, mainly for ceremonial purposes as well as for investment (Donkin *et al*., 2006; Mdladla, 2016; Khowa, 2023a). According to Lebbie, 2004; Webb & Mamabolo, 2004; Bester et al., 2009; Du Toit *et al.*, 2014, South African communal indigenous goats are kept under traditional management practices in communal areas.

The low levels of inputs that farmers can provide (Mpofu, 2002), exposure to diseases and parasites, poor nutrition and harsh climatic conditions are reported to be the main challenges in communal goat production (Webb & Mamabolo 2004; Sebei *et al*., 2004b), causing low productivity due to the compromised production systems. With all those challenges, through the provision of meat, milk, generation of extra cash income and for religious and/or cultural purposes such as marriage feasts, weddings and funerals and controlling bush encroachment, communal indigenous goats play an important role in the livelihood of rural communities (Braker *et al*., 2002; Gwaze, 2009a; Donkin *et al*., 2006; Khowa, 2023b). Communal indigenous goat populations have important socio-economic roles in the livelihood strategies of poor farmers, especially those in rural and hard-to-reach areas (Dube, 2016; Manzi *et al*., 2011; Ofori, 2021).

In every agro-ecological zone that are adapted by communal indigenous goats where they are inhabit, a heterogeneous phenotypic and genotypic characteristics seems to be observed. Nevertheless, their production potential has not been fully harnessed owing to a dearth in research and development work around their use. A phenotypic description can be striking for screening adaptive genetic diversity (Toro & Caballero, 2005). In South Africa, three unimproved Veld ecotype populations has been previously described using description of the phenotypic characteristics (Morrison, 2007). Recent findings on indigenous goats using genome-wide single nucleotide polymorphism (SNP) data confirmed genetic differences and contribution of targeted Southern African goat populations to purebred commercial lines in South Africa (Visser, 2016). These differences further justify conservation efforts for these valuable genetic resources. A greater understanding of how this biodiversity evolved has been achieved, as knowledge of genetics continues to increase (Hall, 2004). The new field of research on goat genetic studies are reported to bring interesting findings as only a limited studies investigating genetic diversity, phenotype-genotype association and signatures of selection are existing (Kijas *et al*., 2013; Brito *et al*., 2015; Nicoloso *et al*., 2015; Lashmar *et al*., 2016; Mdladla *et al*., 2016a). Not any of the noted studies provided clear conservation strategies using the genome-wide single nucleotide polymorphism (SNP) data to unravel the biological relevance of the genome-wide outlier markers. In south Africa, were harsh and extreme production environments are experienced, the adaptive genetic potential of communal indigenous goats is supreme in ecosystems.

Recently, the improvements in goat genetics and other livestock species, the accessibility and continued reduced costs of high output genomic tools joint with genome scans have enabled the development of a Goat 50K BeadChip. According to Tosser-Klopp *et al*. (2014) Goat 50K BeadChip can be used to facilitate the study of genetic diversity and genomic signatures of selection at a genome-wide coverage. Other studies have shown that loci can be identified under adaptive selection for a particular breed or population that can be modelled to understand the genetic adaptation of populations using genome-wide single nucleotide polymorphisms (Mdladla, 2016; Magoro *et al*., 2022).

The surge in inbreeding (*F*) leads to different negative effects such as a reduction in genetic variance, higher frequency of homozygous genotypes for deleterious alleles with a reduction in individual performance (inbreeding depression) and lower population viability (Ouborg *et al*., 2010). In a comprehensive study on the level of inbreeding in goat breeds across the African continent using Goat 50K BeadChip that was conducted, its results reveal that more research still has to be done on the indigenous goats (Nandolo *et al*., 2019; Kropff, 2023). The use of Goat 50K BeadChip indicated that there is a wide variation in the distribution of the number of genomic segments by age, which gives insight into the history of the breeds and further showing that the distributions of the sizes of the ROH in individuals were highly variable across breeds (Nandolo *et al*., 2019; Kropff, 2023).

The erosion and loss of animal genetic resources would compromise the flexibility of future breeding measures (Berthouly-Salazar *et al*., 2012; FAO, 2015a). Conservation of communal indigenous goat populations can be divided into two main objectives: those which have immediate applicability plus future value and those that seek to conserve for the future (Barker, 2001; Lekule & Kyvsgaard, 2003; Oldenbroek, 2007). Goats' genetic resources are endangered and under-conserved, and FAO estimated that about 33 % of the world's goats' breeds being endangered (FAO, 2015b). The South African experience is that the indigenous goat genes are in danger of extinction (Kotze, 2014; Mdladla *et al*., 2016a). These highly valuable genetic resources should be conserved for their adaptive features, traits of scientific and economic interest, cultural-historical values, strong links to regional traditions, and their ability to generate income for poor communities.

For many years, the successful breed improvement programs of the developed high-performance meat type goat breeds such as Boer, Kalahari Red and Savanna goats was made possible by the readily available material provided by communal indigenous goat populations of South Africa. Efficient utilization of the goat genetic resources in South Africa is undermined by the lack of proper breeding definition of communal indigenous goat populations which is a major threat (Hassen *et al*., 2012). There is, however, limited information on the genetic diversity of communal indigenous goat populations kept by rural communities of Southern Africa (Visser, 2016). Characterization of goat populations is important in providing information on established genetic resources and their characteristics thus serve as a guideline on conservation, development, and selection for improved productivity (Huson *et al*., 2014). This information is crucial for the planning of conservation activities and in establishing a niche market for the utilization of indigenous goat genetic resources. Therefore, the purpose of this review is to collate current information on conservation, the production system and the genetic status of communal indigenous goat populations with the view of highlighting opportunities for conservation strategies for sustainable utilization of these genetic resources using genome-wide SNP marker in South Africa.

2.2 South African Goat Genetic Resources

South Africa has several indigenous goat populations with limited genetic population data, and they are associated with different geographical areas (Visser, 2016). The population of goats in South Africa is estimated at 6.8 million (DAFF, 2014; Mdladla *et al*., 2016a; DALRRD, 2018) of which many goat breeds possess two distinct coats, a fine undercoat (down) and coarse guard hair on top (Donkin *et al*., 2006). The South African Boer goat, the Kalahari Red, the Savannah and other indigenous breeds are good examples of the available populations. In South Africa, one of the first breeds to be developed is the Boer goat and it is the most important meat-type breed that has a worldwide reputation of being distributed and utilized (DAFF, 2012). The Boer goat can be traced back to the Dutch farmers of South Africa in its early stage of development as a breed (Casey & Van Niekerk 1988). According to the Boer Goat Breed Association, the earliest breeding stock was a result of crossing between the shorthaired female goats that had white bodies and light-coloured heads with a large dapple-coloured male goat.

In South Africa, the Kalahari Red had a developmental history that is complex when compared to other commercial meat-type goats and it was developed by several breeders, with different breeding objectives. Kalahari Red goats were developed from two lines of the brown lop-eared ‘unimproved’ indigenous goats in South Africa and Namibia and of the Boer goats (Visser, 2016). According to history, back in the 1970s Mr. Voster has once collected red and red-dappled goats in South Africa and Namibia which reveals a record of Kalahari Red breed. In 1991, selection of indigenous brown, and brown and white goats from the former homelands of the Eastern Cape, the Karoo, and Namibia was also conducted by Albie Horn (http://studbook.co.za). In 1957 Messers Cilliers & Sons selected the white Savanna from indigenous goats (Visser, 2016). Savannah goat was first recognized as a distinct breed resulting in the early 1990s which resulted in the formation of the Savanna Goat Breeders Society on November 21, 1993.

In a developing country like South Africa, some animals may belong to (relatively) homogenous groups distinguishable from neighbouring populations on the basis of identifiable and stable phenotypic characteristics (among which may be unique and valuable attributes) that warrant their being distinguished as separate breeds even though parts of the “non-descript” populations are known to be multiple crosses of recognized goat breeds (Morrison, 2007). In about 2500 BC, indigenous goats migrated to Southern Africa (Epstein, 1971; Maree & Plug, 1993) with the local Khoikhoi nomads who moving southwards from Northern Botswana down to the Orange River. Ehret, (1982); Elphick, (1985) reported that at later years the local Khoikhoi nomads followed two additional routes to reach the Southern and Western Cape. In South Africa there are three ecotypes that have been historically defined which include the Nguni, Eastern Cape Xhosa, and Northern Cape Speckled (Morrison, 2007). According to Morrison, (2007) in South Africa, Nguni ecotype was reported to be more in numbers than the other ecotypes appearing in the high rainfall areas of the provinces of Eastern Cape, KwaZulu-Natal, Limpopo, Mpumalanga. From the Eastern province, a Xhosa type was discovered (Roets, 2004; Morrison, 2007) and in Northern Cape province a ‘speckled’ type has originated (Kotze, 2004; Morrison, 2007). All over South Africa, the different ecotypes are kept by breeders and form the majority of the goat populations in the communal areas (Anteneh *et al*., 2004; Bester *et al*., 2009).

2.3 Historical value of Indigenous Goat Genetic Resources

Bester (2009) provided historical records indicating that the initial domestication of goats in Southern African countries was primarily for cultural and religious purposes. Communal indigenous goats constitute a valuable genetic resource for low input village households. Indigenous goats have important socio-economic roles in the livelihood strategies of the poor farmers, especially those in rural and hard-to-reach areas (FAO, 2021a; Dube, 2016). Communal indigenous goat production is described by low input, small flock sizes, poor nutrition, and high levels of diseases and parasite infections as well as low productivity (Van Niekerk & Pimentel, 2004; Bester *et al*., 2009; Gwaze *et al*., 2009b, 2009c). Output of communal indigenous goats in terms of weight gain and kidding per year are very low with high mortality rates even though the production system is sustainable for the resource-poor rural households.

In many parts of Southern Africa, indigenous goats have roles in traditional ceremonies such as marriage feasts, weddings and funerals (Manzi *et al*., 2011; Du Toit *et al*., 2014). The slaughtering of a goat is often a way of welcoming high-status visitors or honouring affine and kin. Goats are also frequently sacrificed, and in some cultures, the intestines of slaughtered goats are consulted as oracles. Indigenous goats are used to strengthen relationships with in-laws and to maintain family contacts by entrusting them to other family members (Dube, 2016) and they are used as a token of appreciation for service rendered (Bozgo, 2012). For these reasons, Du Toit *et al*. (2014) noted that goats are not simply animals, they are a human creation, a social and cultural practice. Indigenous goats hides are used to make special clothes such as skirts and hats as well as mats for traditional healers for their day-to-day use and for spirit mediums to wear during traditional ceremonies (Webb & Mamabolo, 2004; Visser *et al*., 2016; Monau *et al*., 2017).

The role of indigenous goats is recorded as a potential tool to escape extreme poverty and has frequently been claimed (Nsoso *et al*., 2004; Dossa *et al*., 2007). Their outputs, such as meat and milk serve as a good source of protein for both rural and semi-urban people of South Africa (Dube, 2015; Thobile *et al*., 2021) and serve as a good source of income (Pieters *et al*., 2009). Similar trends have been reported in Botswana, where 95 % of the goats consumed in rural and peri-urban areas come from the indigenous goat sector (Nsoso *et al*., 2004). In Zimbabwe, some household's protein supply in rural areas arises from the consumption of indigenous goat (Gwaze, 2009a). (Gwaze, 2009a). Their products are preferred by the majority of smallholder farmers because of their leanness, taste and suitability for special dishes (Du Toit *et al*., 2014). Communal indigenous goat populations can also be sold or bartered to meet family needs such as medicines, medical costs, school fees and village taxes. In this way, they act as a ready source of cash for maintaining rural livelihoods, meeting emergencies and purchasing small household requirements. Indigenous goats provide manure for vegetable gardens and perform valuable sanitary functions by consuming goat dung and controlling insect pests in gardens (Monau *et al*., 2017; Kraai, 2022).

2.3.1 Goat genetic resources populations

The Convention on Biological Diversity’s Aichi Target13 is reflected in the Target for Strategic Priority Area 4 of the Global Plan of Action (GPA) for Animal Genetic Resources (AnGR) and it recommends that: “strategies have been developed and implemented for minimizing genetic erosion and safeguarding genetic diversity” (FAO, 2007b). National Coordinators for the Management of Animal Genetic Resources (172 countries had nominated a National Coordinator as of July 2014) into the Domestic Animal Diversity Information System (DAD-IS) are responsible to AnGR enter data which are indicators that contribute to the measurement of progress toward Aichi Target13 FAO (2012) and are calculated at national, regional and global levels.

Domestic Animal Diversity Information System (DAD-IS) lists 4 956 extant mammalian breeds and 1 970 extant avian breeds. Almost none have been sampled at levels consistent with FAO (2012) guidelines for in-vitro sampling and few of these are well represented in in-vitro collections. There are currently 15 South African goat genetic resources listed on the DAD-IS of FAO and 13 on the Domestic Animal Genetic Resources Information System (DAGRIS) of the International Livestock Research Institute, including those listed in DAD-IS. The list includes the commercial and indigenous goat breeds. Information data of indigenous goats of South Africa is not of good quality for researchers to use it. South Africa and other developing countries face a number of challenges such as lack of accurate number of communal indigenous goats that contribute to poor information on goat production sector and goat production system (Mdladla, 2016). That makes it one of the main challenges when distributing goat populations to breeds and when evaluating the information available for the different breeds (Visser, 2011; Mellor, 2017). Furthermore, the identification system in South Africa does not reflect the genetic differentiation within and between breeds and doesn’t accommodate communal indigenous goat populations that are originate outside the specific locations.

The Animal Improvement Act of South Africa (Act No 62 of 1998) recognizes two groups of goat genetic resources in South Africa as being landrace and exotic breeds. The ‘landrace’ breed group indicates a specified breed or a kind of animal indigenous to or developed in, the Republic of South Africa. In order to build a better understanding of the goat diversity in South Africa and in most of developing countries ad initiatives to compile databases all breeds are important. For many years the Agricultural Research Council has taken up the activity of FAnGR inventories through a network approach by involving species-specific research institutes. According to Simela &

Merkel, (2008) most of initiatives have been ineffective due to the paucity of information available and lack of continuity in documenting more breeds and updating with new information.

There are many non-descript populations that need to be identified, described, characterised, evaluated, geographically positioned and documented (FAO, 2015a). In South Africa, the limited information databases of goat genetic resources are indicated by the shortage of information on these resources, because more diversity that exists in the communal indigenous goat populations remains unknown and undocumented. Official sources of goat statistics are in most of the time inaccurate and questionable and they always they differ. Bester *et al*. (2009) have reported that national surveys are based on questionnaires administered at the household level and do not account for all production systems. Furthermore, due to informal exports and the exchange of animals between communal farmers and household slaughtering the number of goat populations in communal areas sems to not been accurate (Thobile *et al*., 2021). There is a need for approved and supplementary national goat surveys to regulate the state of national goat genetic resources. This can be done by following the universal and standardized protocols to characterize the phenotypic diversity of populations available (FAO, 2012).

2.4 Characteristics of the communal goat production system

In South African there are two main goat production systems which exist, and they are commercial and smallholder or communal farming goats (Benhin, 2006; Selolo *et al*., 2015). Communal farms are predominantly for subsistence and commercial farm is based on large scale farming of goats. In South Africa smallholder communal production accounts for more than 60 % of the total goat inventory (Du Toit *et al*., 2014). Indigenous goat production at villages accounts for more than 60% of the total goat population in South Africa and is an incorporated component of most rural households in communal areas (Shabalala & Mosima, 2002; Du Toit, 2014). The highest proportion of the country's smallholder farmers come from KwaZulu-Natal, Eastern Cape and Limpopo provinces, whilst commercial farmers are mainly in the Northern Cape (DAFF, 2012). Management systems and production in communal farming system differ significantly with those of commercial systems.

In the developing sector of the South African livestock, there is approximately 67% of smallholder farmers coming from a total number 1.3 million and they are not regarded as emerging commercial operations (DAFF, 2017b; Mapiye *et al*., 2018). The majority of herds and flocks that are kept by smallholder farmers are non-descript, crossbred or indigenous cattle, sheep and goats and the herd sizes have been reported to be less than five animals (Mthi *et al*., 2017; Nyamushamba *et al*., 2017). Various studies conducted in the smallholder communal areas showed average flock sizes of between 1 and 120 goats (Webb & Mamabolo, 2004; Dube, 2015). Furthermore, about 70% of the goats are kept under traditional management systems where the farm structure comprises of about twenty (±20) indigenous goats (Monau *et al*., 2020; Zhong *et al*., 2023).

Indigenous goats have variable genetic characteristics that enable them to strive in low input systems utilised by most smallholder farming communities, and they are predominant in the marginalized farming areas (Van Marle-Köster, 2018). Goats for slaughter are mostly marketed directly off the veld through informal trade (Visser, 2018; Khowa, 2023b). Indigenous goats in Southern Africa are generally owned by individual households and are maintained under a communal production system with few or no inputs for housing, feeding and health care (Gwaze, 2009b). In South Africa, there exists a dichotomy in the goat production systems, namely communal and commercial goat production systems. This dichotomy is also noted in the aims for farming, whereby the majority of farmers in the communal system keep livestock for a number of purposes, e.g. milk, meat, and ceremonial slaughtering (Duvel & Afful, 1994).

Most studies target commercial flocks or village communities of smaller geographical extent that contributed to a is limited information on village goat production in South Africa (Mdladla, 2017). in the context of other livestock species, the knowledge of goat farming systems is essential for identifying factors to improve selection programs. The breeds of goats that are kept the farmers is dictated by the production system and defines reasonable strategies for genetic improvement. This is in comparison with the aims of the commercial farmers which are to achieve faster growth, less mortality, high turnover which all translate into higher profits.

The ability of indigenous goats to adapt to harsh environmental conditions of heat and humidity, their ability to use limited forage and resistance to endemic diseases has been noted as their most distinguishable trait (Casey & Van Niekerk, 1988; Donkin et al., 1992; Barry & Godke, 2001; Morand-Fehr et al., 2004; Kunene & Fossey, 2006). (Casey & Van Niekerk, 1988; Donkin, 1992; Barry & Godke, 2001; Morand-Fehr *et al*., 2004; Kunene & Fossey, 2006). Genetic improvement of the commercial farming sector is adequately advanced as compared to the communal indigenous goats and the genetic improvement these communal indigenous goats is considered exceptionally rare or non-existence. The goat production systems for smallholder farmers are receiving enough research attention to improve it. The paucity of information on traits of economic importance such as milk and meat yield and failure to account for the challenges posed by the production system and environmental constraints has led to the limitation of goat genetic improvement programs (Mdadla, 2016).

2.4.1 Constraints to the indigenous goat production system

In many communal production systems, the quality and quantity of forage tend to vary with the harsh environmental conditions that sometimes prevail, leading to nutritional inadequacies (Fresco, 1992; Sangaré & Pandey, 2000; Alexandre & Mandonnet, 2005). Marketing of meat animals by commercial farmers is mostly through a well-organised system with capital resources, infrastructure, institutions, legal frameworks and markets (Roets & Kistern, 2005; Van Rooyen & Homann, 2008). The increasing numbers of goats in this region indicate that their relative importance has not diminished over time and that they still contribute significantly to the world population (Visser, 2019). In the communal goat production systems, the major challenge in the marketing of goats is the unavailability of the formal markets and where available, farmers are not provided with adequate information on prices and market requirements (Roets & Kistern, 2005; Simela & Merkel, 2008). Productivity from goats in the communal farming system, which is based on the extensive system, is said to be poor with a low weaning rate, high mortality rate and low turnover (Bembridge & Tapson, 1993).

Considering the formidable combination of malnutrition, environmental stress, long-term and often massive larval challenge in many communal production systems, indigenous goats are expected to be inherently resistant to haemonchosis and other gastrointestinal infections (Waller & Thamsborg, 2004). It is difficult to associate the high mortality with a single factor, as it is a combination of several factors (Dossa, 2007). The main causes of mortality in goats in order of importance are diseases (scabies, lung infections, abortions and heartwater), predation (Jackals, lynx, snakes and wild dogs), hostile environment and lack of technical support (Hailu, 2006).

Farmers and livestock keepers conduct some sort of selection on phenotypic traits inn order to meet the socio-cultural and religious preferences. This type of selective breeding practice has not been used for production, but the focus was on maintaining and increasing the frequencies of the phenotype(s) for the preferred phenotypic traits. Specific coat colours may have been considered as a preferred trait of choice by smallholder farmers (Manton, 2005; Gwaze *et al*., 2009a) and body frame (Gwaze *et al*., 2009a; Marume *et al*., 2013), which they then apply in their selection for breeding animals. There is no institutional capacity to record and measure the selection pressure applied and monitor the response realized which shows that the selection is unorganized.

2.5 Diversity in Southern African indigenous goat genetic resources

Goat biological diversity involves both phenotypic as well as genotypic variation (Visser, 2004). Biodiversity can be defined at several levels, from phenotypic observations to molecular data. The improvement of domestic animals, including goat, is dependent on variations within and between breeds to meet human needs (Kosgey, 2007). Such variation gives room and opportunity for breeding and selection with regards to among individuals or groups of goats. According to FAO, there are only about 28 breeds recognized in the region (Caballero, 2002; FAO, 2015a). The vast majority of indigenous goats are referred to as the village goat population, a reservoir of genetic diversity that has not been characterized (Morrison, 2007; Lashmar *et al*., 2016; Zhang *et al*., 2024).

Goats are important resources available for endogenous rural development, especially in marginal areas and under a climatic change scenario, but they may be threatened by crossbreeding with and/or replacement by commercial transboundary breeds (Boettcher, 2014; Ginja *et al*., 2017). There are limited characterisation studies on the phenotypic characteristics of South African goats, with a bias towards established commercial breeds (Pieters, 2007). An understanding of the indigenous goat genetic resources is lacking, and there is no comprehensive list of the breeds or goat ecotypes existing in the different goat farming regions.

2.5.1 Phenotypic diversity

The process of identifying distinct breed populations and describing their external and production characteristics in a given environment and under given management is known as phenotypic characterisation of AnGR, it takes into account the social and economic factors (Kunene, 2006). A broad description of indigenous livestock has depended on the phenotypic characteristics and is among the first to be used to determine the relationship between breeds (Yakubu, 2010; FAO, 2011b; Mdladla, 2017). Linear traits (qualitative traits) have been widely used for phenotypic characterisation of FAnGR in Southern Africa (Kotze, 2014). Characterisation of indigenous livestock species is the key to the development of proper strategies for long-term maintenance and use of genetic variation, and for guidance in decisions about future utilization and conservation strategies (Msanga *et al*., 2012). In southern Africa, studies have been conducted to characterise indigenous goats including Mozambican goats (Garrine, 2007), Tanzanian goats (Madubi *et al*., 2000; Nguluma *et al*., 2018), South African goats (Pieters *et al*., 2009; Mdladla, 2016) and Namibian goats (Els *et al*., 2004).

The phenotypic characterisation studies on indigenous goats were undertaken in other parts of the country leaving other regions due to low finances allocated for research on these resources (Pieters *et al*., 2009; Belay, 2017; Madladla, 2017), and may not reflect the current situation, because of changes in population, study site and in production systems (Sölkner *et al*., 1998). In most Southern African countries, communal indigenous goat populations are not adequately characterised to understand the existing diversity that could be of use for decision-making on the development of rational conservation and utilisation strategies. As the first step in breed conservation and assessment for future breeding strategies, it is necessary to create an inventory of communal indigenous goat populations varieties and their characteristics (Selolo *et al*., 2015; Visser, 2016).

2.5.2 Genetic diversity

Genetic diversity within a given farm animal species refers to the variety of genetic variation evolved during domestication and is displayed by the existence of structural variation among genomes of individuals, families, strains and populations (Kotze, 2004; ARC, 2006). Domestication events, relationships among breeds, within-breed genetic diversity and breed structure which are essential for proper breed utilization and establishment of conservation priorities are brought to light by the process of genetic diversity analyses (Toro *et al*., 2009). Molecular genetic studies using DNA information are the central sources of data on genetic relationships among varieties of breeds and strains (Rege & Gibson, 2003). Molecular biology provides tools for the study of within and between-population genetic diversity. As with other livestock species, short tandem repeats (i.e. microsatellites) have thus far been the markers of choice for genetic diversity studies (Groeneveld *et al*., 2010; Lenstra *et al*., 2012; Muema *et al*., 2012; Mekuriaw *et al*., 2012). Several results concerning the survey of goat genetic diversity based on microsatellites have been published, including those surveying breeds from Asia (Li *et al*., 2002; Fatima *et al*., 2008; Ağaoağlu & Ertuğrul, 2012; Sulabda *et al*., 2012), Europe (Iamartino *et al*., 2005; Serrano *et al*., 2009; Bruno-de-Sousa *et al*., 2011; Martinez *et al*., 2015) and Africa (Traoré *et al*., 2009; Missohou *et al*., 2011), and also breeds from Latin American countries such as Brazil (Menezes *et al*., 2006), Colombia (Calvo *et al*., 2012) and Cuba (Chacón *et al*., 2012).

Microsatellites have been widely accepted as useful tools for measuring genetic diversity and divergence within and among populations (FAO, 2011). Their abundance, high level of repeat-number polymorphism, manifested as the occurrence of a large number of alleles per locus, and co-dominant inheritance has facilitated their extensive use in genome mapping, phylogenetic inference and population genetics in farm animals (FAO, 2011). The previous effort to characterize indigenous goats of South Africa at genetic level was done at a research station, using 12 microsatellite markers on a very small population that was under selection (Pieters *et al*., 2009). This population did not represent the variation that occurs in the country and failed to show the inherent genetic variation of the indigenous goat population.

Although the advantages of microsatellites have been well documented as recorded by Singh *et al*. (2014), genome-wide single nucleotide polymorphism (SNP) markers provide new possibilities for genetic characterisation and biodiversity studies (Blasco & Toro, 2014; Toro, 2014). In Africa a powerful tool called Genome-wide SNP genotyping technology for population genetic studies in a variety of indigenous livestock species has emerged (Mbole-Kariuki *et al*., 2014; Khanyile *et al*., 2015; Makina *et al*., 2015). Several SNP assays have been used in the analyses of population diversity and structure of many livestock species (Lin *et al*., 2010; Kanyile *et al*., 2015; Makina *et al*., 2015; Lashmar *et al*., 2016; Mdladla *et al*., 2016a). The commercial Goat50K SNP panel, which was developed in 2012 offers an opportunity for the genetic characterisation of goats. The advent of the 2.66Gb reference goat genome sequenced from a female Yunnan black goat made the frequent use of this technology in goats to become possible (Dong *et al*., 2013) and the accessibility of the first genome-wide Goat SNP52K (containing >50,000 probes) genotyping array (Tosser-Klopp *et al*., 2014).

Kijas *et al*. (2013) reported for the first time the use of the array and differentiated goat populations into breeds providing more evidence for breeds' histories and further identified 10 SNPs on chromosome 1 that were strongly associated with polledness in Boer and Rangeland goats. In Italy, genetic diversity and population structure of goats was conducted using genome-wide Goat SNP52K (containing >50,000 probes) genotyping array (Nicoloso *et al*., 2015). The goat populations were clearly differentiated according to their historical origins and represented the genetic distinctiveness of the Tankwa breed from the domesticated breeds in a study on the commercial, non-descript village and feral goat populations of South Africa using the SNP50 panel (Mdladla *et al*., 2016a; Kropff, 2023). The breed distribution that was reported by Morrison. (2007) is supported by the clustering of the village goat populations. Further investigation of conservation strategies using the genome-wide Goat SNP52K (containing >50,000 probes) genotyping array to discover the adaptive potential of the communal indigenous goat populations must be supported to differentiate these goat populations.

There are several methods of estimating inbreeding from high throughput genomic markers include which include estimation based on runs of homozygosity (ROH) (F_{ROH}), as stated by McQuillan *et al*. (2008), excess homozygosity (Purcell *et al*., 2007), the variance of additive genotypes (VanRaden, 2008), and a maximum likelihood method that takes marker dependencies into account (Leutenegger *et al*., 2003). An approximate measure of inbreeding is the proportion of an individual's genome in ROH runs (Curik *et al*., 2014; Belay *et al*., 2024), and it has been demonstrated that ROH inbreeding coefficients (F_{ROH}) are closer to true inbreeding than pedigree inbreeding coefficient estimates (Keller *et al*., 2011). To date, the most popular of these approaches is the use of ROH, which are continuous stretches of homozygous loci in the genome (Purfield *et al*., 2012). However, if many markers are used (above 10,000), genomic inbreeding estimates can be more powerful in detecting variability and the effects of inbreeding (Wang, 2016).

2.6 Conservation of indigenous goat genetic resources

Animal genetic resources management encompasses all technical, policy, and logistical operations involved in understanding (characterisation), using and developing (utilization), maintaining (conservation), accessing, and sharing the benefits of animal genetic resources" (FAO, 2011a). In animal genetic resources conservation, decision-making regarding breed prioritization should be based on the simultaneous analysis of several different criteria (genetic and demographic characteristics, environmental conditions, the role of the breed in the local or regional economy, etc.) that may contribute to long-term sustainable breeding conditions. There are several challenges associated with the conservation of farm animal genetic resources (Mendelsohn, 2003; Magoro, 2022). A conservation strategy must have clear objectives that are understandable by all stakeholders who will be the drivers for its implementation and eventual success. There are many conservation objectives that can be adapted to meet local conditions. This includes (i) those which have immediate applicability plus future value and those that seek to conserve for the future; (ii) wise use of AnGR is possible without depleting domestic animal diversity; (iii) AnGR with high levels of adaptive fitness to the environment concerned should be used, and sound genetic principles deployed (Barker, 2001; Lekule & Kyvsgaard, 2003; Kosgey, 2007; Oldenbroek, 2007). The erosion and loss of animal genetic resources would compromise the flexibility of future breeding measures (FAO, 2007a). The domestic goat is one of the most important livestock species in animal husbandry that has shown a need to be conserved (FAO, 2015a).

To investigate animal genotypes that are best suited for the production system combined genetic markers that are associated with climate and ecologically important factors Conservation strategies using genome-wide SNP arrays will facilitate an analysis that. Management practices such as husbandry, flock size and the identification of the major production constraints requires a good understanding. In improvement programs that target specific production environment is important for the establishment of traits under selection.

2.7 National initiatives and government policies on the conservation of indigenous goats

A successful animal genetic resources conservation needs to include attention to biological, production, and cultural aspects that affect these populations. All three aspects must be considered if success is to be achieved in adequately conserving genetic resources of domesticated animals, and failure in any one dimension often leads to overall failure. Animal genetic resources conservation has gained importance over the last few decades due to increased recognition that the biodiversity housed in domesticated animals is key to maintaining overall biodiversity. Most indigenous AnGR exists in areas that are geographically remote or are culturally or economically marginalized (Sponenberg, 2016). This setting brings with it challenges in effective conservation. Landrace conservation depends on a process that can be broken down into the categories of Discover, Secure, and Sustain (FAO, 2013; Sponenberg, 2018). Success depends on all three, working together, and failure is assured by failure in any one of the three.

There are several threats to the production of indigenous goat populations in Southern Africa. These include the replacement of local indigenous goat populations with improved and exotic goat breeds (Kotze, 2014). Other Southern Africa countries, except South Africa, do not have coherent policies on conservation indigenous goat population and incentive systems for the farmers that will be involved in those programmes. Some policies take no notice of conservation of indigenous goat populations and undermine traditional production systems, while public agricultural institutions focus research and extension services on a narrow base that excludes local breeds (Halewood & Mugabe, 2002).

DAD-IS lists 4 956 extant mammalian breeds and 1 970 extant avian breeds (FAO, 2000). Few of these are well represented in *in vitro* collections and almost none have been sampled at levels consistent with FAO. (2015b) guidelines for in vitro sampling. The Global Data bank for Animal Genetic Resources, the backbone of DAD-IS, enables National Coordinators to enter breed-specific data, including data on the size and structure of breed populations, required to calculate their risk status. FAO produces biannual Status and Trends Reports (FAO, 2015a). A good and complete inventory of animals and their sources is needed in order to organize breeding and maintenance to avoid erosive losses. For the first report on The State of the Worlds Animal Genetic Resources, a risk status classification based on population size Data was used. The (lack of) availability of global data currently Makes a more elaborate system involving, for example, molecular Diversity indices, population structure/fragmentation, pedigree data, number and size of herds, and geographic distribution in operable.

South African has 15 goat genetic resources is listed on the Domestic Animal Diversity Information System (DAD-IS & FAO) of FAO (http://dad.fao.org; Accessed October 2018) and on the Domestic Animal Genetic Resources Information System (DAGRIS) of the International Livestock Research Institute (ILRI; http://dagris.ilri.cgiar.org; Accessed March 2019) is has 13 and this include those that are listed in DAD-IS. Only indigenous goats that have no improvement initiated were included and those goat breeds that were developed for a specific use that are included from the list. In South Africa, there is no recording that is performed in the smallholder or communal goat sector (Visser, 2018) which is alarming considering that approximately 60% of goats are kept in these systems and they make a significant contribution to household food security. For heterosis and complementarity of traits, local indigenous goats are crossbred with imported breeds which are also used as pure breeds. The ‘exotic’ breeds which comprise predominantly of the dairy and mohair type breeds have been imported from other countries into the Republic of South Africa. South African goats are classified into five groups by descriptors for goats in the Animal Genetic Resources data bank (Morrison, 2007).

Since the inception of national animal recording schemes for dairy, beef and small stock in the early nineteen fifties, genetic evaluations for most of these species are routinely performed and stud breeders have access to estimated breeding values (EBVs) as a selection tool. South Africa has more than 30 registered beef breeds with large variations among breed societies with regard to participation in recording schemes (Van Marle-Koster *et al*., 2013). The national small stock recording was established in 1956 (Schoeman *et al*., 2010) with participation by sheep breeders. The number of traits recorded varies among the breeds with a larger number of phenotypes available for growth traits, compared to limited numbers for fertility traits which contribute to the conservation of FAnGR.

Animal recording by the small-holder and communal farmers is limited to the Kaonafatso ya Dikgomo (KyD) scheme where technical advice on health, production and support with a recording of animal information is provided. This scheme makes provision for weight recordings at birth, weaning, 12 and 18 months (ARC, 2006). The commercial small stock sector consists of 14 sheep breeds, 3 commercial meat goat breeds and the SA Angora goat breed. Participation in animal recording in this small stock sector is limited to a small number of commercial producers, for which genetic analyses are performed. No recording is performed in the smallholder or communal goat sector (Visser, 2018) which is alarming considering that approximately 60% of goats are kept in these systems and they make a significant contribution to household food security. It has also been reported in other studies that there is no genetic improvement in terms of strategic selection or EBV estimation is performed, and genomic applications have been limited to studies on genetic diversity (Mohlatlole *et al*., 2015; Mdladla *et al*., 2016). A dedicated study that covers all the components of conservation strategies for indigenous goats will add value on the importance of these scares' resources.

Interestingly, the African Union developed a Model Law to provide a legal framework for the conservation, evaluation and sustainable use of biological resources, and associated technologies and knowledge but no country had adopted it as of 2007 (FAO, 2007a). Recently, the African Union – Interafrican Bureau for Animal Resources (AU-IBAR) informed the African Member States including South Africa that in the framework on the implementation of the Genetics Project "*Strengthening the capacity of African Countries to Conservation and Sustainable Utilization of African Animal Genetic Resources"* AU-IBAR offered support to South Africa to develop its NSAP for FAnGR as part of the implementation of the Global Plan of Action (GPA) adopted in 2007 in Interlaken, Switzerland.

While genomic methods might help to overcome these data deficiencies, if they are to be applied to livestock conservation, it is important to define the goals of such approaches and how the data could be used to improve or augment the current set of indicators using data that could be collected on trends in effective population size, admixture, inbreeding and genome-wide diversity. The wider application of such data hinges on their applicability to autochthonous, less- commercial breeds. Unfortunately, the data currently provided to FAO does not even allow the reliable calculation of basic trends currently measured via the above indicators (Tittensor *et al*., 2014; FAO, 2015a), yet the livestock genetics and conservation. The available Illumina goat SNP50K panel was used on a number of South African goat populations for genotyping (Lashmar *et al*., 2015; Lashmar *et al*., 2016; Mdladla *et al*., 2016a). The Tankwa feral goat and other goat populations has created more research work on characterization that involve genome sequences (Mohlatlole *et al*., 2015). Two key developments are required to enable the current approach to more directly use genetic or genomic data in the future: first, the livestock conservation genetics community must, therefore, insist that data are collected and analysed in such a way that results are directly comparable and second, to help develop better indicators applied to monitor the genetic trends in domestic populations.

Cardellino & Boyazoglu. (2009) identified that there remains a major need to provide much better links between the major FAnGR databases, which have largely been set up independently and are breed-focused (Groeneveld *et al*., 2010). For other data types, open digital repositories such as Dryad, Zenodo comprise invaluable tools acting as incentives for people to maintain and upgrade their datasets as data can be submitted and authors are provided with a reference which can be cited. This data ecosystem becomes especially important with the myriad of SNP array datasets that are now available and the incompatibility among different versions of these arrays within the same species (Nicolazzi *et al*., 2015). Moreover, to add value to genetic resources, federating gene bank resources is one step That needs to be completed by explicit connection—through Geographical coordinates—with phenotypic data, but also with socio-economic, socio-demographic, climatic, environmental, and policy information. This requires links to existing online digital resources Joost *et al*. (2010) that are currently rarely used by the FAnGR community and need to be listed on such a global portal.

South Africa has a functioning legal framework, and clear policies and programmes, that are prerequisites for effective management of AnGR. The country has its own legislature, the Animal Improvement Act (Act No. 62 of 1998) which notes landrace and exotic breeds as the two groups of goat genetic resources in South Africa. The ‘landrace’ breed described by the Animal Improvement Act as a specified breed or a kind of animal indigenous to, or developed in, the Republic. Clear legislation, and the security which it provides, is important both for economic activities such as international and domestic trade and for the definition of the competences, rights and duties of the stakeholders involved in AnGR management (FAO, 2015). The public sector is largely absent from the animal genetic resource conservation landscape, leaving all activities to commercial players whose main aim is profit (FAO, 2007a).

Strategic approaches for conservation, managing, and utilisation of goat genetic resources at the national levels suited to different needs must be established and implemented in developing countries of Southern Africa. The AU-IBAR requested South Africa to initiate the process of formulating the National Strategies and Action Plan (NSAP) for AnGR and indicated that the various stages of the formulation can include stakeholder consultative meeting, drafting of NSAP and stakeholder validation workshop. The Department of Agriculture, land Reform and Rural Development of South Africa together with members of the National Advisory Committee/ National Working Group for FAnGR and relevant stakeholders developed draft National Strategy and Action Plan (NSAP) document for FAnGR. The NSAP for FAnGR will cover a period of 5 years and will enable the department and relevant stakeholders to jointly implement actions needed. The objectives of the National Strategy and Action Plan for conservation and sustainable use of FAnGR are to (i) To characterize FAnGR for sustainable production systems, (ii) Promote South African participation in conservation and sustainable use of FAnGR at Southern African Development Committee (SADC), African Union (AU), and international level, (iii) Establish sustainable in situ and ex situ conservation of FAnGR in scientifically sound and cost-effective breeding programmes, (iv) Support actions and initiatives concerning the conservation of FAnGR by various stakeholders, (v) Ensure that conservation of FAnGR is in harmony with the sustainable use of natural resources in response to climate change.

2.8 Prioritising populations for conservation

Setting priorities for AnGR conservation requires a process that enables the identification of breeds that contribute most to global genetic diversity and have the greatest potential to contribute to efficient future utilization and further development of that diversity. Additional criteria, such as cultural or heritage values of a breed, will also affect priorities for conservation. Informed decisions need to be taken when prioritising a particular population for conservation based on an inventory of the definite breeds carried out on a global scale through the World Watch List (FAO, 2000) which include the specific population genetic diversity and their characteristics. Weitzman's. (1992) diversity concept is widely used as a formal approach to rational decision–making in livestock conservation. Weitzman's theory was applied in studies on various farm animal species, such as cattle (Thaon d'Arnoldi *et al.*, 1998; Reist-Marti *et al.*, 2003, Simianer *et al.*, 2003; Zander *et al.*, 2013). This approach suggests that the conservation potential is the single most informative criterion to rank breeds with respect to conservation priority.

Prioritization methods are not being applied by managers and policy- makers, and a number of explanations may pertain: first, the method(s) may have not gained enough traction with policy makers to ensure its/their implementation, which may indeed be because genomic methods, which have yet to be systematically implemented, will largely supersede the microsatellite-based approaches implemented thus far and enable conservation prioritization to include genes important in functionally valuable traits (Toro *et al*., 2014). Furthermore, prioritization on the basis of genetic distances (Weitzman,1992) is confounded by genetic isolation of breeds (European Cattle Genetic Diversity Consortium, 2006). Prioritization may not actually be needed, at least in certain regions, where breed societies are active and all or most of the breeds can be maintained. However, recent animal health emergencies (e.g., outbreaks of transmissible spongiform encephalopathies, TSEs) have cast doubt on this simplistic scenario and required the application of careful genetic management during and after the outbreak. While prioritization may be less of a priority in the world's richest regions, it is not expected to be the case in developing countries, where extinction may take a number of forms, including genetic erosion (Berthouly-Salazar *et al*., 2012; FAO, 2015a, b). The methods developed may not have been applied because policy makers and managers are Unaware of their availability, which could be due to a lack of dissemination or penetrance of educational material to the decision makers (Brudford *et al*., 2015).

The conservation potential of a breed basically reflects the amount of expected diversity that can be conserved if a breed is made completely safe. Ndumu *et al*. (2008) further suggested combining the expected diversity with other criteria resulting in the expected total utility as a maximization criterion. The suggested criteria may encompass the presence of special genetic traits such as disease tolerance, production and cultural or environmental values of breeds, inter alia. The approach combines genetic diversity assessed at the molecular level and extinction probabilities estimated by socio-economic factors to derive conservation priorities of breeds based on their conservation potential. Using conservation potentials for prioritizing breeds is highly efficient in the selection of breeds for conservation when the objective of the conservation plan is to maximize the genetic diversity conserved (Reist-Marti *et al*., 2003; Simianer *et al*., 2003; Tada, 2013; Zhong *et al*., 2023). The use of genomic data to manage FAnGR within breeds is, however, continuing a pace and can be demonstrated to be assisting conservation, production and management (Herrero-Medrano *et al*., 2014; Scraggs *et al*., 2014). However, for many breeds, the cost of genetic/genomic analysis vs. the potential economic returns on genotyped stock (with a few exceptions such as TSE resistance) makes its application uneconomic, and therefore it is often not applied. It is unlikely that genotyping costs will reach the level of economic viability for many FAnGR, however, this assumption should be tested by some targeted research across the sector. Individual genotypes, therefore, need to be identified once the aforementioned decisions are made to become part of the conservation scheme, where desirable genetic properties of the sample should: (i) represent the genetic portfolio of the population or breed, (ii) have a maximum effective population size and (iii) conserved special genetic traits.

2.9 Cost implications of conservation

Every sound conservation effort bears a cost that differs with a perspective on the particular population or breed, countries, regions and production environments (Gandini & Oldenbroek, 2007). Although the conservation potential is considered as a good indicator for conservation decisions, it does not give information on how to allocate the conservation budget to maximize conserved diversity.

The complicated step of conservation of animal genetic resources is to sustain the population. This requires attention to the genetic structure of the population as well as to selection for production characteristics that will assure long-term use and function for the breed (FAO, 2013). Breeds that see active use and participation in the marketplace do not become endangered because it is in the financial interest of owners to keep them viable and productive (Sponenberg, 2018). One of the important processes of sustaining breeds is to develop demand for the breed and its products. Sustaining breeds also requires attention to the breed's population structure. This, when combined with selection for production characteristics and promotion of the breed and its products, works to secure the breed's place in the agricultural environment in which breeds compete with one another.

It is necessary to assign appropriate shares of the conservation budget to the different breeds once the decision is made as to which population or breeds should be sampled. While research and application of genomic tools in livestock is occurring in many commercial/transboundary breeds Scraggs *et al*. (2014), its application in less commercial populations is sporadic and the scientific basis of decisions on the management of indigenous livestock, for example in which germplasm to store, assessing the effects of upgrading or evaluating ongoing genetic management is therefore highly Variable (Brown *et al*., 2014; FAO, 2015b). This points to the reality that genetically based prioritization is unlikely to be operational in the absence of other considerations, including commercial reality and the ecosystem/production environment (Sanderson *et al*., 2013). Several methods of estimating the likely cost of conservation efforts have been described elsewhere (Zander *et al*., 2013). Firstly, the costs and effects of the different conservation schemes in terms of reduced extinction probability need to be established and well known.

The conservation costs can be sub-divided into variable costs, which depend on the number of goats cryo-conserved samples and the fixed costs, which are necessary to establish the conservation scheme inter alia. In general terms, it is always possible to identify the optimum conservation scheme for a given investment level within breed when the cost functions for different conservation schemes in the same breed are known. This is demonstrated in Reist-Marti.

(2004) where three out of four different conservation schemes were found to be preferable in at least one out of eight breeds chosen for conservation. If such a planning process is considered in conserving Southern African indigenous goats, factors such as labour–intensive ex situ conservation schemes may be cheaper than cryo–conservation in some countries where the infrastructure for cryo-conservation is not available (Reist-Marti, 2004).

2.10 Summary

Research efforts in indigenous goat should be targeted at aspects ranging from feeding, breeding, disease control and husbandry to obtain a better understanding of indigenous goat production systems in relation to other crop–livestock systems and the changes in socio–economic conditions in smallholder set–ups. Biological factors are not the only factors considered by farmers when adopting technologies to suit their local farming circumstances. Instead, socio–economic factors are also important to the farmer and, therefore, should not be ignored. Both objectively measured variables and subjectively measured variables should be studied to produce more meaningful research results.

Detailed studies of most of the issues raised above would contribute to the management of goat genetic resources and contribute towards improving farmers income and nutrition. Qualitative data can be gathered in a once-off/single visit. The reliability of such data depends on the ability of farmers to recall past events. Smallholder farmers do not usually keep farm records; more reliable data are obtained through monitoring studies and discussions with farmers. By improving existing management, it is possible to increase indigenous goat production in the smallholder sector. Benefits from genetic improvement can only accrue if existing management is improved. The conservation of goat genetic resources is essential in the light of the rapid loss of strains and breeds through dilution and breed replacement.

All varieties of domestic species and species with potential for domestication are considered to be important candidates for conservation. Indigenous goat populations with economic potential, scientific use and cultural or aesthetic interest are of particular importance but all indigenous goat which is unique and endangered should be incorporated into conservation efforts. Molecular markers are an indispensable tool to understand the genetic structures of populations. For the sampling of germplasm to create a gene bank, they are necessary but in no way sufficient to make adequate decisions. In addition to diversity information derived from molecular data, there is a need to be good, specific knowledge and understanding of breed characteristics and values, the risk status of breeds, availability and cost efficiency of possible conservation programmes, among others.

It is therefore recommended to concentrate coordinated genotyping efforts to fill in the still-existing “white spots” on the South African indigenous goat genetic resources and to re-allocate funds to develop a better understanding of the other components of a rational decision-making process. All the different aspects of indigenous goat covered in this review should be incorporated into a model together, rather than individually, to identify combinations that optimize smallholder goat production and improve smallholder household's income and nutrition. The overall goal of the study was undertaken to assess the sustainable utilization, conservation strategies and genetic diversity of South African indigenous goat genetic resources.

CHAPTER 3: STUDY ONE

INFLUENCE OF SOCIOECONOMIC FACTORS ON INDIGENOUS GOAT VALUE AND PRODUCTION CONSTRAINTS IN SELECTED RURAL AREAS OF SOUTH AFRICA

Abstract

The objective of this study was to characterise the socio-economic factors influencing indigenous goat value and production constraints in selected rural areas of South Africa. Individual interviews were conducted in 241 households using semi-structured questionnaires from four randomly selected provinces of South Africa; namely Free State (FS), Gauteng (GP), Limpopo (LP) and North West (NW) respectively. The data collection method used in the study was based on the participatory rural appraisal (PRA) and farming systems research and extension (FSR/E). Data was analysed using Statistical Package for Social Science (SPSS 26.1 for Windows) for multifactorial analysis of variance and covariance. Descriptive statistics were computed using SURVEYMEANS and SURVEYFREQ procedures Statistical Analysis Systems (SAS 9.2, 2014). The major constraints to indigenous goat production were unavailability of feed (85 %) followed by low indigenous goat sales (72 %) and their value by the indigenous farmer (60 % of the households). The logistic regression model identified production system, availability of goat housing, source of breeding bucks and belonging to a production organization as the four main predictors of value of indigenous goats. Odds ratios for the value of the indigenous goats were high for the following predictors: age of the head of household, farm size, production system, mating system, external parasite control and belong to production organization (1.03 – 1.71). Youth-headed indigenous goat farmers practicing uncontrolled mating in semi-intensive production system, controlling external parasites and belonging to producer organization had high probability of valuing the indigenous goats. Odds ratios for selling goats were high for the following predictors: age of the head of household, farm size, production system, mating system, external parasite control, belong to union and source of breeding bucks. To effectively address production constraints faced by indigenous goat farmers, it is therefore, fundamental to consider their socioeconomic profiles.

Key words: *households, breeding bucks, production system, socio-economic, youth.*

3.1 Introduction

An increased contribution to animal production from goats is justified by the presence of 94% of the 674 million total world goat population (FAO, 2021a) of the species being found in the developing countries characterized by inadequate food supply and the need for increased food security for the poor. Through provision of protein mainly from the meat, generation of extra cash income and for religious and/or cultural purposes, communal indigenous goats have played an important role in the livelihood of rural communities (Braker *et al*., 2002; Manzi et al., 2013). Indigenous goat production at villages is an incorporated component of most rural households in communal areas and accounts for more than 60% of the total goat population in South Africa (Shabalala & Mosima, 2002; Du Toit *et al*., 2014). In a total of smallholder household income, 20.20% is projected to be from livestock contribution (Kunene & Fossey, 2006). South Africa has several indigenous goat populations associated with different geographical areas and genetic data on these populations being very limited (Campbell, 2003). The population of goats in South Africa is estimated at 6.8 million of which many goat breeds possess two distinct coats, a fine undercoat (down) and coarse guard hair on top (Donkin *et al*., 2004; DAFF, 2014; Mdladla *et al*., 2016a; DALRRD, 2018).

The ability of indigenous goats to adapt to harsh environmental conditions of heat and humidity, their ability to use limited forage and resistance to endemic diseases has for long been noted as their most distinguishable trait (Casey & Van Niekerk, 1988; Donkin *et al*., 1992; Barry & Godke, 2001; Morand-Fehr *et al*., 2004; Kunene & Fossey, 2006; Khowa, 2023a). Low input village households are dependable on goats because they constitute a valuable genetic resource (Visser, 2019). The low levels of inputs that farmers can provide (Mpofu, 2002), exposure to diseases and parasites, poor nutrition and harsh climatic conditions are mainly the challenges in communal goat production (Webb & Mamabolo, 2004; Sebei *et al*., 2004b), resulting in low productivity. In the marginalized farming areas, indigenous goats are predominant and are able to strive in low input systems of most smallholder-farming that made it possible by the variable genetic characteristics.

Indigenous goats have important socio-economic roles in the livelihood strategies of the poor farmers, especially those in rural and hard-to-reach areas (Dube, 2016; Manzi *et al*., 2013). Those roles include their use as savings, insurance, security, accumulation and diversification of assets, social and cultural functions. They are also valued for their productive performance, adaptation and disease resistance. Other attributes that make them favourable to pastoral production include the small body size, therefore requiring low nutrient levels for survival. They are also suitable for subsistence farming systems because they produce meat in small readily usable quantities (Dube, 2015; Thobile *et al*., 2021*)*.

The knowledge of goat farming systems in the context of other livestock species is essential for identifying factors to improve selection programs in these areas (Visser, 2018). The production system dictates the breeds of goats that are kept and defines feasible strategies for genetic improvement. The challenges to improve their contribution include more efficient use of a bewildering number of potentially important breeds in appropriate production systems that match more efficient use of the available natural resources. The direct benefits include higher productivity, poverty alleviation, improved livelihoods, sustainable agriculture and environmental protection (Monau, 2017). However, better use of the available breeds and increased productivity are constrained by controversy, false perceptions, biases, and inadequate official support and resource use. Most studies target commercial flocks or village communities of smaller geographical extent that contributed to a is limited information on village goat production in South Africa (Mdladla, 2017). Potential productivity is also constrained by poor understanding of many valuable biological attributes and functional values of goats, and of strategies for improved natural resource management in target environments.

Goats are a very valuable genetic resource that is suited for low-input agricultural production systems. They require low inputs and are easy to manage, making them suitable for the resource poor rural households. These characteristics enable them to continue providing milk and meat even when cattle have succumbed to drought (Rege, 1994). The objective of this study was to characterise the socio-economic factors influencing indigenous goat value and production constraints in selected rural areas of South Africa. To generate information with further identification of specific constraints and opportunities in goat production that could assist in the formulation of targeted research that improves goat productivity in the provinces.

3.2 Materials and Methods

3.2.1 Study site

The study was carried out in four randomly selected provinces of South Africa; namely Free State (FS), Gauteng (GP), Limpopo (LP) and North West (NW) respectively. Limpopo and Gauteng provinces experience mild to moderate winters (9.8–20°C), hot summers (21.2–27°C) and average annual rainfall of between 400 and 750 mm per annum. The average summer temperatures in North West province range from 18 to 36°C, with extremes of up to 40°C whilst winter temperatures are moderate and range between 3 and 20°C. Average rainfall of North West province varies between 300 and 600 mm per annum. In Free State province, mean annual temperatures vary between 7 and 10°C in winter and 18 and 30°C in summer, and mean annual rainfall ranges between 300 and 750 mm (Acocks, 1988; Agriculture Geo-Referenced Information System, 2007). In each district municipality between 7 and 70 farmers with indigenous goats were randomly selected (Table 3.1 to 3.4). Each district presented in the current study represents a certain agro–ecological zone. Selection of districts was based on levels of genetic domination of indigenous goats and climatic conditions. These communities are known to raise goats together with other livestock species such as cattle, sheep, chickens and pigs.

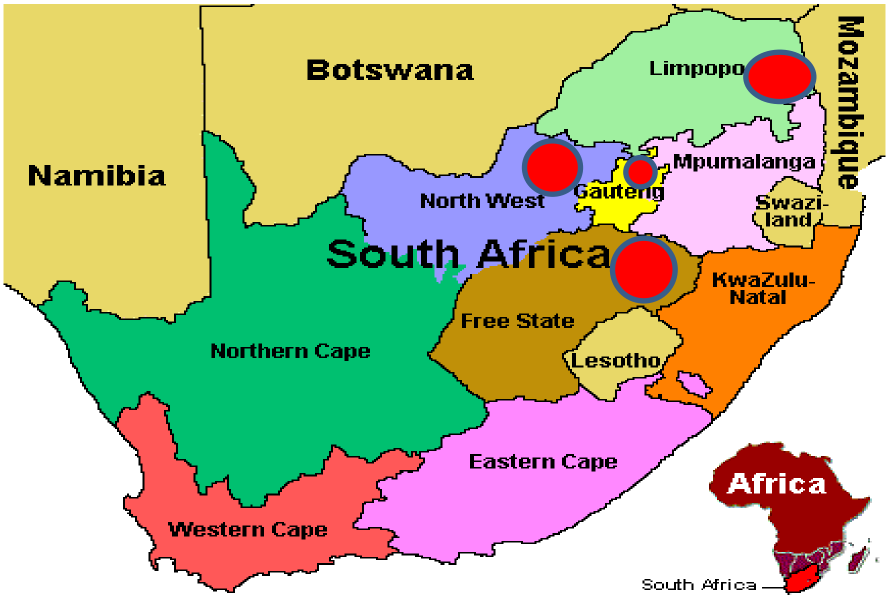


Figure 3.1 Map of South Africa with selected provinces and the district municipalities.

3.2.2 Sampling of households

For each district, 2–6 villages per local municipality were selected and households within a village were chosen using systematic random sampling procedure, where all observations of the frame were given an equal probability of selection (Table 3.1). Sampling of households was based on the ownership of goats and willingness to participate in the study. Primary focus was put on issues related to goat production. Ranking of selection criteria for breeding goats and the constraints on goat production were obtained by consensus. All goat farmers from the selected communities were invited to a central point by chairpersons of each community with the help of a local extension officer working with the communities. The farmers were divided into smaller groups balanced in terms of age and sex to ensure heterogeneity.

Table 3.1 Selected Limpopo farming regions and number of households per village

Province	Metro/District	Local Municipality	Village	No. Household
Limpopo	Vhembe	Mutale	Dhovo	8
			Gogogo	8
			Manentzhe	13
			Mataulu	5
		Makhado	Khomela	10
			Zwhigodini	8
		Thulamela	Khubu	8
			Mulenzhe	7
	Mopani	Baphalaborwa	Madimbo	2
		Greater Letaba	Motupa	4
			Boqa	4
			Femane	4
		Greater Tzaneen	Mamaila KT	3
		Greater Giyani	Malematja	5
		Maruleng	Dombani	3
Total	2	8	15	92

Table 3.2 Selected Gauteng farming regions and number of households per village

Province	Metro/District	Local Municipality	Farms	No. Household
Gauteng	Tshwane	N/A	Jamson park	1
			Rethabiseng	2
			Trigardspoort	2
			Melkhout	2
	West Rand	Westonaria	Enkeldoornpoort	1
		Randfontein	Wheatlands	1
		Mogale City	Rikusrus	1
			Hillside Tarlton	2
			Maanaarand	1
			Hartebeesfontein	1
Total	2	3	10	14

Table 3.3 Selected North West farming regions and number of households per village

Province	Metro/District	Local Municipality	Village	No. Household
		Ganyesa	Kgokgojane	6
			Gataote	6
			Morokwaneng	9
	Dr. RS Mompati	Taung North	De Aar	7
			Leshobo	6
			Dryhart	4
			Mabone	4
		Taung South	Austrey	3
North West		Morokweng	Buxton	6
		Naledi	Maheng	18
		Kagisano	Konke	10
		Moretele	Dikebu	9
	Bojanala	Moses Kotane East	Soulpoort	6
		Madibeng	Fafung	4
			Ramokgatla	5
			Jonathan	6
Total	2	8	15	109

[a]Dr. RS Mompati – Dr. Ruth Segomotsi Mompati

Table 3.4 Selected Free State farming regions and number of households per village

Province	District	Local Municipality	Farms	No. Household
Free State	Motheo	Mangaung	Bloemfontein	2
		Mantsopa	Ladybrand	1
	Thabo Mofutsanyana	Maluti a Phofung	Makwane	5
			Makeneng	4
			Thababosiu	3
			Lejoaneng	2
		Setsoto	Ficksburg	2
		Phumelela	Warden	2
			Reitz	4
Total	2	5	9	25

3.2.3 Data collection

The data collection method used in the study was based on the participatory rural appraisal (PRA) and farming systems research and extension (FSR/E) (Amir & Knipscheer, 1989; Mccrindle *et al.*, 1996; Van Vlaenderen, 1995). Individual interviews were conducted in 241 households using semi-structured questionnaires from four randomly selected provinces of South Africa; namely Free State (FS), Gauteng (GP), Limpopo (LP) and North West (NW) respectively. Initially 20 farmers were subjected to structured interview (Appendix A). Two stage cluster sampling (Thrusfield, 1986) was done where farmers were the primary units and goats were the secondary units. Efforts were made to ensure all members in each group participated in the discussions. Transect walks were made through the grazing areas and assessment of the amounts and state of the feed resources in the grazing lands were also made. The allocation procedure was based on the purposive selection of goat herds on communal grazing within Jericho (North West Province). Thirteen farmers remained in the trial and the farms were visited once a month.

Farmers were specifically asked about their position in household, goat flock size, awareness regarding conservation of indigenous goats, value of conserving indigenous goats, purpose for keeping indigenous goats, mortality rates, management practices on food and water, and other livestock species kept by farmers. The questionnaire also included information pertaining to sales of indigenous goats, breeding and health. Ten trained enumerators were used to conduct the interviews in the vernacular Sepedi, Tsonga, Venda, Tswana, Zulu and Xhosa languages.

3.3 Statistical analysis

Data was analysed using Statistical Package for Social Science (SPSS 26.1 for Windows) for multifactorial analysis of variance and covariance. The Generalised Linear Models procedure was used to analyse the effects of farmers' socio–economic profiles and district on livestock herd/flock sizes and goat mortality. Pair-wise comparisons of the least square means were performed using the PDIFF option. A logistic regression (PROC LOGISTIC) was used to predict the odds of a household to experience unavailability of goat feed, mortality and goat sale. The predictors fitted in the logit model included gender, age of goat ownership, wealth status, household size, production system, land size, livestock herd/flock sizes, type of goat breed owned, availability of supplementary feed, vaccines, housing structure and accessibility of extension and veterinary services. The logit model used for analysis was:

$$Y = \text{Ln}\,[P/1-P] = \beta_0 + \beta_1X_1 + \beta_2X_2 + \beta_3X_3 + ...+ \beta_{12}X_{12} + \varepsilon$$

Where:

P = Probability of a household to value goats, experience unavailability of feed and low goat sales

[P/1−P] = Odds ratio, which refers to the odds of household to experience unavailability of goat feed.

$\beta 0$ = Intercept;

$\beta 1 ... \beta 12$ = Regression coefficients of predictors

X1...X12 = Predictor variables

ε = Random residual error

The prediction of the probability that an event will occur (probability of success) is done by fitting data to a logit function. It makes use of several predictors' variables where Y = 1 for an occurrence and Y = 2 for a non-occurrence. When computed for each predictor (X1... X8), the odds ratio was interpreted as the proportion of households that experienced low goat sales versus those farmers that did not experience low goat sales. Similar ordinal logistic regression models were used to estimate the probability of a household that value the indigenous FAnGR**.**

3.4 Results

3.4.1 Goat ownership patterns and gender participation

The farmers kept a variety of livestock species including cattle, sheep chicken and pigs for household consumption and income generation through sale. Although the farmers were keeping other livestock species, goat farming was observed to be dominant specie kept by farmers in the study. Table 3.5 shows the distribution of the ownership of indigenous goats within the household in each region. Male adults owned the larger proportion of goats in all regions, while female adults own a considerable number of goats in Motheo (33.33%), and Vhembe (16.42%) regions. When the head of the household was male, 88.47% of households owned all the goats, compares with 11.53% when the head of the household was female.

Ownership of goats was shared between the household head and his/her spouse, brothers, sisters and daughters in Thabo Mofutsanyana households. Sharing of ownership between household heads, spouses and sons appeared to be common in Tshwane region.

Table 3.5 Distribution of indigenous goats within households and in relation to gender at different regions of South Africa.

Household with ownership by:	**Mopani** **(*n* = 25)**	**Vhembe** **(*n* = 67)**	**Tshwane** **(*n* = 7)**	**Westrand** **(*n* = 7)**	**Bojanala** **(*n* = 30)**	**DRSMD** **(*n* = 79)**	**Motheo** **(*n* = 3)**	**Thabo** **(*n* = 23)**
Males (%)	96	83.58	100	100	88	78.13	66.67	95.45
Females (%)	4	16.42	0	0	12	21.78	33.33	4.55
Head (%)	84	80.60	71.43	71.43	92	76.46	100	68.18
Spouse (%)	16	19.40	14.29	28.57	8	23.54	0	18.18
Brother (%)	0	0	0	0	0	0	0	4.55
Sister (%)	0	0	0	0	0	0	0	4.55
Sons (%)	0	0	14.29	0	0	0	0	0
Daughters (%)	0	0	0	0	0	0	0	4.55

[a], The ownership categories are listed in the Table. More than one category was involved in some household: Indigenous goats owned by different combinations of household members. [b]Percentages are given in italic to distinguish them from frequencies. [c]Dr. Ruth Segomotsi Mompati – DRSM; [d]Thabo Mofutsanyana – Thabo

3.4.2 Purposes for keeping indigenous goats

Goats were predominantly kept for meat consumption at most regions; Mopani (96%), Vhembe (82.09%), Tshwane (71.43%), Bojanala (100%), Dr. Ruth Segomitsi Mompati (84.9%), Motheo (100%) and Thabo Mofutsanyana (63.64%). The study observed four important functions of goat keeping (Table 3.6) which were sale in times of need (e.g. for food, school and in case of illness), as contribution to social life (e.g. for ceremonies, bride wealth and to help family members), as an investment and consumption of goat meat (mainly for special occasions).

Water from natural water resources (rivers and natural water ponds) in the Westrand was accessed by most goats (71.43%) and Thabo Mofutsanyana (63.63%), whilst dams were the main source for animals in Bojanala (60.00%) and North West (100%). Sixty-six percent of the households kept their goats in kraals at night, while 34 % of the flocks spent the night in open spaces. During the times of limited feed sources, indigenous goats mostly relied on the supplementation feed resource base for their nutrients. Over 68, 77.61, 100, 84, 84.26,100, and 68.19 % of the respondents in Mopani, Vhembe, Tshwane, Bojanala, Dr. Ruth Segomitsi Mompati, Motheo and Thabo Mofutsanyana regions respectively supplemented their goats using different feed resources. Majority of respondent in Westrand (0.0%) kept their indigenous goats extensively not provide supplementations.

Table 3.6 Frequencies of purpose of keeping indigenous goats and management system per region.

Parameters	**Mopani** **(*n* = 25)**	**Vhembe** **(*n* = 67)**	**Tshwane** **(*n* = 7)**	**Westrand** **(*n* = 7)**	**Bojanala** **(*n* = 30)**	**DRSMD** **(*n* = 79)**	**Motheo** **(*n* = 3)**	**Thabo** **(*n* = 23)**
Purpose								
Meat	96.00	82.09	71.43	42.86	100	84.9	100	63.64
Milk	0. 00	0	0	0	0	4.08	0	4.55
Stud breeding	0. 00	0	0	0	0	0	0	4.55
Cash for sale	4. 00	16.42	14.29	0	0	8.34	0	22.73
Investment	0. 00	0	0	0	0	0	0	0
Ceremonies	0.00	0	0	28.57	0	0	0	4.55
Cultural	0. 00	1.49	14.29	28.57	0	2.69	0	0
Water Source								
Dam	56.00	25.36	28.57	14.29	60.00	52.45	100	22.73
Natural Sources	16.00	53.74	57.14	71.43	24.00	12.88	0	63.63
Borehole	28.00	16.42	14.29	14.29	12.00	23.44	0	13.64
Tap	0.0	4.48	0.0	0.0	4.00	11.23	0	0.0
Feed Source								
Grazing	32.00	22.39	0.0	100	16.00	15.74	0.0	31.81
Supplementation	68.00	77.61	100	0.0	84.00	84.26	100	68.19

[a]Dr. Ruth Segomotsi Mompati – DRSM; [b]Thabo Mofutsanyana – Thabo

3.4.3 Management practices

3.4.3.1 Breeding

Goats were largely comprised of indigenous genotypes. Although respondents viewed indigenous goats as less productive, they preferred them because they are perceived to be adapted to the local environment, possess good maternal qualities and produce lean and tastier meat compared to exotic breeds and their crosses. Culling was carried out on old goats (over 6 years), which were either sold or slaughtered. About 99 % of the farmers did not keep records on flock performance. Farmers relied on the ear notch, coat colour and horn shape to identify their goats. In all the surveyed areas, farmers naturally mated their does with visually selected bucks that were bought, exchanged or loaned from other farmers. Goats producers hinted that the most important traits that they would like to improve are related to growth and fertility.

3.4.3.2 Housing

Males were mainly involved in the construction of housing structures for goats in 78 % of the households. Sixty-six percent of the households kept their goats in kraals at night, while 34 % of the flocks spent the night in open spaces. Wood poles and steal housing structures were more popular houses than bricks and fence structures. These observations may play an important role in kids' survivability because the kids were left in the enclosed kraals without feed and sometimes without water depending solely on their mother's milk. A lack of roughage may have had an impact on rumen development and kids became exposed to heart water transmitting ticks at a later stage because some farmers let the kids go out with their mothers for the first time at about four months of age. One of the goat kids necropsied (n = 6) died of starvation.

3.4.3.3 Health

The top three common causes of indigenous goat mortality (diseases, predators and external parasites) were ranked by respondents in order of importance. The major causes of indigenous goat mortality were diseases (65 % of the households), particularly rotten kidney, heartwater and anaplasmosis (38.7 %), followed by predation (60 %) and parasites (48 %). Mortality rate was similar across regions. Average adult indigenous goat mortality was moderate (4.5 %), while about 31.3 % of the kids were lost before 3 months of age for the studied regions. The high kid mortality was attributed to diseases, predation and cold weather. Plant poisonings were recorded and "Krimpsiekte" which is caused by *Cotyledon spp.* and are frequently used as decorative plants and are indigenous in South Africa killed indigenous goats in all regions. The paralysis described by farmers was one symptom of Krimpsiekte that may cause a paralysis lasting several weeks. Few farmers (10 %) vaccinated their indigenous goat heartwater disease. Ethno-veterinary medicines such as *Aloe ferox* and *Aloe vera* were used for treatment of various indigenous goat diseases.

Interviewees also indicated that they used traditional medicines (46 %) and insecticides (12 %) to control ecto–parasites, particularly ticks, lice and fleas. Other remedies used by farmers to control ecto–parasites include paraffin, used car oil and wood ash. Kids were reported to be at the highest risk of predation such as Jackals wild dogs, and Lynx, especially during the day, while adult and growing Does and Bucks were more prone to predation such as dogs, Jackals and Lynx that occurred during nighttime, if they are not provided with any enclosed structure for protection.

3.4.3.4 Marketing of goat

Marketing of goat was largely informal across all the surveyed regions. Goat sales only occurred when there was surplus or in times of emergency. Goats were mainly sold within the local farming communities and to some non–farming communities such as churches, traditional healers and business centres. The cash from sales was mainly used to buy household goods, including food. Sale of non–breeding stock, particularly castrated bucks and old does was common. Religious festivals and ceremonies such as circumcision and weddings periodically influenced the consumption patterns and prices of goats. Few farmers (20 %) purchased breeding stock in form of bucks. Generally, indigenous goats were sold at higher prices than exotic breeds.

3.4.4 Production constraints

The major constraints to indigenous goat production were unavailability of feed (85 %) followed by low indigenous goat sales (72 %) and their value by the indigenous farmer (60 % of the households). Other constraints included lack of extension services (56 %), unavailability of proper housing structures (48 %), veterinary services (45 %), inadequate institutional support (42 %), poor accessibility to markets (37 %) and lack of goat production skills (32 %).

3.4.4.1 Value the indigenous goats

The logistic regression model identified production system, availability of goat housing, source of breeding bucks and belonging to a production organization as the four main predictors of value of indigenous goats in the households (Table 3.7). Odds ratios for the value of the indigenous goats were high for the following predictors: age of the head of household, farm size, production system, mating system, external parasite control and belong to production organization (1.03 – 1.71). Youth-headed indigenous goat farmers practicing uncontrolled mating in semi-intensive production system, controlling external parasites and belonging to producer organization had high probability of valuing the indigenous goats.

Table 3.7 Odds ratio estimates of a household to value the indigenous AnGR in the selected communal areas of South Africa.

Value of indigenous goats' predictor	Odds ratio	Lower CI	Upper CI
Age (youth vs adult)	1.20	0.97	1.29
Farm size (>50 ha vs <50 ha)	1.03	0.93	1.14
Production system (semi-intensive/intensive vs extensive)	1.06	0.75	1.49
Goat housing (kraal vs stall/shed)	0.78	0.71	0.87
Mating system (uncontrolled vs controlled)	1.07	0.80	1.43
Internal parasite control (yes vs no)	0.96	0.67	1.37
External parasite control (yes vs no)	1.71	1.11	2.62
Accessibility of vet and extension services (yes vs no)	1.00	0.88	1.13
Availability of supplementary feed (no vs yes)	0.94	0.79	1.12
Belong to union (yes vs no)	0.85	0.41	0.77
Belong to production organization (yes vs no)	1.69	0.62	4.62
Source of breeding bucks (own vs AI/Rented)	0.89	0.81	0.97

[a]CI – Confidence interval; [b]vs – versus; [c]Vet – Veterinary

3.4.4.2 Unavailability of feed

Genotype was a strong predictor for indigenous goats' unavailability of feed in the communal areas [odds ratio (0.94), 79% confidence interval (0.79 – 1.12). The probability of unavailability of feed was lower in households that owned indigenous goats than those that owned exotic goat breeds. The odds ratios for other feed availability predictors such as production system, land size, cattle herd size, goat and sheep flock sizes, gender, age, wealth status, household size and availability of housing structure were low, ranged from 0.78 to 1.06.

3.4.4.3 Low goat sales

Table 3.8 shows odds ratios for selling goats were high for the following predictors: age of the head of household, farm size, production system, mating system, external parasite control, belong to union and source of breeding bucks. Youth-headed indigenous goat farmers practicing uncontrolled mating using their own bucks in semi-intensive production system and controlling external parasites who belong to a union had high probability of selling goats.

Table 3.8 Odds ratio estimates of a household goat sale in the selected communal areas of South Africa.

Value of indigenous goats' predictor	Odds ratio	Lower CI	Upper CI
Age (youth vs adult)	1.93	0.80	1.09
Farm size (>50 ha vs <50 ha)	1.05	0.94	1.18
Production system (semi-intensive/intensive vs extensive)	1.32	0.92	1.90
Goat housing (kraal vs stall/shed)	0.84	0.76	0.94
Mating system (uncontrolled vs controlled)	1.58	1.16	2.16
Internal parasite control (yes vs no)	0.88	0.59	1.31
External parasite control (yes vs no)	1.67	1.06	2.64
Accessibility of vet and extension services (yes vs no)	0.93	0.81	1.06
Availability of supplementary feed (no vs yes)	0.73	0.60	0.89
Belong to union (yes vs no)	1.63	1.74	3.57
Belong to production organisation (yes vs no)	0.77	0.27	2.22
Source of breeding bucks (own vs AI/Rented)	1.04	0.94	1.14

[a]CI –Confidence interval; [b]vs – versus; [c]Vet = Veterinary

3.5 Discussion

The current study described and documented indigenous goat production systems in Free State, Gauteng, Limpopo, and North West provinces as an essential step towards conservation and sustainable utilisation of indigenous goats. Most of households surveyed in addition to keeping goats, also kept cattle, sheep, chickens and pigs. The combination of livestock owned in these rural farms was similar to other investigations conducted in other rural areas of southern Africa

(Bembridge, 1993; Mahanjana & Cronjé, 2000; Rumosa-Gwaze, 2009; Dube, 2015; Thobile *et al*., 2021). However, with this information it should be recalled that in selection of households one of the criteria was to select farmers keeping goats, thus this probably has led to some of farmers keeping other livestock species to be left out. Jaitner *et al*. (2001) found that small ruminant production ranked close to cattle. The finding that majority of farmers were old showed a critical gap which may exist in the prospects of goat farming in these communities. This would potentially result in future erosion of the available goat management knowledge (Mohlatlole *et al*., 2015; Ofori, 2021). Agriculture training should therefore target younger generations for them to appreciate the benefits and ensure its future continuity.

Four important purposes of goat keeping were found to be sale in times of need (e.g. for food, school and in case of illness), as contribution to social life (e.g. for ceremonies, bride wealth and to help family members), as an investment and consumption of goat meat (mainly for special occasions). This agrees with the findings of Mapiliyao (2010) in Eastern Cape. Goats were commonly used as a source of meat, family income and manure, in the present study. Together these accounted for 99% of the total usage. Fibres, hides, skins and pelts as other important products used in other goat breeds (FAO, 2007). These could be possible opportunities which farmers can exploit to better utilise their goat. The goats were however also kept for cultural purposes and to aid in generation of income during financial distress. These results were consistent to those by Masika & Mafu (2004); Bester *et al*. (2009) and Rumosa-Gwaze (2009). The use of goats for milk production was unpopular as also reported in previous studies (Masika & Mafu, 2004; Tefera *et al*., 2004; Khowa, 2023a). This is because most farmers considered the consumption of goat milk to be highly associated with poverty. It is therefore essential to educate farmers on the rich nutritional attributes of goat milk which can assist in reducing malnutrition in these communities.

Most South African farmers in the rural areas notes that access to water as a challenge that resulted in majority of the animals having to fend for their own water in rivers and natural ponds. Water from natural water resources (rivers and natural water ponds) in the Westrand are accessed by most goats (71.43%) and Thabo Mofutsanyana (63.63%) yet in Bojanala dams were the main source of water for animals (60.00%) and North West (100%). About 8.80 % of South African households do not have access to clean piped water and rivers as well as wells that are shared with livestock are often used as alternative sources of water by households (Sebei *et al*., 2004a). The water sources dry up during the dry seasons and most of the time which makes them unreliable (Sebei *et al*., 2004a). Majority (72.31%) of the farmers depended on unstable water resources which is the main revelation by this study.

The major causes of indigenous goat mortality were diseases, particularly “rotten kidney”, heartwater, anaplasmosis, followed by predation and parasites. The finding that mortality was the major constraint agrees with reports from other developing countries (Donkin *et al*., 2006; Dube, 2016). However, the mortality figures reported in this study were relatively lower compared to those of Sebei *et al*. (2004); Webb & Mamabolo (2004) and Homann *et al*. (2007) which were between 30%-50%. This might be due to a significant number of farmers dipping and deworming of their goats in the current study. The ability of farmers to acknowledge these basic health strategies, illustrates their efforts in reducing production losses. The conventional disease control methods farmers used traditional medicines were also cited by Setlalekgomo & Setlalekgomo (2013).

South Africa has different parts that been considered a heartwater disease area, especial at the dry and hot regions where the tick vector *A. hebraeum* prevails. In the study, ticks were present on some animals with few farmers vaccinating their indigenous goats against heartwater disease with tick control by the farmers being irregular or non-existent. Prevalence of heartwater-endemic in part of Zimbabwe was also reported (Mahan *et al*., 1998). In other studies, the prevalence of heartwater and more risk factors associated with it have been discussed in detail (Bath *et al*., 2005; Swai *et al*., 2008; Swai *et al*., 2009). The present study suggests that the field exposure and continuous tick challenge when maintained under tick infested conditions contributed to the high degree of infection on communal indigenous goats. The finding that heartwater disease was likely to occur in a poor and youth-headed household could imply that such a household did not have money to purchase vaccines or resources to control the disease. In their studies Masika & Mafu (2004) and Slayi *et al*. (2014) observed that there was a high prevalence of heartwater and gall sickness, in the Central Eastern Cape. The erratic dipping programs coupled with failure to mix chemicals properly may have resulted in tick resistance. Therefore, despite farmer efforts in controlling ticks, the ticks still had a significant effect in the flocks.

The findings that the probability of high valuing of goat was high in youth-aged goat farmers is in accordance with Nsoso *et al*. (2004). The probability of valuing goat was also high for the farmers practicing uncontrolled mating in semi-intensive production system, controlling external parasites and belonging to producer organisation (Monau, 2017; Kraai, 2022; Khowa, 2023b). The youth generally perceive agriculture as a non-viable sector of employment and are discouraged by constraints such as limited capital, land, water, access to markets and inadequate involvement in policy dialogue (FAO, 2014). This is unfortunate as they are the future generation of farmers that should ensure the future of the industry. Value addition, processing and niche marketing of indigenous goat products (meat and leather), organising farmers to increase bargaining power and shortening the marketing chain is equally important but needs better understanding of costs and benefits involved.

The observation that the probability to sell goats was high in households that owned large flocks/farms is in accordance with (Peacock, 2005; Pieters *et al*., 2009) who reported that the propensity to sell goats increased with flock size. Noted from the farmers was that their financial needs coupled with the size and appearance of the goat determines the price of goats. It was highlighted that goats were sold regardless of their class; however, most sales were dominantly for castrates, and this was in agreement with the findings by Homann *et al*. 2007) and Gizaw *et al.* (2010). The low probability of selling goats observed for youth-head households could, therefore, be a consequence of limited access to markets, transport, information, credit, agro-inputs and technologies compared to adults (Maree, 1993; Visser, 2018). Youth-headed households are often poorer and have less access to resources required to control diseases than adult-headed households (Dossa, 2008). Therefore, if farmers would participate in the formal market, there would be a need to have high off takes to realize significant profits. Goats for slaughter are mostly marketed directly off the veld through informal trade (Visser, 2018). Also noted in the present study is the non-specificity of the type of animals sold by farmers and a high proportion of farmers selling to meet emergent family needs. This was a result of the fact that farmers did not have stipulated guidelines in selling their goats. This suggests a necessity to explore if organised marketing can improve the benefits reaped by farmers from their investments. Kosgey *et al*. (2008) indicated that farmers would likely not adopt improved management practices whilst proceeds from sale of animals are low. Thus, goat marketing would have to be addressed in order to win the hearts of farmers towards the conservation and improvement of indigenous goats. Accessibility of veterinary services influences goat mortality and, consequently, the number of goats available for sale (Sebei *et al*., 2004; Khowa, 2023b).

3.6 Conclusions

The study presented a detailed description of the state of indigenous goat production in the investigated areas. The indigenous goats value, age of indigenous goat ownership, production system, flock size, type of goat breed owned, accessibility of veterinary services, availability of supplements and vaccines influence indigenous goat farmer's production constraints such as feed availability, goat mortality, prevalence of diseases and goat sales. To improve indigenous goat production, it is, therefore, critical to consider producers' socio–economic profiles. To facilitate conservation and utilization of these valuable genetic resources, it is also imperative to further characterize them both phenotypically and genetically.

CHAPTER 4: STUDY TWO

PHENOTYPIC DIVERSITY OF SOUTH AFRICAN INDIGENOUS GOAT POPULATION IN SELECTED RURAL AREAS

Abstract

Phenotypic characterisation of indigenous goat populations is crucial in providing information on goat types and their attributes and may play an important role as guideline for conservation and sustainable us of these resources. The objective of this study was to characterise indigenous goat populations in rural areas of South Africa. Appearance of indigenous goat phenotypes and their typical features were observed and measured from 297 individual goats. FREQ procedure of Statistical Analysis System was used to determine the descriptive statistics of the qualitative phenotypic variables. To detect the statistical differences for quantitative traits, the General Linear Model procedure of SAS was computed, whereas Fisher's Least Significant Difference test was used to separate the least square means ($P<0.05$). Horns and toggles were the most dominant phenotypes found in the different regions, while the beard had low proportions across regions. Black coat colour was the dominant colour (9.68 – 69.57 %) of most of the populations in Mopani, Vhembe, Tshwane, Westrand, Bojanala, Motheo and Thabo Mofutsanyane regions. There was a significant ($P<0.05$) difference in all phenotypic measurements, with higher ($P<0.05$) values for body length (48.23 cm), body weight (26.86 kg) and wither height (64.61cm) observed in indigenous goats of Dr. Ruth Segomotsi Mompati (DRSM) region. Goats in Tshwane, Westrand and DRSM had significantly similar body length whilst also those in Motheo, Thabo and Vhembe had significantly similar body length. The indigenous goats of Thabo Mofutsanyana region had the highest ($P<0.05$) value for rump length (17.52 cm), however have the shortest tail length (7.17 cm) compared to those at other regions. Results from the study shows considerable phenotypic heterogeneity in qualitative traits of indigenous goat population and their distributions in different regions.

Key words: *body length, characterisation, coat colour, phenotypes, regions*

4.1 Introduction

Goats in general are known to have the ability to survive and reproduce in harsh environmental conditions and on poor quality fibrous feeds. In developing countries, livestock production is mostly subsistence oriented and fulfils multiple functions that contribute more for food security (Roessler *et al*., 2008; Duguma *et al*., 2010). Majority of South African goats are indigenous goat breeds which are kept by small holder farmers in communal areas (Matshaba *et al.,* 2010). Indigenous goats, like all other livestock species are recognized as important components of livestock biodiversity (Nsoso *et al*., 2004; Bekalu, 2016).

Characterisation of livestock breeds based on their morphological trait's variations (Mavule *et al*., 2016; Delgado *et al*., 2001) is the first step towards the use of the available Animal Genetic Resources (Kunene *et al*., 2007; Lanari *et al*., 2003). Phenotypic quantitative characteristics are measures of animal body parts (Belay, 2017; FAO, 2012; Pieters *et al*., 2009) and are more directly associated to production characteristics when compared to phenotypic qualitative characteristics (Manzi *et al*., 2011; Jimcy *et al*., 2011).

Phenotypic quantitative characteristics are measures of animal body parts (Capote *et al*., 1998; Pieters *et al*., 2009; FAO, 2012) and are more directly associated to production characteristics when compared to phenotypic qualitative characteristics (Manzi, 2011; Jimcy, 2011; Belay, 2017). Furthermore, characterisation of livestock breeds based on their morphological trait's variations (Mavule, 2016; Delgado *et al*., 2001) are the first step towards the use of the available Animal Genetic Resources (Kunene, 2007; Lanari *et al*., 2003). A general description of indigenous livestock has for many years relied on the phenotypic characteristics and is among the first to be used to determine the relationship between breeds (Yakubu, 2010; FAO, 2011b; Mdladla, 2017).

Morphological diversity is a good reflector of ecological selection regimes and history of a breed (Kotze *et al*., 2014; González *et al*., 2011; Jordana, 1993). In addition, phenotypes are an expression of genetic characteristics, modified by environmental conditions and variance in both genetics and environment may affect phenotypic variance (Kunene *et al*., 2014; Yakubu *et al*., 2010; Riva, 2004).

Idowu & Adelabu. (2018) stated that coat colour and certain characteristics provide goats with unique abilities. Coat colour is very amiable and irregular including black and brown, pied and mixed colour (Adedeji, 2012). It is influenced by a large number of genes that are involved in determining the presence, distribution and biochemical activities of the melanocytes (Okourwa, 2015; Fontanesi *et al.*, 2011).

Although phenotypic characterisation is important in breed identification and classification, it is scanty in Gauteng, Free State, North West and Limpopo provinces. It is in the context of these assertions that this study depended on phenotypic measurements and geographic locations to unearth the characteristic of genetic diversity amongst indigenous goat populations. The objective of this study was to characterise indigenous goat populations in selected rural areas of South Africa based on a set of phenotypic traits.

4.2 Materials and methods

4.2.1 Study site

Surveys were conducted in 2013 at Mopani and Vhembe District Municipalities of Limpopo Province; Bojanala and Dr. Ruth Segomotsi Mompati Districts Municipalities of North West Province; Tshwane Metro Municipality and Westrand District Municipality of Gauteng Province and at Motheo and Thabo Mufutsanyana District Municipalities of Free State Province.

4.2.2 Sampling of households and data collection

For each district, 3-8 villages were selected and households within a village were chosen using systematic random sampling procedure. A total of 297 does, were sampled from the 4 studied provinces of South Africa. The number of does sampled in each area were: Gauteng province: Tshwane Metro Municipality = 36, Westrand District Municipality = 42, Free State province: Motheo District Municipality = 23 and Thabo Mufutsanyana District Municipality = 36, North West province: Bojanala District Municipality = 34, Dr. Ruth Segomotsi Mompati (DRSM)

Districts Municipality = 44, Limpopo province: Mopani District Municipality = 46, Vhembe District Municipality = 36.

4.2.3 Data collection

Age of each animal was determined by the dentition method. Only goats with two pairs of incisors and above (24 months old and above) were considered in order to minimise age effects. A scale was used to determine body weight (BW) of each animal sampled. Goats were weighed in the morning before feeding to minimize post-prandial gut variation (Yakubu *et al*., 2010). A textile measuring tape was used to obtain different body measurements from each sampled animal (with records taken to the nearest cm) after restraining and holding the animal in an unforced position. The body parts were measured as described by Yakubu *et al*. (2010). Phenotypic qualitative traits recorded were head length (HL), head width (HW), ear orientation (EO), ear length (EL), heart girth (HG), body length (BL), wither height (WH), thorax depth (TD), rump height (RH), rump width (RW), rump length (RL), neck circumference (NC) and tail length (TL). Records were also taken on qualitative traits such as coat colour pattern, colour, horns length, ear orientation and presence or absent of beard and toggles.

4.2.4 Statistical analysis

Frequencies and percentages of occurrence of qualitative traits were generated using the FREQ procedure of Statistical Analysis System (SAS 9.2, 2014). To detect the statistical differences for quantitative traits, the General Linear Model procedure (PROC GLM) of the SAS was computed, whereas Fisher's Least Significant Difference (LSD) test was used to separate the least square means ($P<0.05$). The following model was used:

$$Y_{ik} = \mu + A_i + e_{ik}$$

Where:

Y_{ik} -	Observations on linear body measurements
μ -	Underlying constant common to all observations
A_i -	Fixed effect of districts
e_{ik} -	Random residual / error

4.3 Results

4.3.1 Indigenous goat phenotypic diversity

A considerable diversity of phenotypic characters such as horns, beard and toggles of indigenous goat population distributions in different regions of South Africa (%) are presented in Table 4.1. The three common phenotypes of indigenous goat found in rural communities of South Africa include: presence and absence of horns, beard and toggles. Horns and toggles were the most dominant phenotypes found in the different regions, while the beard phenotype observed in the current study had low proportions across regions. Beard and toggles phenotypes were observed to be high in Motheo region (69.57% and 86.96 % respectively). In Tshwane district there was a low observation of beard phenotype (25.81%), and the toggle phenotype (26.47%) are observed to be low in Vhembe region.

Table 4.1 Diversity of phenotypic characters of indigenous goat population distributions in different regions of South Africa (%).

Regions	*n*	Horns	Beard	Toggled
Mopani	46	100.00	34.78	73.91
Vhembe	34	100.00	41.18	26.47
Tshwane	31	100.00	25.81	70.97
Westrand	33	100.00	30.30	63.64
Bojanala	34	100.00	26.47	82.35
DRSM	44	100.00	65.91	38.64
Motheo	23	100.00	69.57	86.96
Thabo Mofutsa	36	100.00	47.22	61.11

[a]Dr. Ruth Segomotsi Mompati – DRSM; [b]Thabo Mofutsanyana – Thabo Mofutsa

4.3.2 Body hair coat colour and Coat colour pattern characteristics

The proportions of the different body hair coat colour and patterns of indigenous goat populations in different regions of South Africa (%) are presented in Table 4.2. Each population observed possessed multiple variants of body hair coat colours, even though there were great variations among the different populations in the proportion of specific body hair coat colours characterising them. Black body hair coat colour was the dominant colours (9.68 – 69.57%) of most of the populations in Mopani, Vhembe, Tshwane, Westrand, Bojanala, Motheo and Thabo Mofutsanyane regions. The second most popular body hair coat colour that was dominant appeared to be a white colour (2.94 – 55.56%) in most of the populations in Mopani, Vhembe, Tshwane, Westrand, Bojanala, Motheo and Thabo Mofutsanyane regions. Except for DRSM region which comprised large proportions (59.09%) of light red and fawn (38.64%) body hair coat colour. The fawn body hair coat colour was also observed in Vhembe region (17.65%) amongst other regions.

Farmers in Thabo Mofutsanyana region preferred a patchy coat colour pattern indigenous goat (69.444 %) than farmers in Tshwane region (19.35 %) who enjoy keeping indigenous goats with plain coat colour pattern (58.06 %). The higher proportion spotted coat colour pattern (44.12%) was observed in Vhembe and Bojanala regions and appear to be distributed relatively fairly between the different regions than other observed coat colour patterns.

Table **4.2** The proportions (%) of the different coat colour and coat colour patterns of indigenous goat populations in different regions of South Africa.

Regions	***n***	**Coat colour**					**Coat colour patterns**		
		White	**Black**	**Dark red**	**Light red**	**Fawn**	**Plain**	**Patchy/Pied**	**Spotted**
Mopani	46	6.52	69.57	13.04	10,87	0.00	10.87	50.0	39.13
Vhembe	34	2.94	38.24	23.53	17.64	17.65	14.71	41.17	44.12
Tshwane	31	48.39	9.68	41.93	0.00	0.00	58.06	19.35	22.58
Westrand	33	30.30	12.12	57.58	0.00	0.00	15.15	39.40	45.45
Bojanala	34	52.94	20.59	26.47	0.00	0.00	11.76	44.12	44.12
DRSM	44	0.00	0.00	2.27	59.09	38.64	13.64	43.18	43.18
Motheo	23	47.83	52.17	0.00	0.00	0.00	8.70	65.21	26.09
Thabo Mofutsa	36	55.56	27.78	16.66	0.00	0.00	16.67	69.44	13.89

[a]Dr. Ruth Segomotsi Mompati – DRSM; [b]Thabo Mofutsanyana – Thabo Mofutsa

4.3.3 Head region characteristics

Table 4.3 shows the proportions (%) of the different head region characters (horn shape and horn growth direction) of South African indigenous goats. The curved horn shape significantly dominated (50.00 – 65.22%) all regions except in Vhembe (32.35%) and DRSM (20.45%) regions. The straight and spiral shaped horn shape were observed to be dominant in Vhembe (41.18%) and DRSM (45.45%) regions. The backward horn growth directions constituted higher proportion in DRSM (43.18%), Vhembe (44.12%), Motheo (65.22%), Mopani (65.33%), Thabo (66.67%) and Tshwane (80.65%). Sideways and upright growth directions were observed to be dominant in Bojanala (64.71%) and DRSM (34.09%), respectively.

Table 4.3 Proportions of the different head region characters (horn shape and horn growth direction) of South African indigenous goats (%).

Regions	***n***	**Horn shape**			**Horn direction**		
		Curved	**Spiral**	**Straight**	**Backward**	**Sideways**	**Up straight**
Mopani	46	50.00	21.74	28.26	65.22	8.70	26.08
Vhembe	34	32.35	26.47	41.18	44.12	41.17	14.71
Tshwane	31	64.52	35.48	0.00	80.65	0.00	19.35
Westrand	33	60.61	0.00	39.39	33.34	36.36	30.30
Bojanala	34	52.94	8.82	38.24	11.76	64.71	23.53
DRSM	44	20.46	45.45	34.09	43.18	22.73	34.09
Motheo	23	65.22	0.0	34.78	65.22	34.78	0.00
Thabo Mofutsa	36	58.33	30.56	11.11	66.67	13.89	19.44

[a]Dr. Ruth Segomotsi Mompati – DRSM; [b]Thabo Mofutsanyana – Thabo Mofutsa

4.3.4 Ear region characteristics

The proportions of the different ear region characters (ear orientation and ear direction) of South African indigenous goats (%) are presented in Table 4.4. The ear orientation and ear direction are the most prominent ear region characters on indigenous goats that were observed. Mopani, Motheo and Thabo Mofutsanyane regions have the higher proportion of erected eared goats, whilst Vhembe, Tshwane, Bojanala and Dr. Ruth Segomotsi Mompati regions have the higher proportion of semi-pendulous eared goats. However, indigenous goats in Westrand region have the higher proportions of pendulous ears. The higher proportion of stiff sideways ear direction was observed in indigenous goats of Westrand (87.88%), Thabo Mofutsanyana (77.78%), Bojanala (70.59%), DRSM (63.64%) and Vhembe (61.76%) regions, whilst the higher proportion of those with soft hanging ear direction were observed in Mopani (89.13%) and Tshwane (64.52%) region.

Table 4.4 Proportions of the different ear region characters (ear orientation and ear direction) of South African indigenous goats (%).

Regions	***n***	**Ear orientation**			**Ear direction**	
		Erect	**Pendulous**	**Semi-Pendulous**	**Soft hanging**	**Stiff sideways**
Mopani	46	60.87	6.52	32.61	89.13	10.87
Vhembe	34	5.88	2.94	91.18	38.24	61.76
Tshwane	31	35.48	0.00	64.52	64.52	35.48
Westrand	33	30.30	51.52	18.18	12.12	87.88
Bojanala	34	29.41	29.41	41.18	29.41	70.59
DRSM	44	11.36	43.19	45.45	36.36	63.64
Motheo	23	56.52	4.35	39.13	47.83	52.17
Thabo Mofutsa	36	72.22	11.11	16.67	22.22	77.78

[a]Dr. Ruth Segomotsi Mompati – DRSM; [b]Thabo Mofutsanyana – Thabo Mofutsa

4.3.5 Body region characteristics

The linear body measurements (cm) of South African indigenous goats are presented in Table 4.5. There was a significant ($P<0.05$) difference in all phenotypic measurements understudy, with higher ($P<0.05$) values for body length (48.23cm), body weight (26.86cm) and wither height (64.61cm) observed in indigenous goats of DRSM region. Goats in Tshwane, Westrand and DRSM had similar ($P>0.05$) body length whilst also those in Motheo, Thabo and Vhembe had significantly similar ($P>0.05$) body length. However, those in Mopani had significantly lower body length compared to those in other regions. Indigenous goats in Mopani Region have significantly higher ($P<0.05$) values for thorax depth (23.77cm), rump height (57.78cm) and tail length (7.93cm). The indigenous goats of Thabo Mofutsanyana region had the highest ($P<0.05$) value for rump length (17.52cm), however have the shortest tail length (7.17cm) compared to the indigenous goat of all regions.

Table 4.5 Least Square Means ± standard error for the quantitative body characters of indigenous goats in different regions of South Africa.

Traits (cm)	**Mopani**	**Vhembe**	**Tshwane**	**Westrand**	**Bojanala**	**DRSM**	**Motheo**	**Thabo Mof**
N	46	34	31	33	34	44	23	36
Body length	36.08^{c} ± 1.07	38.44^{b} ± 1.08	46.97^{a} ± 1.16	48.21^{a} ± 1.14	39.06^{b} ± 1.10	48.23^{a} ± 1.07	39.07^{b} ± 1.08	39.69^{b} ± 1.11
Body weight	22.59^{cd} ± 0.93	21.92^{de} ± 0.94	22.45^{cde} ± 1.01	25.21^{b} ± 0.99	20.96^{e} ± 0.95	26.86^{a} ± 0.93	25.26^{ab} ± 0.94	23.64^{bc} ± 0.96
Heart girth	73.23^{b} ± 1.04	75.12^{a} ± 1.05	74.07^{ab} ± 1.13	74.07^{ab} ± 1.10	73.55^{ab} ± 1.07	74.82^{ab} ± 1.03	70.04^{c} ± 1.05	74.29^{ab} ± 1.08
Wither height	61.76^{bc} ± 0.90	61.50^{bc} ± 0.91	63.05^{ab} ± 0.97	61.81^{bc} ± 0.95	61.13^{c} ± 0.92	64.61^{a} ± 0.89	62.39^{bc} ± 0.91	61.56^{bc} ± 0.93
Thorax depth	23.77^{a} ± 0.38	23.65^{abc} ± 0.39	23.64^{abc} ± 0.42	23.34^{abc} ± 0.41	23.07^{bcd} ± 0.40	23.68^{ab} ± 0.38	22.89^{cd} ± 0.39	22.41^{d} ± 0.40
Rump height	57.78^{a} ± 1.27	53.65^{bcd}± .27	54.19^{bc} ± 1.37	51.88^{cd} ± 1.34	51.73^{d} ± 1.30	55.05^{b} ± 1.26	53.40b^{cd}±1.31	53.27^{bcd}±1.31
Rump length	15.03^{d} ± 0.55	16.07^{bc} ± 0.55	15.86b^{cd}±0.59	15.56^{cd} ± 0.60	16.42^{bc} ± 0.56	16.68^{ab} ± 0.54	15.37^{cd} ± 0.55	17.52^{a} ± 0.57
Rump width	14.58^{bc} ± 0.43	15.62^{a} ± 0.44	15.91^{a} ± 0.47	14.40^{c} ± 0.46	14.29^{c} ± 0.45	15.46^{a} ± 0.43	15.17^{abc}±0.44	15.33^{ab} ± 0.45
Tail length	7.93^{a} ± 0.25	7.84^{ab} ± 0.25	7.90^{ab} ± 0.27	7.54^{abc} ± 0.26	7.49^{bc} ± 0.25	7.24^{c} ± 0.25	7.29^{c} ± 0.25	7.17^{c} ± 0.26

$^{a, b, c, d,e}$ Values with different superscripts within the same raw differs significantly (P<0.05); Dr. Ruth Segomotsi Mompati – DRSM; Thabo Mofutsanyana – Thabo Mof

4.4 Discussions

The results show the presence of clear morphological variations between and within the indigenous goat populations in different areas of South Africa. Horns and toggles were the most dominant phenotypes found in the different regions, while the beard phenotype observed in the current study had low proportions across regions. The presence of horns in indigenous goats is an important adaptive feature for self-defensive mechanism to fight predators or where animals had to fight competitors for feed and water and even for does during mating (Katongole *et al*., 1996; Mdladla, 2016). The low occurrence of polledness in indigenous goat populations has been reported in Ghana (Hagan *et al*., 2012). The morphological differentiation was also observed in other species such as Zulu sheep populations in South Africa using multivariate analysis (Mavule *et al*., 2016).

Beard and toggles phenotypes were observed to be high in Motheo region. In Tshwane district there was a low observation of beard phenotype, and the toggle phenotype are observed to be low in Vhembe region. Beard and toggles have been associated with many benefits in some studies (Adebayo & Chineke, 2011). Prominent among the benefits of toggles and beard are the thermoregulatory functions of beard and wattle and the association of these traits with reproduction such as higher prolificacy, higher milk yield, higher litter size, fertility index and conception rate (Osinowo *et al*., 1988 and Yakubu *et al*., 2010). Although further conclusions cannot be drawn on the current study regarding toggles/wattles based on the collected data. Yakubu *et al*. (2010a) reported an associated taboo towards toggled village goats which might be the case in the communities in the study.

Farmers relied on coat colour and patterns to identify their goats. Each population observed possessed multiple variants of body hair coat colours, even though there were great variations among the different populations in the proportion of specific body hair coat colours characterising them. Black body hair coat colour was the dominant colours of most of the populations in Mopani, Vhembe, Tshwane, Westrand, Bojanala, Motheo and Thabo Mofutsanyane regions. Morphological differences have important socio-cultural and economic values to the rural communities and as a result, most farmers have specific consideration and choices for goat coat colors (Mahanjana & Cronje 2000; Gwaze *et al*., 2009b). In Vhembe region, black goats are more preferred for rituals (Mashau, 2013) and are also believed to have good adaptation to cold weather as the black pigment helps warming them up faster than goats with other coat colours (Hassen *et al*., 2012). In Ghana, dark coat colours have been linked to environmental adaptation (Hagan et al. 2012).

The second most popular body hair coat colour that was dominant appeared to be a white colour in most of the populations in Mopani, Vhembe, Tshwane, Westrand, Bojanala, Motheo and Thabo Mofutsanyane regions. This is similar with the results of Hassen *et al*. (2012) on Ethiopian indigenous goats where he found that white colour has socio-cultural and economic values to African people. For example: black goats are less preferred in the Amhara region (Ethiopia) and Zululand region (South Africa) because they are believed to bring bad luck in the family (Pieters, 2009). Except for DRSM region which is comprised of a large proportion of light red and fawn body hair coat colour. The fawn body hair coat colour was also observed in Vhembe region amongst other regions. The body hair coat colour has a direct effect on goat marketing value (Mahanjana & Cronje, 2000; Kotze *et al*., 2014). These marketing abilities on indigenous goats brought by their unique coat colours and certain characteristics were stated by Idowu & Adelabu. (2018) in their studies. However, in West Africa, based on the information gotten from the farmers, it was discovered that there is no preference coat colour amidst the farmers, but black coat colour is highly priced followed by brown herd in agreement with Adedeji *et al*. (2011).

The majority of smallholder farmers in all districts studied preferred patchy coat colour pattern. The plain coat colour patterns showed lower proportion in all the regions understudy except in Tshwane region, whilst the spotted coat colour pattern was distributed relatively fairly between the different districts. The variation in colours observed in the current study was not surprising, as it has been documented that South African indigenous goats have a variety of colours (Campbell, 2003; Morrison, 2007; Mdladla, 2016; Mdladla, 2017). This shows that South African indigenous goats in different areas of South Africa share some common characteristics.

Only nine basic phenotypic measurements (BL, BW, HG, WH, TD, RH, RL, RW and TL) consistently could be important in differentiating among indigenous goat populations, then acquiring a substantial number of measurements. Some of the measurements selected in the current study are similar to those obtained by earlier researchers (Traoré *et al*., 2008; Yakubu *et al*., 2010a; Yakubu *et al*., 2010b; Okpeku *et al*., 2011) in morphological differentiation of indigenous goats. The study revealed a significant (P<0.05) difference in all phenotypic measurements understudy, with higher (P<0.05) values for body length, body weight and wither height observed in indigenous goats of DRSM region. This was in agreement with the report of (Alade, *et al*., 2008; Sowande, *et al*., 2009; Semakula, *et al*., 2010; Okbeku *et al*., 2011). The morphometrical studies involving Sahelian goat are scant: Mohmmed and Amin. (1996) reported mean HW in non-pregnant Sahelian does in Nigeria of 60 cm; the mean HW of the Red Sokoto goat, which is considered a transition breed between Sahelians and Djallonkés present in Southern Niger, was 58.2 cm (Alade, 2008; Dossa *et al*., 2007; Bourzat *et al*., 1993). These values are, in general, consistent with that of HW reported here for the Sahelian goat (Sowande, O.S., Oyewale, B.F., Iyasere, O.S., 2009) which are similar to the results from this study.

Indigenous goats in Mopani region have significantly higher (P<0.05) values for thorax depth, rump height and tail length. In other studies, an average value for thorax depth was reported in the coastal goat population of Benin and were on average 24.69 cm (Dossa *et al*., 2007). The indigenous goats of Thabo Mofutsanyana region had the highest value for rump length, however, have the shortest tail length compared to the indigenous goat of all regions. Morphometric measurements can be used to describe the animals’ production status, and breed characteristics (Cam *et al*., 2010). Previous studies have used multivariate analysis of morphological parameters to explain population structure, facilitate breed identification, and estimate genetic variation within and between indigenous goat populations from different agro-ecological zones (Tsegaye *et al*., 2013).

4.5 Conclusions

Results from this study shows considerable phenotypic heterogeneity in qualitative traits of indigenous goat populations kept under extensive production system and their distributions in different regions of South Africa. From the three phenotypes of indigenous goats found in rural communities of South Africa include: presence and absence of horns, beard and toggles while the beard phenotype observed in the current study had low proportions across regions. Black coat colour was the dominant colour of most of the populations. There was a significant difference in all phenotypic measurements understudy, with higher values for body length, body weight and wither height observed in indigenous goats. This phenotypic information could be useful to regulate the different phenotypes within a region or country and design some criteria for characterisation and description of the indigenous goat populations into breeds. Further complementary research into the effects of these traits and the underlying genes on economic factors should be undertaken for smallholder farmers-oriented breeding plans. The assessed phenotypic traits coupled with genetic information could be a powerful tool towards the promotion of conservation and utilization of indigenous goat genetic resources. For this reason, the level and distribution of genetic variation between South African indigenous goat populations using Single Nucleotide Polymorphisms require investigation.

CHAPTER 5: STUDY THREE

GENETIC DIVERSITY OF SOUTH AFRICAN INDIGENOUS GOAT POPULATION FROM FOUR PROVINCES USING GENOME-WIDE SNP DATA

This chapter was orally presented at the SASAS 2024 Congress, and a publication came out in South African Journal of Animal Science.

PUBLICATION:

Chokoe, T.C., Tada, O., Hadebe, K., Muchadeyi, F.C., Dzomba, E.F., Matelele1, T.C., Mphahlele1, T.D., Mpofu, T.J., Nephawe K.A and Mtileni, B. (2025). Utilisation of genome-wide SNP data revealed Genetic Diversity of South African indigenous goat population. *South African Journal of Animal Sciences (in-press)*.

CONFERENCE PROCEEDING: APPENDIX H

Chokoe, T.C., Tada O., Mdladla-Hadebe, K., Muchadeyi F., Dzomba, E., Matelele, T.C., Mphahlele, T.D., Mpofu, T.J., Nephawe, K.A and Mtileni, B.J. (2024). Utilisation of Genome-Wide SNP Data Revealed Genetic Diversity in South African Indigenous Goat Population. The 54th South African Society of Animal Science Congress – East London, South Africa, 02 – 05 July 2024.

Abstract

Genome-wide assessments of the genetic landscape of Farm Animal Genetic Resources (FAnGR) are key to developing sustainable breed improvements. Understanding the FAnGR adaptation to different environments and supporting their conservation programs from community initiative to national policymakers is very important. The objective of the study was to investigate the genetic diversity and population structure of communal indigenous goat populations from four provinces of South Africa. Communal indigenous goat populations from the Free State (FS) (n = 24), Gauteng (GP) (n = 28), Limpopo (LP) (n = 30), and North West (NW) (n = 35) provinces were genotyped using the Illumina Goats SNP50 BeadChip. An Illumina Goats SNP50 BeadChip data from commercial meat-type breeds: Boer (n = 33), Kalahari Red (n = 40), and Savanna (n = 31) were used in this study as reference populations. The H_o revealed that the genetic diversity of a population ranged between 0.39 ± 0.11 H_o in LP to 0.42 ± 0.09 H_o in NW. Analysis of molecular variance revealed variations of 3.39% (p < 0.0001) and 90.64% among and within populations, respectively. The first two Principal Component Analyses (PCAs) revealed a unique Limpopo population separated from GP, FS, and NW communal indigenous goat populations with high levels of admixture with commercial goat populations. There were unique populations of Kalahari and Savanna that were observed and admixed individuals. Marker F_{ST} (Limpopo versus commercial goat populations) revealed 442 outlier single nucleotide polymorphisms (SNPs) across all chromosomes, and the SNP with the highest F_{ST} value (F_{ST} = 0.72; chromosome 8) was located on the *UHRF2* gene. The study revealed that the SNPs identified by the first two principal components show high F_{ST} values in LP communal goat populations and allowed us to identify candidate genes which can be used in the development of breed selection programs to improve this unique LP population and other communal goat population of FS, GP, and NW, and find genetic factors contributing to the adaptation to harsh environments. Effective management and utilization of South African communal indigenous goat populations is important, and effort should be made to maintain unique genetic resources for conservation.

Keywords: *genetic diversity, communal indigenous goat population, Heterozygosity, commercial breeds, SNP genotype*

5.1 Introduction

South Africa has a great diversity of agro-ecological zones and abundant Farm Animal Genetic Resources (FAnGR). It has more than 6 million indigenous goats, which are distributed across geographic regions of South Africa (DAFF, 2014). The majority of South African goats are indigenous and are kept by small holder farmers in communal areas under extensive production system (Matshaba *et al*., 2010). The four provinces combined in this study contribute more than 51% of the communal indigenous goat populations of the country (DAFF, 2014; DALRRD, 2018). Morphological differences have important socio-cultural and economic values to the rural communities and as a result, most farmers have specific considerations and choices for goat coat colors (Gwaze *et al*., 2009b; Mahanjana & Cronje, 2000; Chokoe *et al*., 2020). Diversity in indigenous goats is important for maintaining biodiversity and is the basis of conservation and genetic improvement. Although indigenous goats in Southern Africa have low growth rates, small body size, low milk yield, and low carcass weights, their characteristics such as adaptation to local feed resources and response to environmental factors; heat tolerance, and disease and parasite tolerance have a potential for improvement and conservation of these resources (Mdladla *et al.*, 2018; Monau *et al*., 2020).

Indigenous goat populations have also been used to produce improved breeds with good meat quality and high reproduction, such as the renowned Boer, Savanna, and Kalahari Red breeds. The Boer goat can be traced back to the Dutch farmers of South Africa in its early stage of development as a breed (Casey & Van Niekerk, 1988). According to the Boer Goat Breed Association, the earliest breeding stock was a result of crossing between the shorthaired female goats that had white bodies and light-colored heads with a large dapple-colored male goat. Kalahari Red goats were developed from two lines of the brown lop-eared ‘unimproved’ indigenous goats in South Africa and Namibia, and of the Boer goats (Campbell, 2003). In 1991, selection of indigenous brown, and brown and white, goats from the former homelands of the Eastern Cape, the Karoo, and Namibia was also conducted by Albie Horn (http://studbook.co.za). In 1957, Messers Cilliers and Sons selected the white Savanna from indigenous goats (Campbell, 2003). The Savannah goat was first recognized as a distinct breed in the early 1990s, which resulted in the formation of the Savanna Goat Breeders Society on 21 November 1993.

Furthermore, the migration and evolution of goats have always been closely linked with human migration (Campbell, 2003), and understanding their evolution can shed light on understanding human migration and culture. The history of indigenous FAnGRs and their adaptation to marginalized production systems, unfavorable environmental conditions, and human selection pressures is an important contributor to their diversity and survival. In turn, these FAnGRs dominate the communal production systems, which are often under extensive management with minimal production inputs. The societal importance of communal indigenous goats, including during marriage, cleansing, birth, death, and initiation ceremonies plays an important role to be termed the so-called "poor man's cow", as they refer to their role as the source of food and income (Monau *et al*., 2020).

It is expected that the effect of natural selection (i.e., adaptation to the specific environment) is more ostensible in the communal indigenous goat population and has played an important role in their development, while commercial breeds are subjected to more intense artificial selection (Onzima *et al*., 2018). Therefore, communal indigenous populations will tend to show the ability to use low-quality fodder, resistance to gastro-intestinal parasites, diseases, heat tolerance, and water scarcity. A small population with a cumulative effect on the overall expression of the phenotype highlights that adaptation is a complex trait that involves many biological processes and quantitative trait loci (Kim *et al*., 2016; Yang *et al*., 2016; Mwacharo *et al*., 2017).

The most promising method for the investigation of genetic diversity and population structure is the analysis of single nucleotide polymorphisms (SNPs), which started its journey over a decade ago through advances in availability of reference genomes and development of high-throughput genotyping platforms (Guo *et al*., 2018). Furthermore, the recent developments in genomic technologies resulting in the availability of the Illumina Goat 50K SNP BeadChip (Tosser-Klopp *et al*., 2014; Zhong *et al*., 2023) have presented the opportunity to search for genomic regions that may have undergone selection. Such studies in cattle (Makina *et al*., 2015; Zhao *et al*., 2015), sheep (Moradi *et al*., 2012; McRae *et al*., 2014) chickens (Stainton *et al*., 2015), and pigs (Ai, 2013; Ai *et al*., 2014) each have identified genes that have undertaken a positive selection and are likely to contribute directly to phenotypic variation. Furthermore, genetic diversity studies on local and international goat breeds, e.g., Italian (Nicoloso *et al*., 2015), Moroccan (Benjelloun *et al*., 2015), and South African (Lashmar *et al*., 2015; Mdladla 2016; Magoro *et al*., 2022; Kropff, 2023), were conducted. Additionally, regarding goat genetic diversity, more studies on goat 52 K single nucleotide polymorphism chip have been available for some time (Tosser-Klopp *et al*., 2014; Zhang et al., 2021)) and has already been used for national and multi-country goat diversity studies (Ağaoağlu & Ertuğrul, 2012; Brito *et al*., 2017; Mdladla, 2016). Using this standardized tool for genotyping, the AdaptMap initiative (Stella *et al*., 2018) gathered a dataset that includes genotypes of 148 goat populations which successfully investigated the distribution of goat genetic variation around the world, compared the present-day diversity patterns to those observed in ancient goat samples and in other ruminant livestock species, as well as reconstructed admixture and migration events that have shaped goat post-domestication history.

Studies on population structure and genetic diversity are important for describing the natural selection history and genetic relationships among FAnGR (Mukhongo *et al*., 2014). The genome-wide assessments of the genetic landscape of FAnGRs' are a key aspect of developing sustainable breed improvement strategies and understanding adaptations to extreme environments (Mdladla *et al*., 2017; Xu *et al*., 2018; Zhong *et al*., 2023). Additionally, it has value in supporting conservation programs from community initiatives to national policy makers. To facilitate the rapid adaptation to changing environments, maintaining local genetic resources is very much required. The objective of this study was to investigate the population structure and genetic diversity of communal indigenous goat populations from four provinces of South Africa.

5.2 Materials and Methods

All work was conducted according to the guidelines provided by the animal research ethics committee (TREC) of the University of Limpopo (UL); Registration Number: **TREC/114/2024: PG (Appendix B).**

5.2.1 Population description and sampling

A total of 117 Communal indigenous goat populations were systematic random sampled from Free

State (*n* = 24), Gauteng (*n* = 28), Limpopo (*n* = 30) and North West (*n* = 35) provinces of South Africa (Figure 5.1). Sampling strategy targeted the major goat producing provinces of South Africa (Figure 1). From each animal, blood samples were collected by jugular venipuncture into 6-ml EDTA vacutainer tubes (Greiner Bio-One, GmbH). The DNeasy" Blood and Tissue Kit (Qiagen) was used to extract Genomic DNA, as per the manufacturer's instructions. A 1% agarose gel electrophoresis and Qubit" 3.0 Fluorometer (Life Technologies) used to determine DNA quality and quantity respectively. Descriptions of sampling locations and farms have been described in detail in (Mdladla *et al*., 2017).

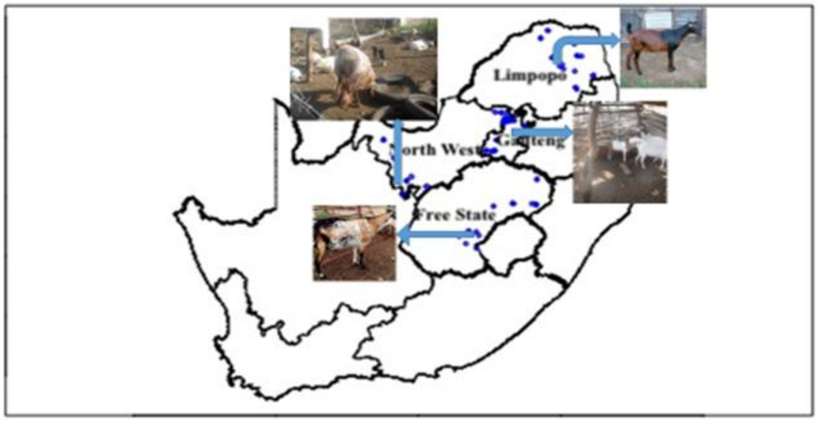


Figure 5.1 South African map showing geographical location of communal indigenous goat populations.

5.2.2 Genotyping and Quality control

The Illumina Goats SNP50 BeadChip (Tosser-Klopp *et al.*, 2014) was used to genotype DNA samples by using the Infinium assay compatible with the Illumina HiScan SQ genotyping platform at the Agricultural Research Council-Biotechnology Platform, South Africa. The BeadChip was developed by the International Goat Genome Consortium (IGGC) with more than 50K SNPs across the whole genome with an inter-SNP spacing of approximately 40 kb (Tosser-Klopp *et al.*, 2014). The genotype input file was converted into a PLINK and SNP calling rate using the Illumina

Genome Studio v2.0 (Purcell *et al*., 2007) map/ped input file. Information on the chromosome number, chromosomal position, and Golden Helix SVS v8.3.4 (Golden Helix, Bozeman, MT, USA) were used to update the SNP marker information. PLINK was used to perform individual and SNP quality control procedures (Purcell *et al*., 2007). The mind function procedure was used for analyses of individuals with a missing genotype call rate of greater than 5%, which were excluded for further analysis. The three samples that did not meet the quality control threshold (95%) included 2 individuals from Limpopo and 1 from Gauteng, and they were removed from the final dataset. The removal of SNPs with less than 95% call rate (*n* = 683), and less than 5% minor allele frequency *(n* = 1228) and HWE exact test *(n* = 123) resulted in a total of 47,908 autosomal SNPs available for downstream analysis. The average genotyping rate in the remaining 117 samples was 0.99. Additionally, to evaluate population structure and relatedness, commercial populations represented by Boer (*n* = 33), Kalahari Red (*n* = 40), and Savanna (*n* = 31) reference population data obtained from a previous study (Mdladla, 2016) were included. To prepare dataset 2, the same QC criterion was used, resulting in 46,081 SNPs and 195 individuals. In addition, a genome-wide identity-by-descent (IBD) similarity matrix was used to calculate and prune related individuals and the '–indep-pairwise 50 5 0.2-' command was used to remove one of every pair of SNPs with $r^2 > 0.2$ within 50-SNP sliding windows in PLINK (Purcell *et al*., 2007) for dataset 3. From the IBD threshold of greater than 0.40, denoting substantial relatedness, twenty-seven animals were removed, therefore data set 3 consisted of 20,873 SNPs and 168 individuals.

5.2.3 Genetic diversity

Minor allele frequency (MAF) was estimated for each of the four communal indigenous goat populations using PLINK (Purcell *et al*., 2007). The fixed alleles (MAF = 0.00), rare alleles (>0.00–<0.05), intermediate alleles (≥0.05 <0.10), and common alleles (≥0.10 and ≤0.5) were categories for alleles that were used in different bins based on their frequency. PLINK was used to estimate within-population genetic diversity, observed heterozygosity (H_o), and the expected heterozygosity (H_E) (Purcell *et al*., 2007). The observed heterozygosity (H_o) estimates for each population were calculated from observed genotype frequencies obtained from PLINK (Purcell *et al*., 2007) as follows: (N-O)/N (where N is the number of non-missing genotypes and O is the number of observed homozygous genotypes for a given individual). Expected heterozygosity (H_E)

estimates for each population were calculated from expected genotype frequencies as follows: (N-E)/N (where N is the number of non-missing genotypes and E is the number of expected homozygous genotypes for a given individual). Allelic richness (R_t) over all loci for each population was computed using ADZE Allelic Diversity Analyzer: Version 1.0.

5.2.4 Population structure analysis

AMOVA was executed using dataset 2 and analyzed using ARLEQUIN 3.5 after conversion map/ped file conversion to arp file using PGDSpider. Two groups: The commercial and communal indigenous goat populations were created by doing the significance of variance components for each hierarchical comparison (among populations, among individuals, among individuals within populations). The pairwise fixation indexes (F_{ST}) (Weir and Cockerham 1984) were used as a measure of genetic differentiation between population pairs using Golden Helix SVS v8.3.4 (Golden Helix, Bozeman, MT, United States). The Principal Component Analysis (PCA) was carried out using Golden Helix SVS v8.3.4 (Golden Helix, Bozeman, MT, USA), and to infer the most probable number of ancestral populations, ADMIXTURE 1.21 was used (Alexander *et al.*, 2009) using default settings. ADMIXTURE was run from K = 2 to K = 5. To explore the most probable number of clusters (K), ten-fold cross-validation (CV = 10) was specified, with the error profile obtained thereafter used as described by (Alexander *et al.*, 2009). The GENESIS software was used for graphical display of the admixture output and was also used to visualize admixture plots (Buchmann & Hazelhurst, 2014).

5.2.5 Identification of signatures of selection

Identification of signatures of divergent selection between populations using population differentiation (*Fst*) was calculated using Golden Helix SVS v8.3.4 (Golden Helix, Bozeman, MT, USA) between the Limpopo population versus commercial goat populations: Boer, Savanna, and Kalahari Red. Outliers were identified, and a region was considered to be a high-F_{ST} outlier if it corresponded to the upper 1% of the empirical genome-wide distribution of F_{ST}. The second approach used PCAdapt (Luu, 2017) to find outlier SNPs. We first assessed the optimal Principal Components (PC) from 1 to 10 and then the candidate SNPs significantly correlated to the optimal

PCs. All outlier SNPs detected using both methods were mapped to gene-associated regions based on the goat genome annotation (ARS 1) on the BioMart database (www.ensembl.org/ biomart). The genes in regions with evidence for selection were searched against the Kyoto Encyclopedia of Genes and Genomes (KEGG, http://www.genome.jp/kegg/) pathways and literature search.

5.3 Results

5.3.1 Quality control and Genetic diversity

The mean minor allele frequencies (MAFs) for Gauteng, Free State, Limpopo, and North West were 0.33 ± 0.11, 0.33 ± 0.11, 0.29 ± 0.12, and 0.33 ± 0.11, respectively, with an overall mean of 0.32 ± 0.12 across the Communal indigenous populations. Figure 5.2 presents minor allele frequency distribution for different categories in each population. The number of fixed SNPs (MAF = 0.00) varied from 5 in North West populations to 151 in Limpopo. Polymorphic SNPs were high (<90%) across all populations. The allelic richness for Gauteng, Free State, Limpopo, and North West were 1.99 ± 0.02, 1.99 ± 0.02, 1.99 ± 0.05, and 1.99 ± 0.01, respectively, and with the mean number of alleles per locus being 1.99±0.03 across the communal indigenous populations.

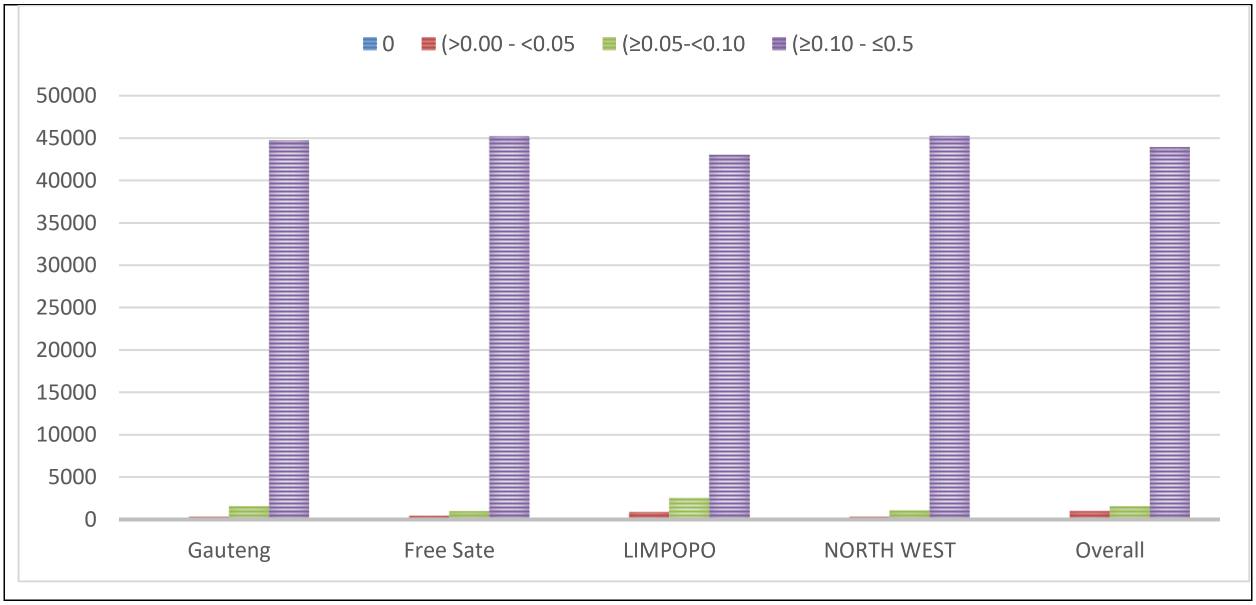


Figure 5.2 Distribution of minor allele frequencies (MAF) in Communal indigenous goat populations.

The H_o reflects the genetic diversity and history of a population, with Free State and Gauteng having an H_E of 0.40±0.13 and H_O of 0.41±0.09; North West recording an H_E of 0.39 ± 0.1 and H_O of 0.42 ± 0.09; and Limpopo recording an H_E of 0.38 ± 0.14 and H_O of 0.39 ± 0.11.

5.3.2 Source of variation and population structure

Analysis of AMOVA revealed variation of 3.39% ($p< 0.0001$) and 90.64% among and within populations, respectively (Table 5.1).

Table 5.1 Analysis of Molecular Variance analysis using different data sets of commercial goat populations.

Source of variation	Degrees of difference (d.f)	Sum of Squares	Variance components	Percentage of variation
Among populations	1	80565.150	341.26752 Va	3.39
Among population within groups	5	99867.875	185.19042 Vb	1.84
Among individuals within populations	182	1814879.906	416.85973 Vc	4.12
Within populations	189	1727110.000	9138.14815 Vd	90.64

The PCA of the Communal indigenous goat and commercial goat populations is presented in Figure 3. The analysis ignores population membership but reveals clear population structures as samples from the same population cluster together. The first two PCs, separated Limpopo population (Cluster 1), and Cluster 2, consisting of Gauteng, Free State, and North West populations, whilst Cluster 3, Cluster 4, and Cluster 5 consisted of commercial goat populations. Additionally, outliers were evident for the Cluster 2 populations in Cluster 3. The Communal indigenous goat populations provided weak sub-structuring with an overlap of populations from Free State, Gauteng, and North West.

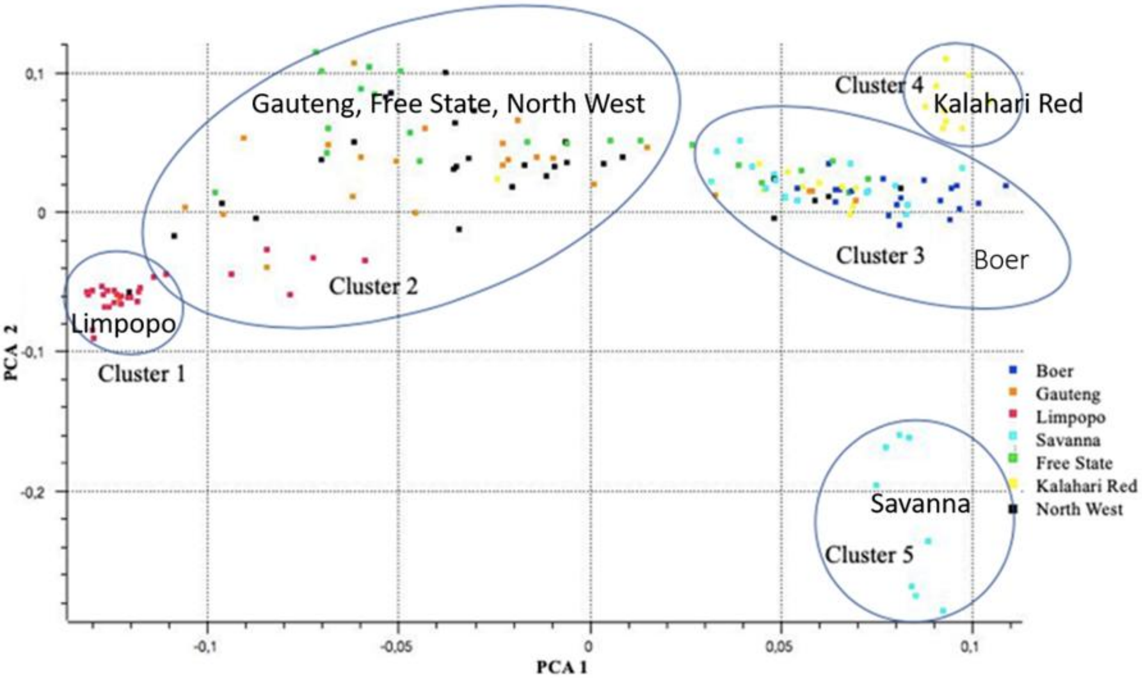


Figure 5.3 Plot of two principal components showing genetic relationships among the commercial goat populations: Boer, Kalahari Red and Savanna with the Communal indigenous goat populations from Free State, Gauteng, Limpopo and North West.

In Figure 4, ADMIXTURE was used to further understand the degree of admixture in the populations and increased *K* from 2 to 5, where *K* is the assumed number of ancestral populations. K = 2, Limpopo separated, and a subset of Kalahari Red was revealed. K = 3 revealed two sub-groups of the Savanna goats and Boer that shared genetic background with the Savanna. The analysis suggested *K* = 3 (CV error = 0.65048) as the most likely number of genetically distinct groups, reflecting three genetic backgrounds (Figure 5.5). At K = 4, communal indigenous goat populations from Gauteng, Free State, and North West showed clear evidence of genetic heterogeneity, with shared genome ancestry with other populations. Increasing values of *K* to 5 indicated higher levels of breed homogeneity in the Limpopo population, shown as Cluster 1 of PCA (Figure 5.4). Increasing *K* beyond 5 did not reveal any new distinct clusters or patterns.

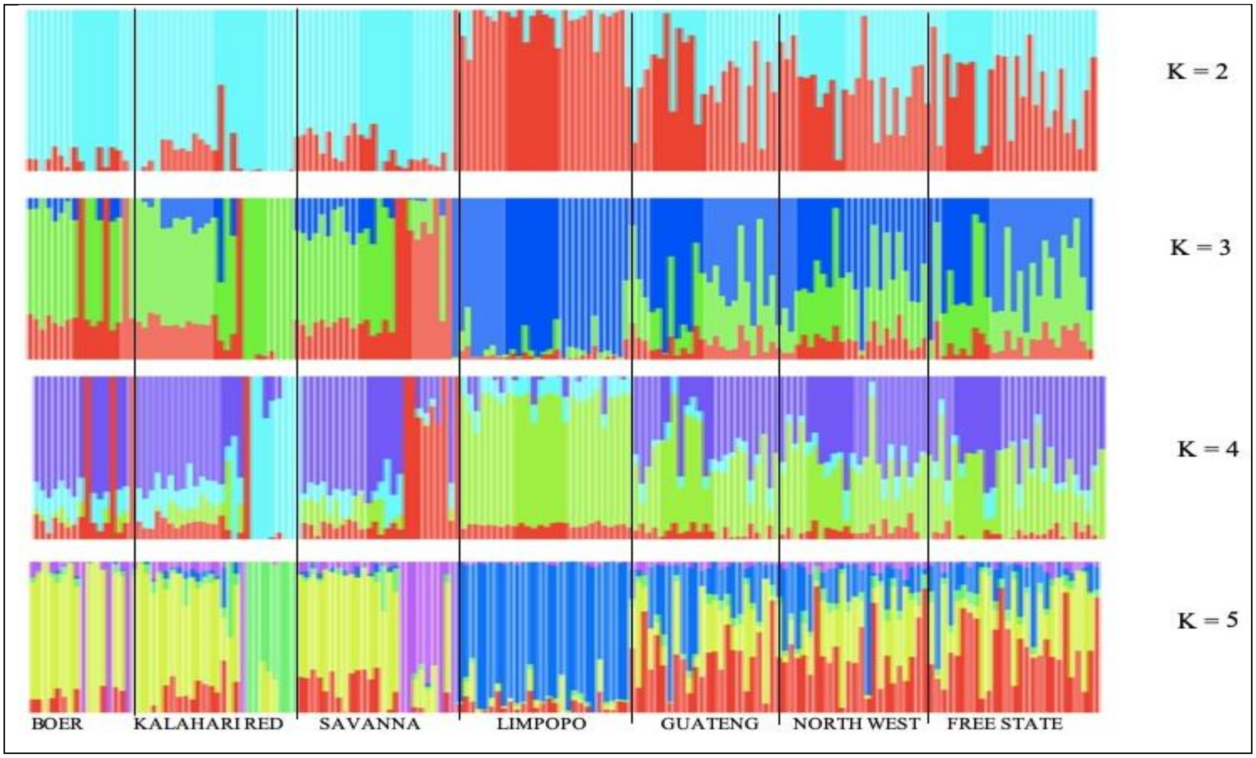


Figure 5.4 Population structure plots showing proportions of ancestral populations for each individual for K = 2 to 5.

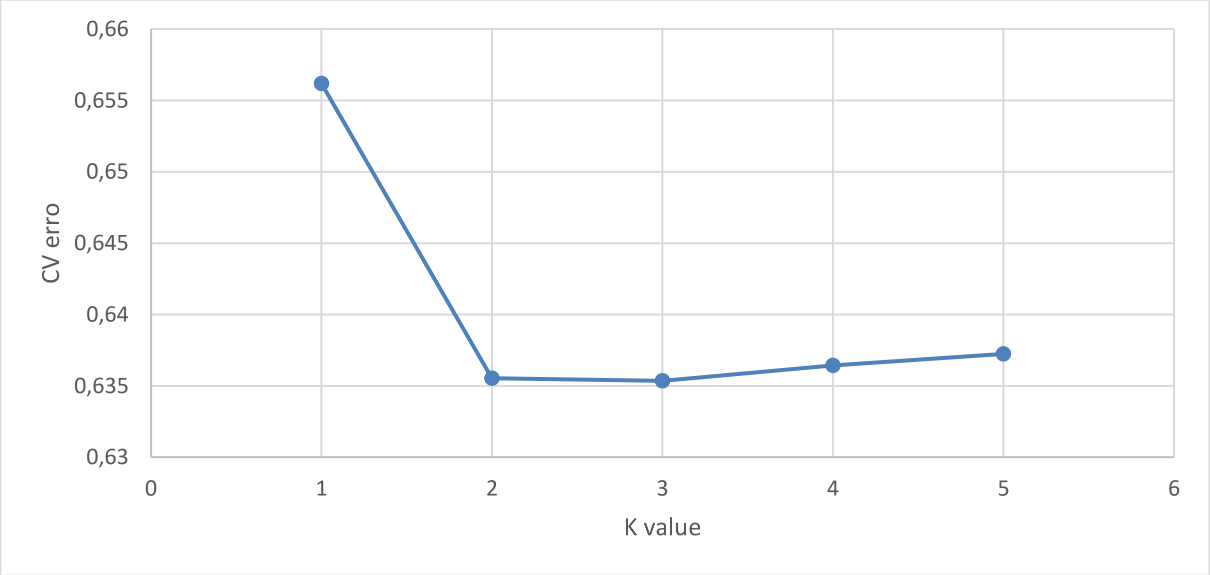


Figure 5.5 Cross-validation (CV) error for the optimal *K* value.

The pairwise mean F_{ST} supports the population relationships based on PCA and ADMIXTURE. High F_{ST} (F_{ST} = 0.084) was shown between the Limpopo population and commercial goat populations (Boer, Kalahari Red, and Savanna). A low F_{ST} value (range 0 to 0.038) within the Communal indigenous goat populations was found, indicating a low genetic differentiation between these populations as shown in Figure 5.6 and and APPENDIX C.

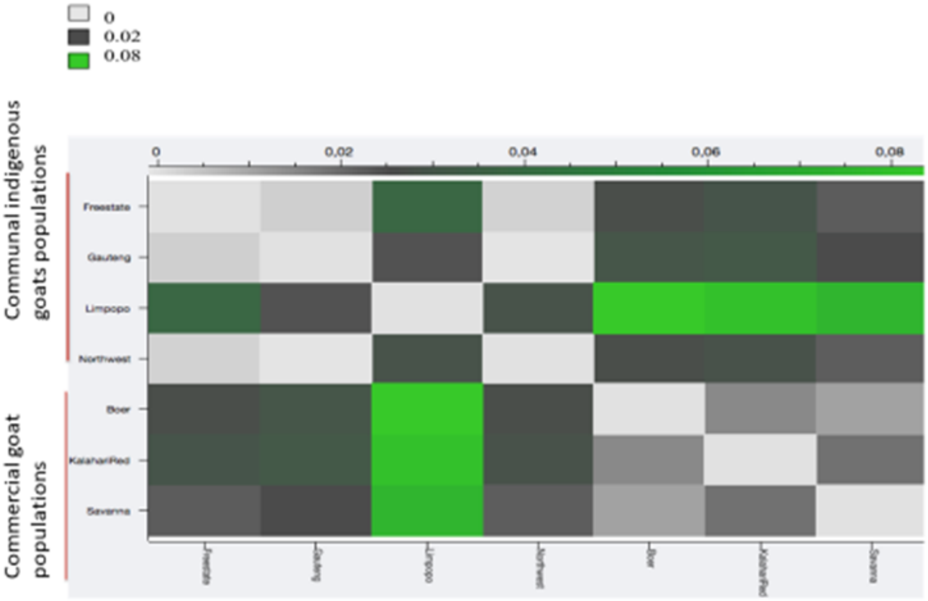


Figure 5.6 F_{ST} distances for Communal indigenous goat population from Free State, Gauteng, Limpopo and North West with commercial goat populations.

5.3.3 Candidate genes under selection

A total of 442 differentiated SNPs with an F_{ST} threshold ≥ 0.47 were considered to be under selection. The distribution of F_{ST} across all chromosomes is shown in Figure 5.7. Outlier SNPs were found across all chromosomes with varying numbers. In general, bigger chromosomes had a higher number than the smaller chromosomes. Chromosome 8 had the highest number with 37 SNPs, and chromosomes 28 had 4 SNPs.

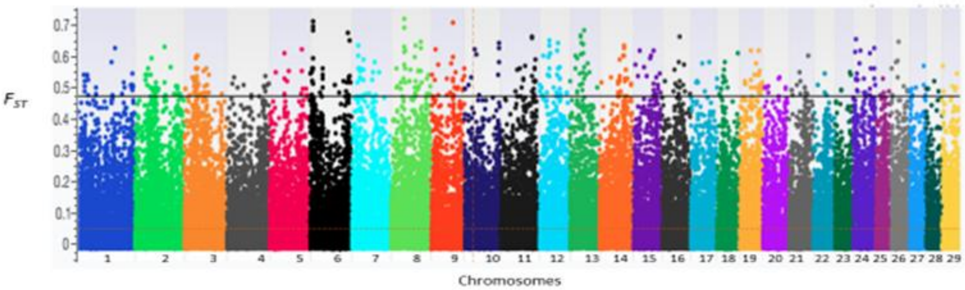


Figure 5.7 Manhattan plot Limpopo versus commercial goat populations Boer, Savanna and Kalahari Red.

Table 5.2 shows the top ten SNP and additional file 1, Table S1 has the full list of outlier SNPs. The SNP with the highest F_{ST} value (F_{ST} 0.72) was at chromosome 8 and sits on the *UHRF2* gene. The 133 candidate genes (APPENDIX D) were adjacent to these outlier's loci that were associated significantly with pathways involved in the immune system, thermoregulation, and longevity (APPENDIX E). The other four important genes from the top ten outlier SNPs that were found include with the F_{ST} value (F_{ST} 0.69) at chromosome 8 which sits on the *GLDC* gene, F_{ST} value (F_{ST} 0.68) at chromosome 6 which sits on the *NDST3* gene, F_{ST} value (F_{ST} 0.68; 0.67) at chromosome 13 which sits on the *CFAP61* and CUBN genes, respectively.

Table 5.2 Top ten outlier SNPs for the estimated chromosomes and genes using F_{ST}.

Marker	CHR	Position	F_{ST}	Gene	Gene Description
snp28078-scaffold300-3412212	8	38197294	0.72	UHRF2	ubiquitin like with PHD and ring finger domains 2
snp19368-scaffold1958-104157	6	8034538	0.71	-	
snp3556-scaffold1110-106176	9	59365070	0.70	-	
snp19366-scaffold1958-28303	6	8110392	0.69	-	
snp28077-scaffold300-3369813	8	38154895	0.69	GLDC	glycine decarboxylase
snp51703-scaffold760-153052	6	7438269	0.68	NDST3	N-deacetylase and N-sulfotransferase 3
snp32526-scaffold371-1443673	13	39230563	0.68	CFAP61	cilia and flagella associated protein 61
snp48555-scaffold690-432877	6	104631767	0.67	-	
snp49002-scaffold7-1603772	13	30788222	0.67	CUBN	cubilin
snp49005-scaffold7-1739012	13	30652982	0.66	CUBN	cubilin

Outlier detection using principal components (PCs) shows the decay of eigenvalues confirmed to the use of K = 2 as optimal (Figure 5.8a). The Q-Q plot confirmed the expected uniform distribution of the *p*-values (Figure 8b). Figure 8c shows a Manhattan plot indicating the outlier SNPs that have been detected based on the expected FDR equal to 10%.

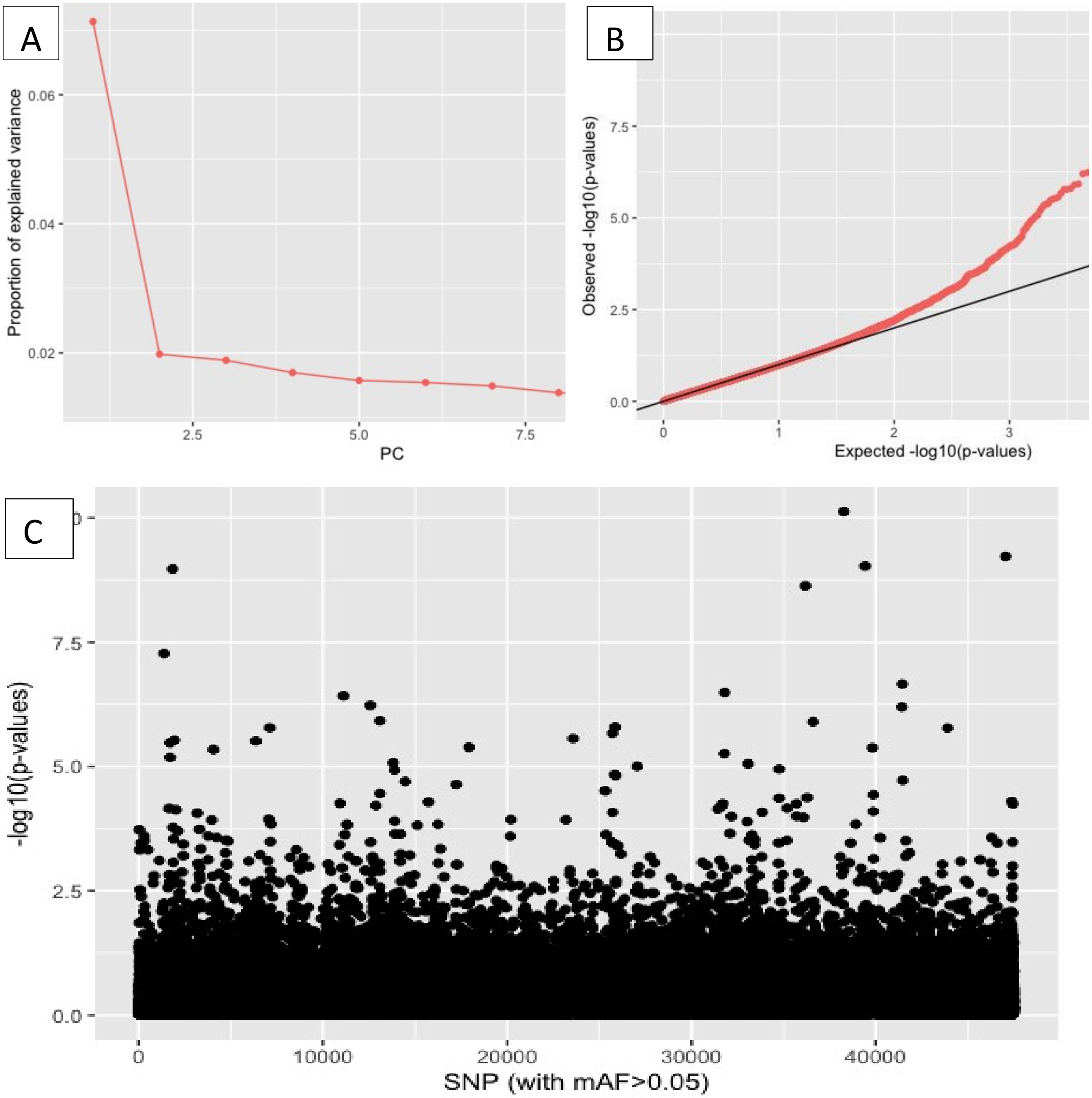


Figure 5.8 Detection of outlier SNPs using Principal Components (PCs). a) shows the scree plot of the PCs; b) Q-Q plot for the distribution of the p-values; and c) Manhattan plot for the SNP.

The results show that twenty-five outliers were significant to each PC, however, only 5 could be retained (Table 5.3). The 5 SNPs were found on chromosomes 10, 15, 20 and 21 and were associated with the PC2. In this study, the gene search did not reveal any genes.

Table 5.3 Outlier SNPs using Principal Components.

Marker	**Chromosome**	**Position**	**PC**
snp2141-scaffold1065-308545	10	74803720	2
snp32432-scaffold37-603475	15	12584499	2
snp32448-scaffold37-1273016	15	13254040	2
snp34005-scaffold40-2680622	20	50848470	2
snp15603-scaffold165-514510	21	53972419	2

PC – principal component

5.4 Discussion

The ability to adapt to a changing environment is the genetic diversity of indigenous FAnGR, as they provide information to support improvement and conservation efforts. To design genetic improvement and conservation strategies at national and global levels, information on within and between genetic diversity and population structure becomes paramount (Tittensor *et al.*, 2014). In this study, population structure and genetic diversity of communal indigenous goat populations from the goat producing provinces of Free State (FS), Gauteng (GP), Limpopo (LP), and North West (NW) provinces were investigated.

Communal indigenous goat populations are genetically diverse, exclusive, and are adapted to particular production systems, and their value of diversity has been strongly emphasized (Morrison, 2007; Mdladla *et al*., 2017; Zhong *et al*., 2023). The overall mean of the minor allele frequency (MAF) was 0.32 ± 0.12 across the communal indigenous goat populations. It has been indicated that the communal indigenous goat populations were more diverse than the commercial goat populations with regards to the observed within-population diversity measures. These results support the findings by Mdladla, (2016) on the Communal indigenous goat population, where goat ecotypes of Venda and Zulu showed the maximum number of alleles per locus.

The number of fixed SNPs (MAF = 0.00) varied from five in NW populations to 151 in LP populations. Polymorphic SNPs were high (<90%) for all populations. The mean MAFs were estimated on 49,942 SNPs and 117 (<0.95 call rate) individuals for FS, GP, LP, and NW, respectively, with an overall mean of 0.32 ± 0.12 across the communal indigenous goat populations. The results are comparable to the results from Lashmar *et al*. (2015), who recorded 43,759 (82.03%) observed for the South African Angora breed and Mdladla *et al*. (2017) observing the overall proportion of informative SNPs (87.09%). In this study, the level of polymorphic SNPs was at a 95% call rate threshold, which was similar to the study of Mdladla, (2016), whilst in Lashmar *et al*. (2015)'s study, it was a 98% call rate threshold, which was higher for the Angora goat breed. The importance of the differences in the SNP quality control thresholds has to be emphasized, as it has an influence on the resultant proportion of useful SNPs.

Analysis of the distributions of alleles across populations is important for evaluating genetic diversity and population relationships (Kalinowski, 2004). Allelic richness was identical to allele frequency, implying that there was no bias based on sample size. The low levels of allelic diversity indicate that the communal indigenous goat populations are experiencing low levels of nonrandom mating when bred and not maintaining allelic diversity over the entire populations. The level of allelic diversity in this study was similar to that reported for nine Chinese cashmere goats, but lower than in the Chinese cashmere (Kalinowski, 2004) and Swiss (Glowatzki-Mullis *et al*., 2008; Liu, 2013) goat populations. The high mean number of alleles per locus and expected heterozygosities indicated that the overall gene diversity was high in the population.

A key point to design/update breeding programs and conservation strategies is represented by genomic characterization of the genetic diversity of breeds. Communal indigenous goat populations from the four provinces of FS, GP, LP, and NW have not been comprehensively studied for population structure and diversity, thus genetic characterization of these populations is of paramount importance. Heterozygosity was calculated to determine genetic variation ranging from 0.42±0.09 in NW and 0.39 ± 0.11 in LP. Monau *et al*. (2020) reported heterozygosity values ranging from 0.387 in Swazi goats and 0.41 in Tswana goats, whilst Mdladla *et al*. (2016) reported similar values for communal indigenous goat populations. Nicoloso *et al*. (2015) showed levels of H_o ranging from 0.35 to 0.41 for 14 Italian goat breeds using the same SNP Beadchip, whilst Brito *et al*. (2017) revealed low values in Nubian goat populations (0.338) and high values in (0.413) rangeland goat populations. Management practices that caused breed segregation were reported to be responsible for the low H_o that characterizes the Malawi populations, whereas the high H_o observed for populations in East Africa most likely mirror admixture by crossbreeding (Colli *et* *al*., 2018). An increase in heterozygosity due to pastoralism and nomadism was frequently reported in sheep (Zhao *et al*., 2017; Tapio *et al*., 2010) and is consistent with specific geographical patterns in Iranian goats (Vahidi *et al*., 2014). These similarities between the studies in heterozygosity values may be attributed to the overlap of geographical locations and the use of population types under similar production environments used. More similarities in H_E and H_o in some of the populations may be due to the use of populations/breeds which were previously not used during the development of the 50 K SNP panel, as it was noted in other Southern African indigenous goat populations such as the Binga, Chipinge, Matopo, and Shurugwi goat populations of Zimbabwe (Zvinorova, 2017). This can suggest that these values represent the genetic diversity levels of the communal indigenous goat populations.

In the study, it was shown that populations can be exploited through appropriate breeding strategies to improve productivity, as large within-population variation (90.64%) was observed. It was revealed that the level of the among-population genetic variation was lower than that reported in commercially developed breed populations including Angora with 16.12% (Ozeje, 2002; Pieters, 2007). This high within-population variation is supported by population structure analysis. The PC1 and PC2 show the highest level of genetic heterogeneity and weak sub-structuring in the FS, GP, and NW provinces, which might be triggered by continuing crossbreeding with improved breeds to improve their productivity practiced in these regions (farmer communication). Limpopo Communal goat populations and commercial breeds had the highest F_{ST} (0.084), while GP populations had a low F_{ST} value (range 0 to 0.038). Indigenous breeds in the Southern African regions have shown high genetic diversity, but weak population sub-structuring (Onzima *et al*., 2018). The highest genetic distance (F_{ST}) was observed to be higher than 0.25, moderate to between 0.05 and 0.25, and the lowest estimate below 0.05 when microsatellite markers were used (Kalinowski, 2004). Many authors in sheep studies for genetic distance among most of the populations recorded F_{ST} values (0.101), (0.042) and almost negligible (<0.05) and/or moderate ($0.05 < F_{ST} < 0.25$) (Yang *et al*., 2016; Ahmed *et al*., 2014). Significant genetic distance estimates among populations were revealed by some of the authors. Among the goat populations, there is relatively low to moderate genetic sub-differentiation. An indication of significant differentiation among populations is considered to be a fixation index (F_{ST}) of about 0.15 (Brito *et al*., 2017).

The commercial goats from different geographical areas and breeding backgrounds provided stronger sub-structuring. According to Mdladla *et al*. (2016), samples were taken from a farm with closed populations of Savanna and Kalahari Red in Griquastad, Northern Cape, and these populations were used as reference populations. The Kalahari Red and Savanna populations that were found to be kept in commercial farms, corporations, and research stations showed levels of admixture. In shaping the differentiation of breeds, isolation by geographical distance can play an important role, however, in the populations under study, management and breeding strategies seem to have more effect. The PCA, ADMIXTURE, and pairwise F_{ST} results agree, thus emphasizing the exclusive genetic diversity and clustering populations according to the breed type and production system of communal indigenous goat population of Limpopo.

Searching for genomic regions that show high levels of differentiation between populations or by looking for regions of low genetic diversity within a population is possible by detection of signatures of selection from genotype data (Bertolini *et al*., 2018; Zhang *et al*., 2021). In this study, 442 and 5 SNPs based on the F_{ST} and PC analysis, respectively, were identified. The 5 SNPs were related to PC2, which showed communal indigenous goat population of Limpopo as having a unique genetic background. The SNP with the highest F_{ST} value (F_{ST} 0.72) was identified to be at chromosome 8 and sits on the *UHRF2* gene. Islam *et al*. (2019), reported that selected genes in other studies on sheep were mostly enriched in biological processes, including metabolic processes, regulation of biological processes, developmental processes, and reproductive processes. An additional four important genes from the top ten outlier SNPs were discovered with the F_{ST} value (F_{ST} 0.69) at chromosome 8 sits on the *GLDC* gene, F_{ST} value (F_{ST} 0.68) at chromosome 6 sits on the *NDST3* gene, and F_{ST} value (F_{ST} 0.68; 0.67) at chromosome 13 sits on the *CFAP61* and *CUBN* gene, respectively. The candidate genes found in this study were involved in pathways involved in metabolism, disease response, thermoregulation, and longevity. In other studies that investigated coat color, (Bertolini *et al*., 2018) detected regions on chromosomes 5, 13, and 18 in the black vs. white comparison, regions on chromosomes 5, 9, and 13 in the white vs. black and red comparison, and regions on chromosomes 8, 22, and 29 in the red vs. white comparison. Analysis of the data by (Bertolini *et al*., 2018) for the three groups of solid coat colors detected signatures of selection near at least five genes that are known to be involved in the color and pattern definition of the coat: *ADAMTS20, MC1R, ASIP*, *SOX18,* and *TIMP3*. Two of these genes (*MC1R* and *SOX18*) were specifically detected in the comparison between solid black and solid white individuals, whereas the remaining three were identified in both solid black vs. solid white and solid black and red vs. solid white groups.

The 133 candidate genes were adjacent to the outlier's loci that associated significantly with pathways involved in the immune system, thermoregulation, and longevity. In the study, chromosome 8 had the highest number with 37 SNPs, and chromosomes 28 had 4 SNPs. The results show that twenty-five outliers were significant to each PC, however, only 5 could be retained, which were found on chromosomes 10, 15, 20, and 21, and were associated with the PC2, while the gene search did not reveal any genes. Rahmatalla *et al.* (2017) has emphasized that studying differences in different genes could elucidate the underlying genetics of the differences between Sudanese goat breeds in regard to bone formation and body measurement characteristics, which is applicable to the South African communal indigenous goat populations. Significant roles in the processes of oocyte maturation, regulation of follicular growth, and ovulation in livestock is played by other enriched pathways, such as bile secretion (hsa04976), retrograde endocannabinoid signaling (hsa04723), the hippo signaling pathway (hsa04390), the oxytocin signaling pathway (hsa04921), and ovarian steroidogenesis (hsa04913) (Yang *et al*., 2016).

Genetic diversity observed between these communal indigenous goat populations with more attention on Limpopo populations provide a unique opportunity to conserve the population. The study confirms the observation that communal indigenous goat populations kept closer to the metropolitan cities have different production values, and therefore market seems to be more of a breeding factor for GP communal indigenous goat population. Crossbreeding with commercial goat populations, especially the use of the dominant Boer goat bucks, was in evidence. The impact of crossbreeding if not given attention by policy makers will have a negative impact on the genetic diversity of the communal indigenous goat populations and to their genetic merit, and thus conservation programs will be affected.

5.5 Conclusions

The communal indigenous goat populations showed a weak sub-structuring with admixed individuals with evidence of gene flow and shared genome ancestry with commercial goat populations, while the Limpopo population separated to form its own cluster. Further research is required to identify the genomic regions which are associated with different important environmental adaptation and economical traits in communal indigenous goat populations using the recent updated Illumina Goat 50K SNP BeadChip in other goat producing provinces of South Africa. The patterns of genetic diversity and population structure showed that effective management and utilization of South African communal indigenous goat populations is important, and effort should be made to maintain these unique genetic resources for conservation.

CHAPTER 6: STUDY FOUR

CONSERVATION STATUS AND HISTORICAL RELATEDNESS OF SOUTH AFRICAN INDIGENOUS GOAT POPULATIONS FROM COMMUNAL FARMING SYSTEM USING GENOME-WIDE SNP MARKER

Abstract

The objective of this study was to determine the conservation status and historical relatedness of South African communal indigenous goat populations using genome-wide SNP markers. Indigenous goats form the majority of populations in smallholder; low input, low output production systems and are considered an important genetic resource due to their adaptability to different production environments and support communal farming. Effective population size (N_e), inbreeding levels, and the runs of homozygosity (ROHs) are effective tools for exploring the genetic diversity and understanding the demographic history in efforts to support breeding strategies to use and conserve genetic resources. Across populations, the current N_e of Gauteng was the lowest at 371 animals, while the historical N_e across populations suggests that the ancestor N_e has decreased by 53.86%, 44.58%, 42.16% and 41.16% in Free State (FS), North West (NW), Limpopo (LP) and Gauteng (GP), respectively, over the last 971 generations. Genomic inbreeding levels related to ancient kinship (F_{ROH} >5Mb) was highest in FS (0.08±0.09) and lowest for Eastern Cape (EC) (0.02±0.02). A total of 871 ROH island regions which include important environmental adaptation and hermo-tolerance genes such as *IL10RB, IL23A*, *FGF9*, *IGF1*, *EGR1*, *MTOR* and *MAPK3* were identified (occurring in over 20% of the samples) in FS (*n* = 37), GP (*n* = 42), NW (*n* = 2) populations only. The mean length of ROH across populations was 7.76Mb and ranged from 1.61Mb KwaZulu-Natal (KZN) to 98.05Mb (GP and NW). Distribution of ROH according to their size showed that the majority (*n* = 1949) of the detected ROH were >5Mb in length than the other categories. Assuming two hypothetical ancestral populations, the population from KZN and LP are revealed, supporting PC 1. The genomes of KZN and LP shared an origin but have substantial admixture from the EC and NW populations. The findings revealed that the occurrence of high N_e and autozygosity varied largely across breeds in communal indigenous goat populations at recent and ancient events when a genome-wide Single nucleotide polymorphism (SNP) marker was used. The use of Illumina goat SNP50K BeadChip shows that there was a migration route of communal indigenous goat populations from the northern part (LP) of South Africa to the eastern areas of the KZN, that confirmed their historical relatedness and which coincide with the migration periods of the Bantu nation.

Keywords: *runs of homozygosity; effective population size; populations; genomic inbreeding*

6.1 Introduction

There are currently 15 South African goat genetic resources listed on the DAD-IS of FAO and 13 on the Domestic Animal Genetic Resources Information System (DAGRIS) of the International Livestock Research Institute, including those listed in DAD-IS. In the country, indigenous goat ecotypes have been used as triple purpose animals (e.g skin, milk and meat); and depending on the region, the animal characteristics, and the geographical isolations, they began to diverge into breeds/populations (Visser *et al*., 2016). These ecotypes have generally been named after their place of origin (e.g Northern Cape Skilder) and/or their prominent characteristics (e.g Xhosa lobbed ear) and on basis of the people who own them (e.g Nguni) (Morrison, 2007). These ecotypes are widely spread across all major agro-ecological regions of South Africa displaying adaptability traits to a specific habitat or production environment and represent a significant resource to satisfy present and future demands for sustainable farming in a changing environment.

Improvement of indigenous livestock has been practised through the introduction of high performing breeds (exotic and improved breeds) and as a result of indiscriminate mating and breeding, the majority of communal indigenous goat populations are crossbreds (Mdladla *et al*., 2016a). The majority of the smallholder farmers have small herds or flocks where herd sizes could be less than five animals with the majority of these herds being non-descript, crossbred or indigenous cattle, sheep and goats (Mthi *et al*., 2017; Nyamushamba *et al*., 2017). The reduction in local indigenous populations suggests a need for conservation of local genetic resources through implementing a national conservation strategy. Various studies conducted in the smallholder communal areas showed average flock sizes of between 1 and 120 goats (Webb & Mamabolo, 2004, Dube, 2015). Furthermore, about 70% of the goats are kept under traditional management systems where the farm structure comprises of about twenty (±20) indigenous goats (Monau *et al*., 2020). A detailed information on the phenotypic, genetic diversity and population structure of goat's ecotype populations become important to guide conservation strategies through utilisation of these populations. According to (FAO, 2015b), conservation and characterisation of animal genetic resources is critical because of their contribution to the sustainable livelihoods of rural communities that depend on them for food security. Conservation frameworks should incorporate both genetic diversity and breed merits for prioritizing breeds/populations from community to national level to support breeding programs of current populations.

In South African more extensive research studies on genetic diversity analyses were done using microsatellite markers that were instrumental in providing an insight into the genetic structure and variation among South African goat populations (Kotze *et al*., 2004; Visser *et al*., 2004; Kotze *et al*., 2014). Kotze *et al*. (2014) observed average heterozygosity of 63% in Kalahari Reds using 18 microsatellites markers nine of which were used in the study by Visser *et al*. (2004). Recently, microsatellites have been used to study genetic variation of the Tankwa feral goat population, which showed it to be highly divergent from the other farmed populations (Kotze *et al*., 2014). In spite of their common use in most livestock diversity studies, microsatellites are often criticized for their usual location in the non-coding regions of the genome and for not being directly associated with genes that affect phenotypes. This has led to low-density microsatellites finding little application in studies of adaptive genetic diversity of local breeds.

The completion of the first draft of the goat genome (Dong *et al*., 2013) made it possible for the development of high-density markers (Tosser-Klopp *et al*., 2014). The Illumina goat SNP50K BeadChip includes 53 347 SNPs (Tosser-Klopp *et al*., 2014) that have found utility in South African population genetic studies in Angora (Lashmar *et al*., 2016), commercial, indigenous and village goat populations (Mdladla *et al*., 2017) as well as investigate genetic adaptation to environmental pressures (Mdladla *et al*., 2018). The use of the tool has been described in other African countries (Zvinorova, 2017; Onzima *et al*., 2018) and in specialised breeds (Martin *et al*., 2016). In South Africa, research work on the use of Illumina goat SNP50K BeadChip to determine the differences of indigenous communal goats at a point of genetic background is limited as compared to the studies where microsatellites were used. Therefore, while much work on South African commercial, indigenous and village goat populations has focused on genetic studies and investigation on genetic adaptation, less work has focused on conservation status and historical relatedness of communal indigenous goat populations.

The presence of the extent of an effective population size (*Ne*), is an important population genetic parameter that has recently received a great deal of research attention (Zhao *et al*., 2014), determining population demographic development (Deng *et al*., 2019; Sobrinho *et al*., 2024) and demographic processes such as migration and admixture (Nicoloso *et al*., 2015), and having profound implications for understanding the architecture of the animal genome (Alvarenga *et al*., 2013; Lashmar *et al*., 2016; Zhong *et al*., 2023). In addition, *Ne* is widely regarded as one of the most critical population parameters because it measures the rates of genetic drift and inbreeding as well as affects the efficacy of systematic evolutionary forces such as mutation, selection, and migration (Shina *et al*., 2013). It also helps to discover population demographic history and allows for the prediction of the behaviour of genetic diversity through time. The *Ne* is estimated using the r^2 coefficient and measures the observed range and the amount of genetic variation within a frame of population genetics (Berihulay *et al*., 2019). It also provides information on the degree of inbreeding of the population under consideration (Flury *et al*., 2010; Asadollahpour *et al*., 2023). The *Ne* determines the amount of genetic variation, genetic drift, and linkage disequilibrium (LD) in populations (Liu *et al*., 2017). Implementation of a national conservation strategies for FAnGR must be based on a better understanding on the degree of inbreeding of the populations, genetic variation, genetic drift, and linkage disequilibrium (LD) in populations.

An increase in inbreeding (*F*) over generations leads to a reduction in genetic diversity (Onzima *et al*., 2018). Higher frequency of homozygous genotypes for deleterious alleles with a reduction in individual performance (inbreeding depression) and lower population viability (Ouborg *et al*., 2010). Offsprings may inherit autozygous chromosomal segments from both parents that are identical by descent (IBD), when they are inbred, i.e., segments that are derived from a common ancestor (Brownman & Weber, 1999). The result is the runs of homozygosity (ROH), also known as the continuous homozygous segments in the genome. The ROH are contiguous lengths of homozygous segments of the genome where the two haplotypes inherited from the parents are identical (Gibson *et al*., 2006).

The extent of ROH can be used to estimate the inbreeding coefficient (Bosse *et al*., 2012; Marras *et al*., 2015; Peripolli *et al*., 2018), to disclose the genetic relationships among individuals, usually estimating with high accuracy the autozygosity at an individual and/or population level (Ferenčaković *et al*., 2011, 2013) Autozygosity is the homozygous state of identical-by descent (IBD) alleles, which can result from several phenomena such as genetic drift, population bottlenecks, mating of close relatives, natural and artificial selection (Curik *et al*., 2014; Lashmar et al., 2016). The level of selection pressure on the populations can also be established by the use of ROH (Zhang *et al*., 2015). Distant from more recent inbreeding may also be distinguished by the length and frequency of ROHs since the length of IBD segments follows an inverse exponential distribution with a mean of 1/2 *g* Morgans, where *g* is the number of generations from a common ancestor (Howrigan *et al*., 2011). Effective populations (*Ne*) and ROH have been studied in humans (Gibson *et al*., 2006), cattle (Ferenčaković *et al*., 2011; Marras *et al*., 2014; Mastrangelo *et al*., 2016), pigs (Ai *et al*., 2013; Shina *et al.*, 2013) sheep (Mastrangelo *et al*., 2017) but less comprehensively in other livestock species, such as goats for designing conservation strategies especially on the communal indigenous goats of South Africa. The objective of this study was to determine the conservation status and historical relatedness of South African communal indigenous goat populations using genome-wide SNP markers.

6.2 Materials and Methods

In this chapter, the procedures for which animal samples were collected followed the recommendation of directives as provided by the research ethics committee of the University of Limpopo; Registration Number: **TREC/114/2024: PG. (APENDIX B)**

6.2.1 Sample collection and genotyping

A total of 117 communal indigenous goat populations were sampled from Free State (*n* = 24), Gauteng (*n* = 28), Limpopo (*n* = 30) and North West (*n* = 35) provinces of South Africa. Additionally, genotypes of communal indigenous goat populations from (Mdladla, 2016) representing Eastern Cape (*n* = 20), KwaZulu-Natal (*n* = 30), Limpopo (*n* = 30) and North West (*n* = 20) provinces were included for further analysis.

All animals were genotyped using the Illumina GoatSNP50 BeadChip (Illumina Inc., San Diego, CA, USA) using the Infinium assay compatible with the Illumina HiScanSQ genotsyping platform at the Agricultural Research Council – Biotechnology Platform in SouthAfrica. A number of quality control measures were applied to all SNPs as follows: SNPs were removed if they had a call rate <95 %, a minor allele frequency (MAF) <0.05 and if deviated from the Hardy-Weinberg equilibrium (for a *P*-value cut-off of 0.00001), had no assigned genomic locations and on sex chromosomes were also excluded from the analysis. The parameter '–cow' was used to indicate the number (i.e., 29) of autosomes in the goat genome since cow and goat have the same number of autosomes. The final dataset included 47 778 SNPs and 207 individuals.

6.2.2 Genetic diversity indices

Historical and recent effective population sizes (N_e) for each breed were estimated with the *SNeP* (Barbato *et al*., 2015), which is based on the relationship between linkage disequilibrium (LD), N_e and recombination rate. The different SNP marker distance bins used for r^2 analysis were used to obtain different estimates of *Ne* at different time points by calculating the number of generations (t) in the past as 1/2c. To verify the accuracy of the coefficient of inbreeding the genomic coefficient was estimated via two methods. (1) PLINK (Purcell *et al*., 2007) was used to measure the inbreeding coefficient based on the difference between the observed and expected numbers of homozygous genotypes (F_{HOM}) using the function het. The calculation formula was as follows:

$$F_{HOM}= (E_{HOM} - O_{HOM})/ (L- E_{HOM}),$$

where L is the number of genotyped autosomal SNPs, E_{HOM} is the number of expected homozygous genotypes and O_{HOM} is the number of observed homozygous genotypes. The inbreeding coefficient based on the proportion of autosomes covered in runs of homozygosity per individual (F_{ROH}) was determined using *detectRUNs* (Biscarini *et al*., 2018). F_{ROH} was calculated as follows:

$$F_{ROH} = L_{ROH}/L_{AUTO},$$

where L_{ROH} is the total length of ROH on autosomes and L_{AUTO} is the total length of the autosomes covered by SNPs, which was 2450.71 Mb. Furthermore, the correlation between F_{ROH} and F_{HOM} was calculated for the four populations.

6.2.3 Distribution of Runs of homozygosity

Runs of homozygosity (ROH) were identified in every individual using *detectRUNS* Biscarini *et al*. (2018) using a sliding window of a specified length or number of homozygous SNPs to scan along with each individual's genotype at each SNP marker position to detect homozygous segments. The parameters and thresholds applied to define a ROH were (i) a sliding window of 50 SNPs across the genome; (ii) the minimum number of consecutive SNPs included in a ROH was 50; (iii) the minimum length of a ROH was set to 1 Mb to avoid short and common ROH that occur throughout the genome due to LD (Shi Y & Manley, 2007); and (iv) a maximum of five SNPs with missing genotypes were allowed in a ROH. ROH was divided into five physical length categories (1-5Mb, 5-10Mb, 10-20Mb, 20-30 Mb and <40 Mb). The mean number of ROH per individual, the average length of ROH, the total number of ROH per animal, the percentage of chromosomes covered by ROH and mean ROH were calculated on *detectRUNS*. The genomic inbreeding coefficient based on ROHs (F_{ROH}) was also calculated as the sum of the length of the autosome covered by ROHs divided by the overall length of the autosome covered by the SNPs as described by McQuillan *et al*. (2008). Means and standard deviation (sd) of F_{ROH} were calculated as the sum of the lengths of $F_{ROH\text{1-5Mb}}$, $F_{ROH\text{5-10Mb}}$, $F_{ROH\text{10-20Mb or <20Mb}}$.

To identify the genomic regions that were most associated with ROH, the percentage of the occurrences of a SNP in ROH was calculated by counting the number of times the SNP was detected in those ROH across individuals, and this was plotted against the position of the SNP along the chromosome. This percentage threshold was normalised to 70%, 50% and 20% of individuals per population to be an indication of a possible hotspot of ROH in the genome. The function of these genes and pathways in which they are involved were assessed using the Kyoto Encyclopedia of Genes and Genomes (KEGG, http://www.genome.jp/kegg/) database and literature search.

6.2.4 Population structure

Principal component analysis (PCA) was calculated and plotted in Golden Helix SNP and Variation Suite (SVS) V8.1 (Golden Helix, Inc. 2012). For the analysis of ancestry proportions (admixture) with K set from 2 to 10, the ADMIXTURE *v1.3.0* program (Alexander *et al*., 2009) was used. The default parameter of PLINK *v1.9* (50 SNPs step 5 SNPs, r^2 0.5) was used to subject the whole genotype data set to linkage disequilibrium (LD) pruning (Purcell *et al*., 2007) prior to use in admixture analysis. Finaly, to visualized admixture plots GENESIS software was used (Buchmann & Hazelhurst, 2014).

6.3 Results

6.3.1 Genetic diversity indices.

Variation of the estimated N_e at *t* generations ago (from 12 to 983) is presented in Figure 6.1. As expected, N_e decreased progressively across generations, however, N_e was higher than 150 for all breeds at 12 generations ago. The variation in N_e across generations was smallest for Gauteng ($N_e = 371$) and Free State ($N_e = 386$) whilst Limpopo had the highest ($N_e = 723$). Ancestral populations exhibited considerably larger N_e values, with the largest historical N_e values ($N_e = 5772$).

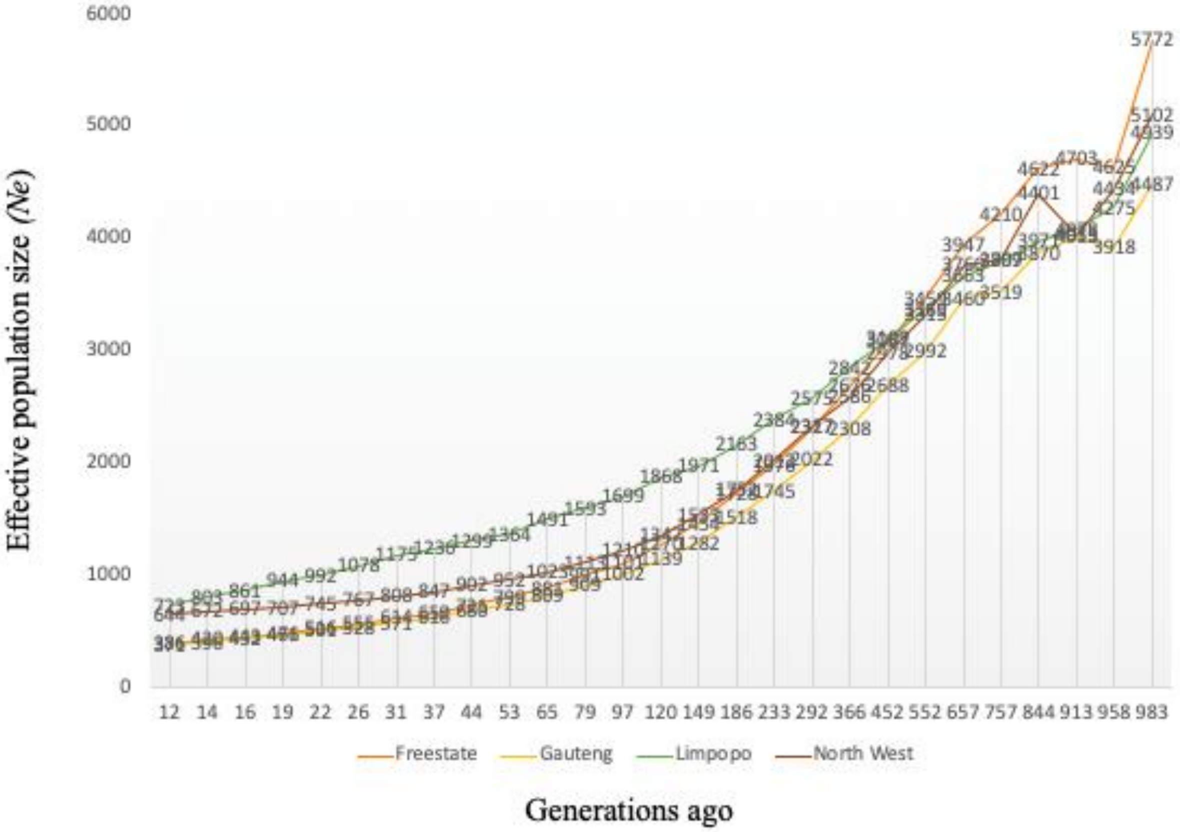


Figure 6.1 Effective population size (*Ne*) for the communal indigenous goat populations from Free State, Gauteng, Limpopo and North West.

The average inbreeding coefficient (F_{IS}), was lowest in Free State (F_{IS} = 0.03±0.09), followed by 0.04±0.09 in Gauteng, 0.05±0.01 in North West and highest in Limpopo (F_{IS} = 0.09±0.05). Overall, the inbreeding level was 0.06±0.08. The average F_{ROH}, its range of variation across populations and its distribution are summarised in Table 6.1. Genomic inbreeding coefficients (F_{ROH}) based on the distribution of the length of runs of homozygosity by class are described in Table 6.2 and by chromosome in Figure 6.2. F_{ROH} differed significantly among populations across the length categories. The genomic inbreeding coefficients of the shortest ROH (0-5Mb; related to ancient kinship) per animal ranged from 0.02±0.02 in the Eastern Cape population to 0.08 ±0.10 in North West population. The F_{ROH} of Eastern Cape, Limpopo populations increased with category size, whilst decreased in Free State. Gauteng F_{ROH} decreased from 0.07±0.09 to 0.05±0.09 for F_{ROH} >20Mb and increased at >20Mb. In KwaZulu-Natal, F_{ROH} increased to up to 0.08±0.09 at <20Mb and decreased for >20Mb category.

Table 6.1 Distribution of runs of homozygosity inbreeding coefficients (F_{ROH}) within each population.

Class (Mb)	**Eastern Cape (*n* = 20)**	**Free State (*n* = 24)**	**Gauteng (*n* = 28)**	**KwaZulu-Natal (*n* = 25)**	**Limpopo (*n* = 55)**	**North West (*n* =55)**
0-5Mb	0.02±0.02	0.08±0.09	0.07±0.09	0.04±0.07	0.03±0.04	0.08±0.10
5-10Mb	0.02±0.01	0.06±0.09	0.06±0.09	0.05±0.08	0.03±0.04	0.07±0.09
10-20Mb	0.02±0.01	0.06±0.08	0.05±0.09	0.08±0.09	0.03±0.05	0.07±0.09
>20Mb	0.03±0.01	0.06±0.04	0.08±0.12	0.06±0.05	0.07±0.03	0.08±0.09

Chromosomal distribution of inbreeding showed higher inbreeding levels in chromosome 15, in Gauteng chromosome 19, in KwaZulu-Natal in chromosome 19 followed by chromosome 16. In the North West chromosomes 22 and 19 had the highest inbreeding coefficients compared to other chromosomes.

Figure 6.2 Distribution of inbreeding coefficients (F_{ROH}) based on runs of homozygosity (ROH) for each chromosome.

6.3.2 Distribution of Runs of Homozygosity (ROH)

A total of 3383 ROH were identified across populations, although the frequency and length of ROH differed per population. Among the 207 animals, only 1 animal in the Eastern Cape population was lacking ROH, whilst 206 (99.52%) had at least one ROH longer than 1 Mb. The mean number of ROH per population was 24.36, 23.92, 21.47, 9.13 and 9 in Gauteng, Free State, North West, KwaZulu-Natal, Limpopo and Eastern Cape, respectively (Figure 6.3).

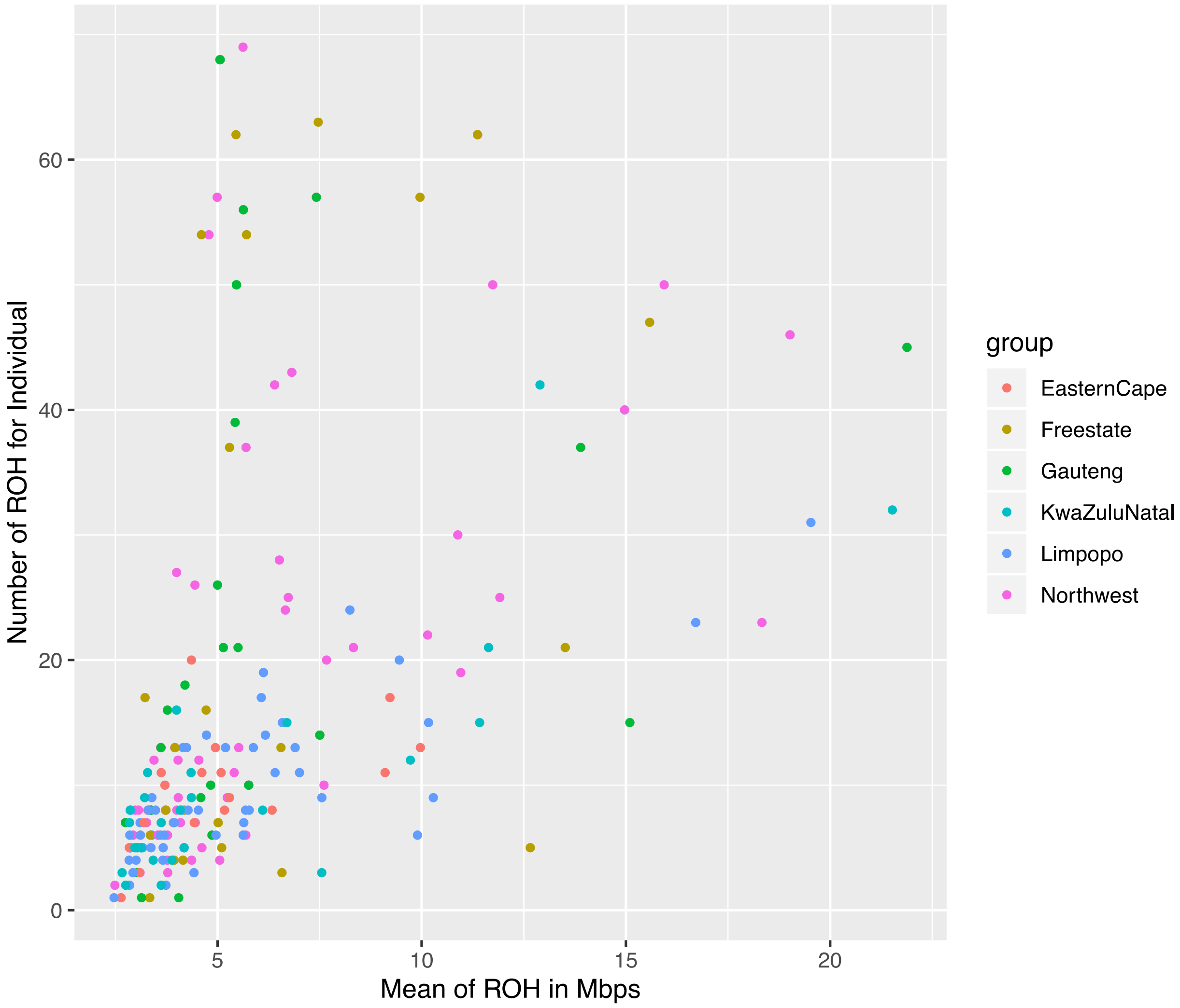


Figure 6.3 The genomic length with mean runs of homozygosity (ROH) per individual and the number of ROH for individuals.

The mean ROH length was 7.76 Mb across population. The longest segment (SNP position 39467151 -137516937) was observed in the Gauteng and North West populations was 98.05 Mb in length (1992 SNPs) found on chromosome 1. In KwaZulu-Natal, Free State and Eastern Cape the longest segments were found on chromosome 9 (83.54Mb; 1691 SNPs), chromosome 7 (73.33Mb; 1449 SNPs) and chromosome 7 (51.81Mb; 1034 SNPs), respectively. ROH shorter than 5Mb predominated (*n* = 1949) across all populations (Table 6.1) accounting for 57.61% of all detected segments and differed per population. These short segments accounted for 72.22% in the Eastern Cape population, followed by Limpopo (*n* = 322; 64%), KwaZulu-Natal (*n* = 151;

57.20%), Gauteng (*n* = 390; 57.18%), North West (*n* = 645; 54.61%) and Free State (*n* = 311; 54.18%).

Table 6.2 Number of runs of homozygosity (*n*ROH) and length (in Mb) categorised by ROH length class (ROH_{1-5Mb}, ROH_{5-10Mb}, $ROH_{10-20 Mb}$, $ROH_{20-40 Mb}$ and $ROH_{>40 Mb}$).

Class (Mb)	**Eastern Cape (*n* = 20)**	**Free State (*n* = 24)**	**Gauteng (*n* = 28)**	**KwaZulu-Natal (*n* = 25)**	**Limpopo (*n* = 55)**	**North West (*n* =55)**
0-5Mb	130	311	390	151	322	645
5-10Mb	34	146	193	46	100	271
10-20Mb	8	77	68	34	47	163
20-40Mb	7	34	19	27	25	72
>40Mb	1	6	12	6	8	30
Total	**180**	**574**	**682**	**264**	**502**	**1181**

The relationship between the mean number of ROH and the length of the genome covered by ROH per individual varies considerably among animals and populations. The number of ROH per chromosome displayed a specific pattern with the larger numbers found for chromosome 1, 2 and 3, a number that tended to decrease with chromosome length, and the smallest number on chromosome 26 with 44 segments. Chromosome 1 had the highest number of ROH and Eastern Cape did not have ROH on chromosome 23 and 28 (Figure 6.4).

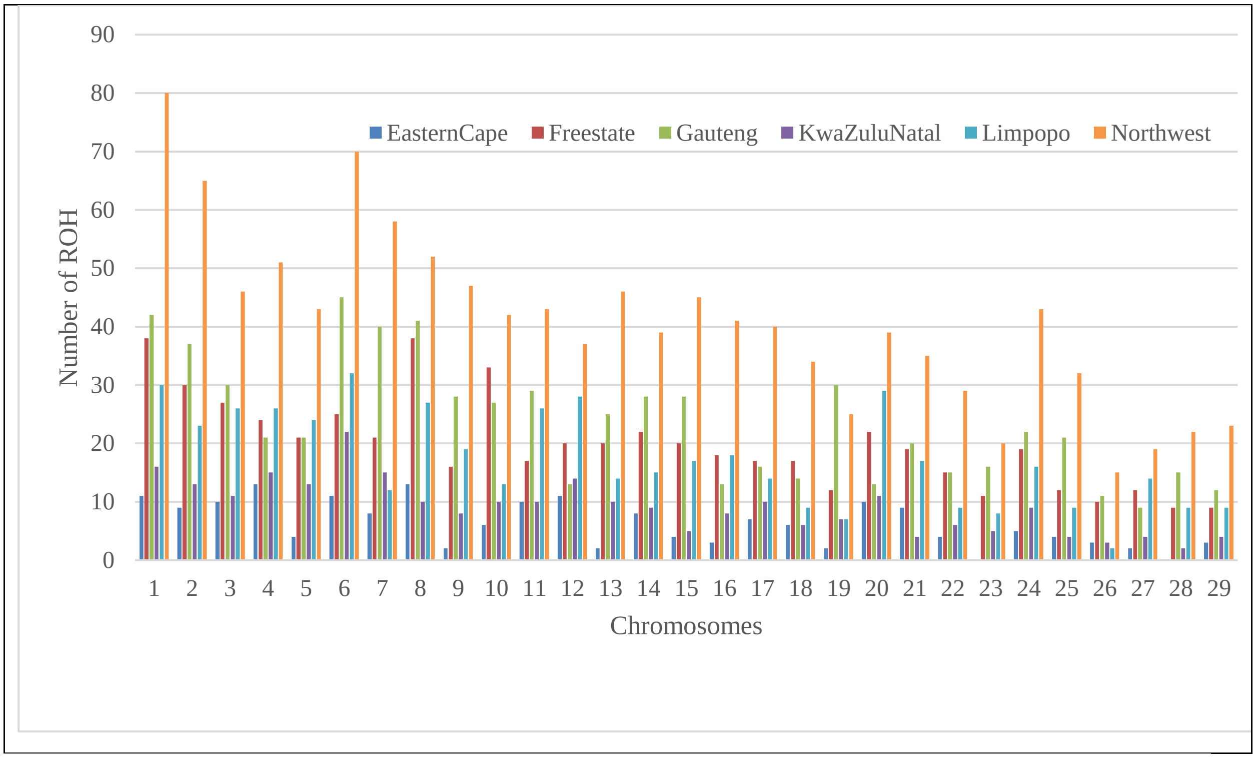


Figure 6.4 Number of runs of homozygosity (ROH) per chromosome identified across all populations.

The proportion of chromosomes covered by ROH is illustrated in Figure 6.5. Overall, the highest coverage by ROH was observed on chromosome 1, 2, 6 and 8 at 0.37, 0.31, 0.38 and 0.33, respectively. For the Eastern Cape population, chromosome 4 and 8 0.07%, whilst Free State, Limpopo and North West had the highest proportion on chromosome 1 with 0.06%. Gauteng and KwaZulu-Natal had the highest at chromosome 6 with 0.06 and 0.08%, respectively.

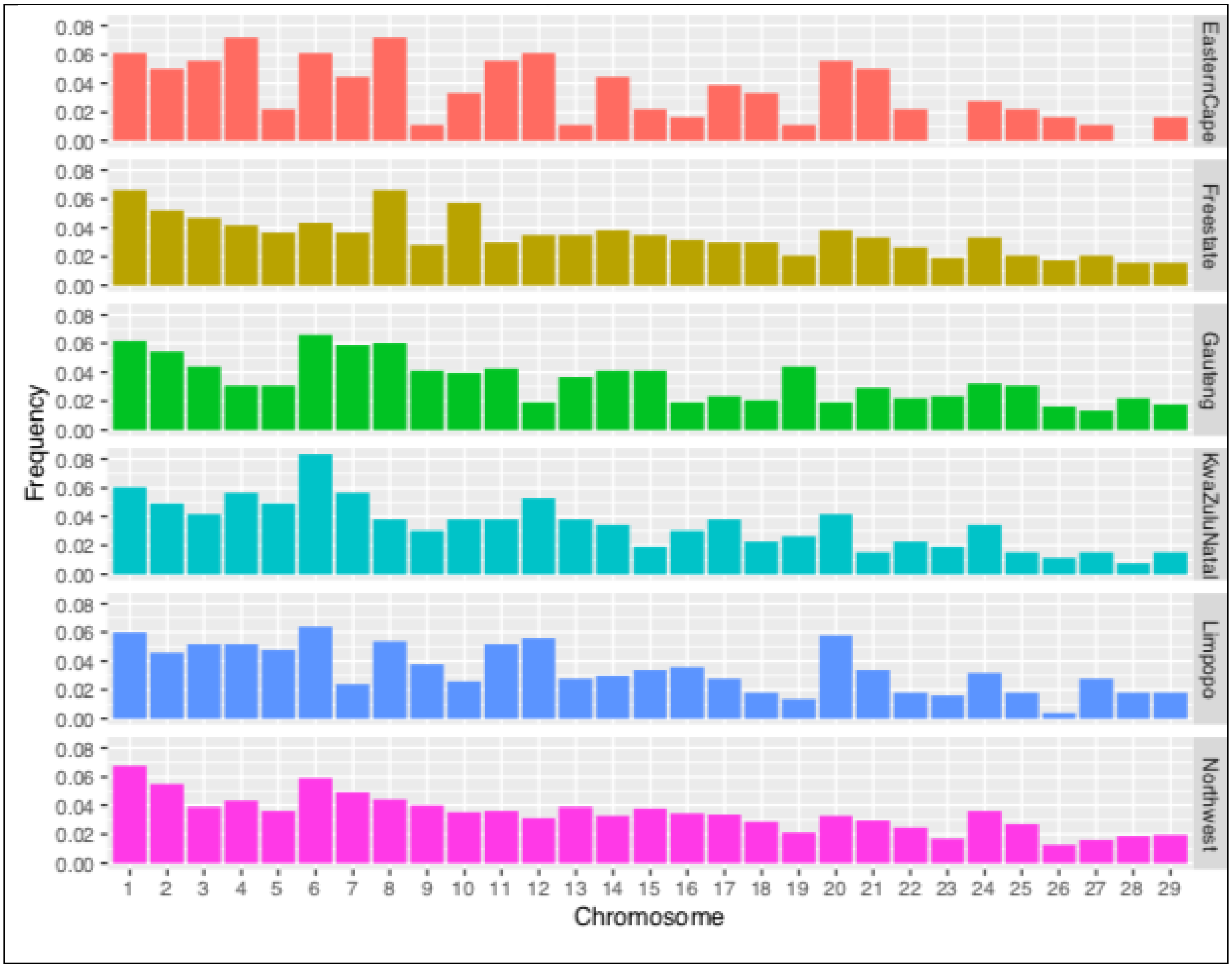


Figure 6.5 Frequency of runs of homozygosity (ROH) per chromosome per population.

To identify the genomic regions that were most associated with ROH, the percentage of SNPs in ROH was assessed by analysing the frequency of a SNP occurring in those ROH across different individuals (20%), and this was plotted against the position of the SNP along the chromosome (Figure 6.6). The threshold of 70% and 50% of the individuals did not yield ROH islands across populations thus 20% was used. Several genomic regions were identified that frequently appeared in a ROH within individual animals (Table 6.3 and APPENDIX D). We identified 58 ROH islands at the 20% threshold in the Free State (*n* = 28) and Gauteng (*n* = 29) provinces. No ROH islands were observed in the Eastern Cape, KwaZulu-Natal, North West and Limpopo at the set thresholds. The ROH hotspot with the highest occurrences (SNPs = 149) in Gauteng was located on chr7 (7.69Mb). Chromosome position, start and end position of ROH, ROH length and number of SNPs within the genomic regions of extended homozygosity are reported in Table 6.3 and APPENDIX

F. A total number of 871 genes inside the ROH islands. An additional APPENDIX shows the KEGG 292 pathways associated with the genes (APPENDIX G).

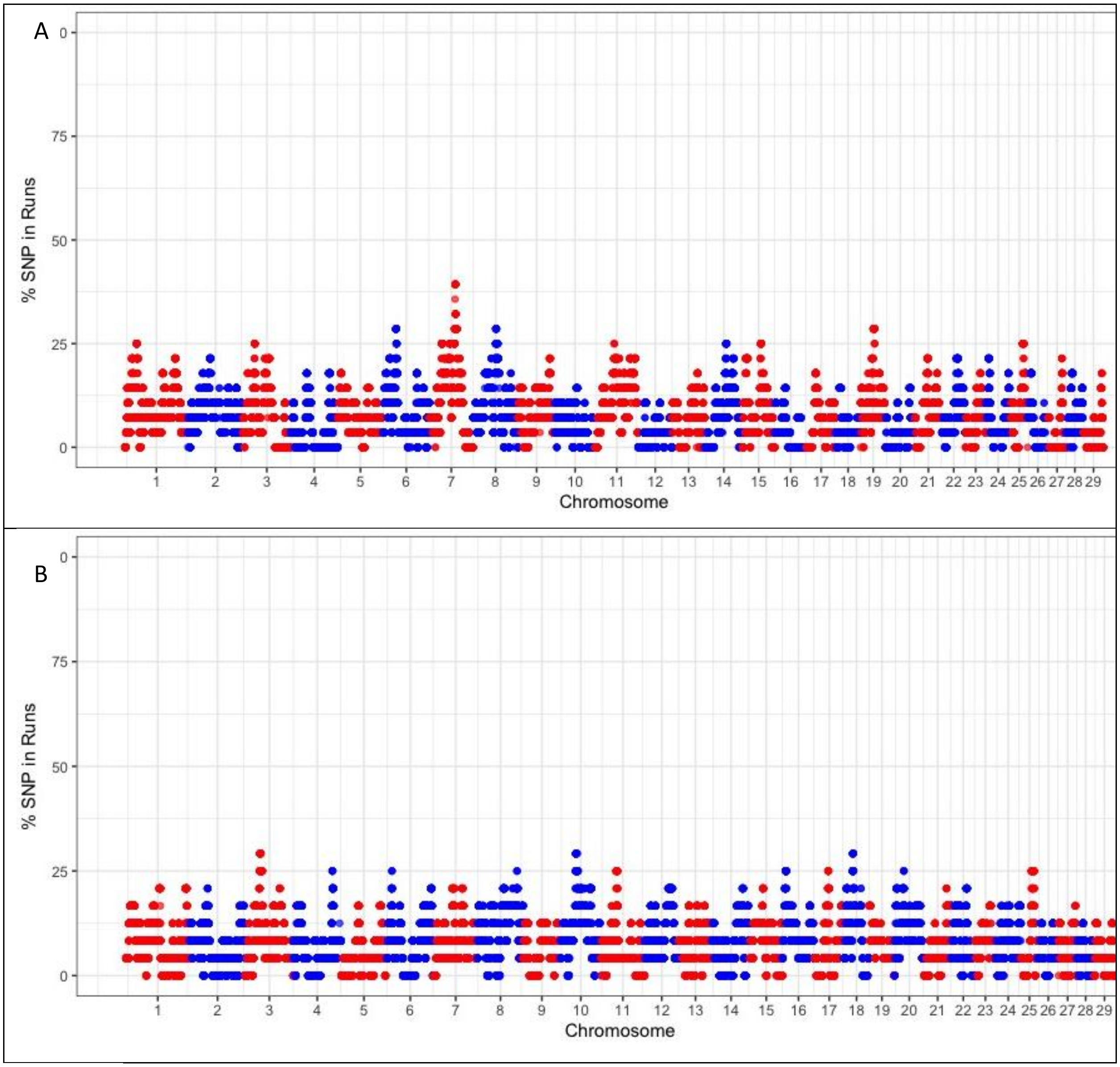


Figure 6.6 Manhattan plot of occurrences (%) of a SNP in ROH across populations. The X-axis represents the distribution of ROH across the genome, and the Y-axis shows the frequency (%) of overlapping ROH shared among samples.

Table 6.3 Regions of the ROH islands at 20 % across Gauteng and Free State populations by length.

Population	**Position (chr: SNP 1: SNP 2)**	***n*SNP**	**Length (Mb)**
Gauteng	3:54056151:55070625	22	1.01
Freestate	7:48193142:49278113	19	1.08
Freestate	20:21671108:22811848	22	1.14
Freestate	15:30999298:32153016	30	1.15
Gauteng	15:7897116:9088595	28	1.19
Gauteng	9:76995912:78321101	30	1.33
Gauteng	8:53874425:55257845	34	1.38
Freestate	20:4743026:6211601	32	1.47
Gauteng	19:27892936:29379671	33	1.49
Freestate	6:11346351:12878262	32	1.53
Freestate	20:19597454:21199311	37	1.60
Freestate	14:73908424:75554996	30	1.65
Gauteng	24:7056817:8823189	37	1.77
Gauteng	1:122842771:124683449	34	1.84
Freestate	22:36144242:37987490	36	1.84
Gauteng	15:43908135:45815862	33	1.91
Gauteng	21:30374560:32314473	45	1.94
Freestate	6:107507640:109477575	40	1.97
Gauteng	14:51115518:53088572	38	1.97
Gauteng	25:29189441:31200199	43	2.01
Freestate	25:25914911:28121785	48	2.21
Freestate	10:73412812:75622539	47	2.21
Gauteng	2:53997579:56229103	44	2.23
Freestate	4:94620783:96868758	55	2.25
Freestate	10:70170521:72471193	48	2.30
Freestate	1:81289909:83642225	50	2.35
Gauteng	11:85024580:87384856	47	2.36
Gauteng	8:60260123:62640344	51	2.38
Freestate	18:6154744:8563747	54	2.41
Gauteng	7:29457232:31898006	46	2.44
Freestate	1:145037345:147663352	55	2.63
Freestate	8:62328607:64991613	62	2.66
Gauteng	11:45829634:48502615	52	2.67
Freestate	11:36630830:39372620	53	2.74
Gauteng	1:17079512:19890667	60	2.81
Gauteng	11:95518465:98340959	43	2.82
Freestate	17:32672670:35522389	54	2.85
Gauteng	6:31221691:34180737	60	2.96
Freestate	8:94585706:97590188	52	3.00
Gauteng	19:31681378:34691035	57	3.01
Gauteng	1:28400001:31438929	61	3.04

Table 6.3 Regions of the ROH islands at 20 % across Gauteng and Free State populations by length (continued).

Population	Position (chr: SNP 1: SNP 2)	*n*SNP	Length (Mb)
Freestate	12:57673212:60742379	61	3.07
Gauteng	6:15586763:18769652	60	3.18
Gauteng	3:62095554:65301414	62	3.21
Gauteng	8:55933868:59160945	67	3.23
Freestate	25:28641340:31924694	69	3.28
Freestate	16:5685888:9117064	69	3.43
Freestate	10:48160488:51636811	64	3.48
Gauteng	11:50602742:54104265	72	3.50
Gauteng	15:9294238:12900069	70	3.61
Freestate	18:20922080:24775492	76	3.85
Freestate	12:63521630:67564200	87	4.04
Gauteng	22:35705179:39950926	81	4.25
Gauteng	7:45438722:51833004	126	6.39
Freestate	10:36878056:43333293	124	6.46
Freestate	3:33683337:40785725	140	7.10
Gauteng	7:60187788:67883046	149	7.70

6.3.3 Population structure

For population structure analysis further quality control parameters were effected in PLINK v1.90 (Purcell *et al*., 2007): to removed linked SNPs using the --*indep-pairwise 50 5 0.5* command and related individuals (IBS >0.65). The database for population structure included 32886 SNPs and 189 individuals across populations. The plot of the first (PC1) and second eigenvectors (PC2) (Figure 6.7), shows weak differentiation among the clusters of admixed populations. PC1 shows cluster 1 and 2 consisting of populations of KwaZulu-Natal and Limpopo, respectively. The Eastern Cape population (Cluster 3) revealed a separate cluster (with three outliers). Clusters 4 consists majority of North West and Gauteng, whilst cluster 5, was Free State.

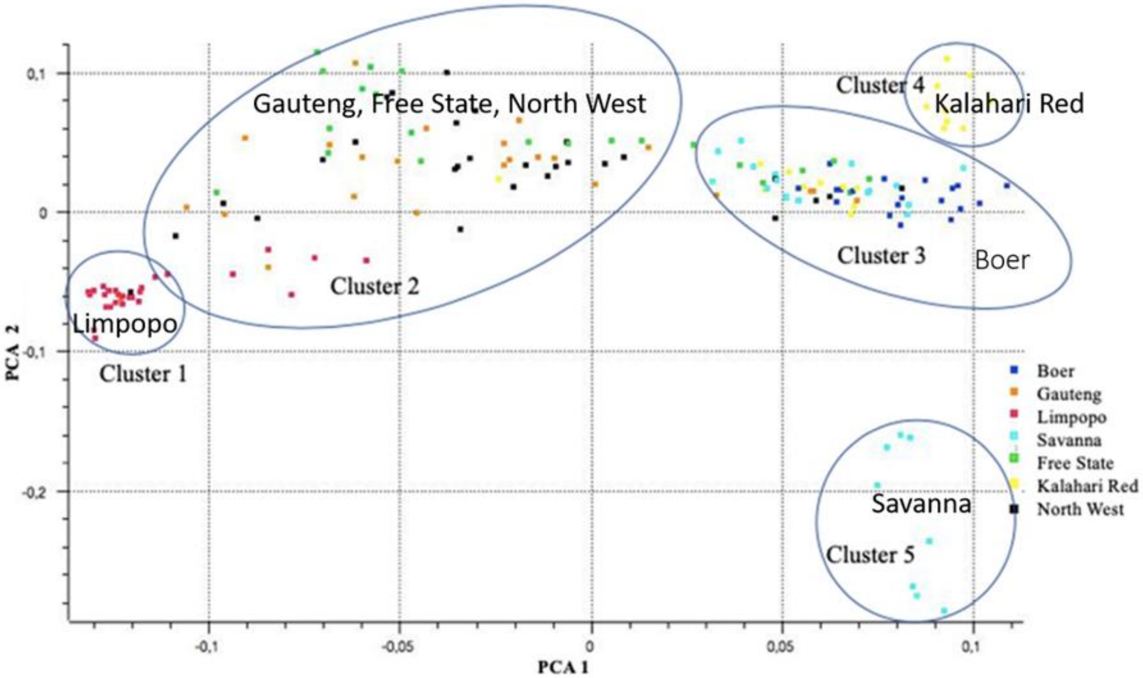


Figure 6.7 A plot of principal components (PCA) analysis showing differentiations among the clusters of admixtures across six communal indigenous goat populations.

For the further understanding of the degree of admixture within the populations, the ADMIXTURE 1.3 (Alexander *et al*., 2009) software was used for K = 2 to 10 hypothetical ancestral populations, only K= 2 to K = 6 is plotted since no further clusters were observed after K = 6 (Figure 6.8). Assuming two hypothetical ancestral populations, the population from KwaZulu-Natal and Limpopo are revealed, supporting PC 1. The genomes of KwaZulu-Natal and Limpopo shared an origin but have substantial admixture from the Eastern Cape and North West populations. K = 3 as the most likely number of genetically distinct groups within our populations presenting the lowest cross-validation error (0.4617), reflecting a clear cluster of the Limpopo populations. Free State and Gauteng and North West showed similar genetic heterogeneity patterns with a considerable level of admixture. North West revealed a high level of within-population genetic differentiation as there are individuals closer to Eastern Cape and another subpopulation closer or clustering with Free State. This is also in agreement with the second PC coordinate analysis in showing genetic heterogeneity within the population. Moreover, with the increment of the value of K (K = 4 to K = 6), Free State and Gauteng show a higher level of genetic heterogeneity than the other populations.

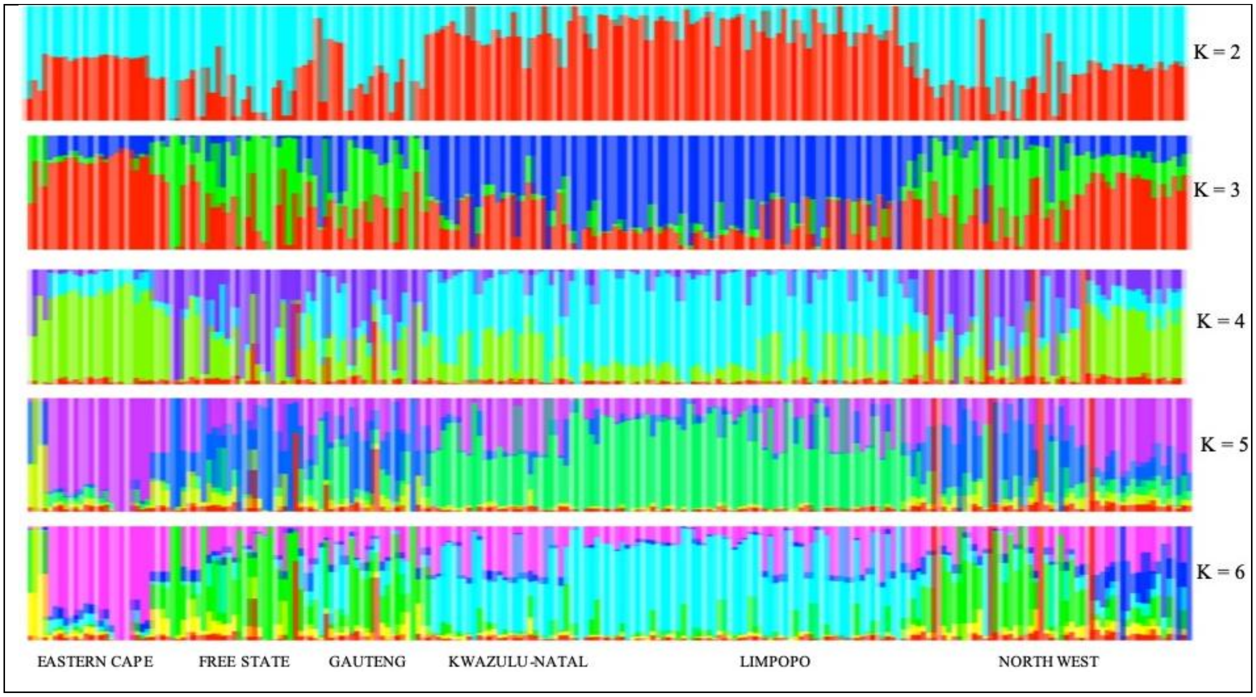


Figure 6.8 Clusters inferred from ADMIXTURE at K = 2 - 6. The cluster membership of each sample is shown by the colour composition of the vertical lines, with the length of each colour being proportional to the estimated membership coefficient.

6.4 Discussion

In chapter 5, the genetic diversity and population structure of goat populations in South Africa was revealed. The main links to the development of commercial goat populations is represented by indigenous goat population and may potentially be relevant as a future source of untapped adaptable genetic material (Visser, 2016). Therefore, improving our understating of within-ecotype relationships among the major goat producing provinces in South Africa offers a rare opportunity enhancing efficient use of the breeds and implementing conservation programs. This study investigated the indications for population status on inbreeding and runs of homozygosity in the indigenous goat population. Data from a previous study (Mdladla, 2016) enabled a broad geographical coverage of South Africa and represents populations from the major goats producing provinces within the country.

Effective population size (N_e) is a crucial population genetic parameter because of its relationship to the loss of genetic variation, increases in inbreeding, the accumulation of mutations, and the determination of the accuracy of genomic selection (Goddard, 2009; Berihulay, 2019). Gauteng had the smallest estimated N_e among the population and Limpopo had the highest. It was also observed in other studies that effective population size (N_e) showed a reduction to 132 in the Kingdom of Eswatini and highest in South Africa 12 generations ago (Visser *et al*., 2016). It is recommended that to prevent a reduction of the adaptive value in populations, N_e values between 50 and 100 animals and 50 to avoid inbreeding depression (Meuwissen, 2007). A study by Colli *et al*., (2018), reported a large N_e in local goat breeds, such as those from Africa, Spain and Central-Southern Italy local goats breeds and a small *Ne* in the Angora, Boer, Nubian, Cashmere, Saanen and Alpine populations.

The rapid increase pattern in *Ne* may also include bottlenecks associated with domestication, selection and breed formation, and the endangerment of the breed (Shina *et al*., 2013). A study by Mdladla *et al*., (2016) based on SNP data and using the same method reported large N_e for all investigated breeds (ranging from 140 to 348). Furthermore, a study by (Mdladla *et al*., 2016a) revealed that the ecotype goat was slightly higher in effective population sizes than the Tankwa and commercial goat populations across generations. From a conservation standpoint, the indigenous goat population should top the priority in the population studied due to their diminishing effective population size and increased inbreeding coefficients.

Runs of Homozygosity (ROH) can disclose the genetic relationships among individuals, estimating with high accuracy the autozygosity at the individual and population levels and can elucidate about selection pressure events (Purfield *et al*., 2017). If long ROH accumulates in the genome of some individuals, they could seriously impact the overall biological fitness (Manunza *et al*., 2016), therefore, it was an important objective to investigate and understand the level of homozygosity among the populations. In this study, only 1 animal was lacking ROH, whilst 206 (99.52%) had at least one ROH longer than 1 Mb. The genomic inbreeding coefficients (F_{ROH}) values found in the study for the Ethiopian goats were $F_{ROH > 1\mathrm{Mb}}$ values (Nandolo *et al*., 2017). Similar results were found by Nandolo *et al*. (2019) with more African goats (Cameroon, Ethiopia, Kenya, Madagascar, Malawi, Mali, Mozambique, Nigeria, Tanzania, Uganda, and Zimbabwe) using a clustering algorithm. In this study, differences in terms of total number and length of ROH were short (>5Mb) were more abundant (57.61%). Onzima *et al*. (2018) reported results that showed lower than the $F_{ROH > 2\mathrm{Mb}}$ for Kenya, Uganda, and Mozambique goat breeds when Goat

50K BeadChip was used. On the other hand, the Eastern Cape population showed very low amounts of ROH. This has been suggested to be consistent with recent admixture in the individuals in Chinese cattle (Xu *et al*., 2019). Long segments were abundant in the North West population. Ismal *et al*., (2019) recent study revealed a high mean ROH in the long length category (>30 Mb), and their study suggested that inbreeding is more recent and is indicative of demographic decline. Considering the extensive management systems of goats in the region, these results might be likely, even if some researchers have argued that such extensive systems may lead to inbreeding especially where goats are on an extensive system or are shepherded with other flocks for some part of the year (Tefera *et al*., 2004; Gwaze *et al*., 2009). The lower inbreeding levels in African goats could be due to the openness of the breeding systems in most of Africa that led to the loose definition of livestock breeds in the region (Manunza *et al*., 2016).

One of the main advantages of genomic coefficients is the availability of chromosomal inbreeding coefficients (Mastrangelo *et al*., 2016). ROHs, representing the level of genomic autozygosity, are continuous homozygous segments at the individual and population levels that can be used as a measurement of inbreeding; more in-depth ROHs are the result of demography, natural and artificial selection, and inbreeding (Purfield *et al*., 2012). In this chapter, we do not discuss in detail all the genomic regions associated with ROH but focus on some selected regions that show associations with several specific traits related to livestock breeding. We identified five genes reported to be associated with the important traits of goats (Figure 6.5) identified by the selection signature. Overall, the highest coverage by ROH was observed on chromosome 1, 2, 6 respectively. Gene INHA, located on chromosome 2, was reported as a candidate gene for litter size in goats (Hou *et al*., 2012). Significant QTL for milk production traits such as milk yield and milk protein have been reported on chromosome 2 in sheep (García-Gámez *et al*., 2013). Gene INHA, located on chromosome 2, was reported as a candidate gene for litter size in goats. The *PPP1R36* and Heat Shock Protein A2 (*HSPA2*) (*CHI10*, 26.402–26.719 Mb) identified in these communal indigenous goats are involved in heat stress response and in other studies, *HSPA2*, *DNAJC24*, and *DNAJC*13 are associated with the heat shock family of genes (Shi & Manley, 2007). The presence of multiple genes associated with heat stress would seem to suggest that the trait is under intense selection pressure in tropically adapted breeds (Onzima *et al*., 2018).

In accordance with Nothnagel *et al*. (2009), these regions in humans, when they are present in more than 50% of the individuals of a population, can indicate a strong selection occurrence. The occurrence of ROH hotspots in genomic regions that harbour candidate genes may be involved in selection pressure in response to production and environmental conditions. This study identified 58 ROH hotspots in Gauteng and Free State populations and revealed 871 genes and 292 KEGG pathways. This threshold did not yield any results and only in 20% ROH islands were detected in the communal indigenous goat population. The 20% threshold has been used in indigenous Chinese pigs, Jinhua (Xu *et al*., 2019). ROH islands can be defined as genomic regions with reduced genetic diversity and, consequently, high homozygosity around the selected locus that might harbour targets of positive selection and are under strong selective pressure (Peripolli *et al*., 2018; Pemberton *et al*., 2012). According to Onzima *et al*. (2018), the minimum expected length of homozygous DNA segments is based on the time frame of approximately 25 generations, over which goats are believed to have been characterized in separate breeds.

This study explored the population genetic structure of the indigenous goat population in the context of all South African goat populations. In accordance with our earlier studies (Mdladla *et al.*, 2017; Lashmar, 2015), the principal component analysis (PCA), the ADMIXTURE analyses based on the SNP array and sequence data sets capitulated the major genetic division among the South African goat populations from two large geographic regions: Eastern Cape and Limpopo. The KwaZulu-Natal and Limpopo population`s genomes shared an origin yet with significant admixture from the Eastern Cape and North West populations. Some signals of admixture and underlying genetic relationships among the populations were generated by analysis of population admixture (Ismal *et al*., 2019). A migration route of ancient goat from the northern part of South Africa to the eastern areas of the KZN, during their migration periods of the Bantu nation, is supported by this study as observed.

6.5 Conclusions

The results of this study indicated a greater negative impact of inbreeding in recent times which is important for planning conservation strategies. It was revealed that the occurrence of high N_e and autozygosity varied largely across ecotypes in communal indigenous goat populations at recent and ancient events when a genome-wide SNP marker was used. The use of Illumina goat SNP50K BeadChip shows that there was a migration route of communal indigenous goat populations from the northern part (Limpopo province) of South Africa to the eastern areas of the KwaZulu-Natal, that confirmed their historical relatedness, and which coincide with the migration periods of the Bantu nation. The communal-traditional indigenous goat farming system and adaptation to different climatic conditions had an influenced on the results in this study. The study deepened the understanding of the conservation status and selection mechanisms of goats in communal indigenous goat production setting. For effective conservation programs and utilisation of South African communal indigenous goat populations, effort should be made to establish a conservation program for the unique genetic resources of indigenous goat populations.

CHAPTER 7

GENERAL CONCLUSIONS, RECOMMENDATIONS AND POLICY IMPLICATIONS

7.1 Conclusions

Recently, indigenous goats were among the most important Farm Animal Genetic Resource (FAnGR) in South Africa. For socio-economic, food security and cultural importance in smallholder farming systems in rural areas, FAnGR are significant. In the last decades, the diversity and purity of indigenous goat populations have experienced a severe decline due to indiscriminate breeding and improvement strategies. One of the major drawbacks has been the lack of understanding of the breeds/population characteristics (phenotypic and genotypic) and traditional management systems in which the majority of the goat population exists.

Characterisation of the socio-economic profiles, phenotypic and genetic characterisation of breeds represents a vital step to guide decisions making on management and conservation of communal indigenous goat population. The study provides a high-resolution representation of the genome-wide diversity and population structure of communal indigenous goat populations from major goats producing provinces in South Africa using a medium-density single nucleotide polymorphism (SNP) array. Sustainable utilization of communal indigenous goat populations is the key to effective breed improvement, efficient conservation, goat management and marketing. This entails comprehensive information on communal indigenous goat population's identity and their distinctive characters, as well as their environmental adaptation.

The study showed that a significant number of farmers were above 60 years of age, and this is a critical gap which may impact knowledge transfer on current improvement and conservation programs especially if it is combined by illiteracy. The study revealed that the goat's body size and appearance determine the goat price as well as the financial needs of the farmer. Adult-headed households are richer while youth-headed households are often poorer and have less access to resources required to control diseases.

Farmers relied on coat colour and patterns to identify their goats. Black coat colour was the dominant colour of most of the populations. In communal indigenous goats it was observed that there was a significant difference in all phenotypic measurements understudy, with higher values for body length, body weight and wither height. This phenotypic information could be useful to regulate the different phenotypes within a region or country and design some criteria for characterisation and description of the indigenous goat populations into breeds. Further complimentary research into the effects of these traits and the underlying genes on economic factors should be undertaken for smallholder farmers-oriented breeding plans. The assessed phenotypic traits coupled with genetic information could be a powerful tool towards the promotion of conservation and utilization of indigenous goat genetic resources. For this reason, the level and distribution of genetic variation between South African indigenous goat populations using Single Nucleotide Polymorphisms (SNPs) were investigated.

This study applied a high-density SNP data to investigate genetic diversity, admixture and population structures of communal indigenous goat populations. Population structure analysis showed admixed populations, which highlight the genetic dilution that is experienced in the smallholder communal setting. Results revealed that the shared signatures are due to crossbreeding practiced among the farmers. In spite of the complex admixture events that most populations have experienced, the Limpopo population has a unique genetic background suggestive of distinctive characteristics and can be clearly discriminated, which is probably due to differences in a production environment and genetic isolation. The frequency and distribution of ROH, inbreeding levels based on the two approaches revealed regions of high homozygosity and suggests a lack of effective management of inbreeding. For example, the Limpopo population had the highest effective population size, however, evidence of high recent inbreeding cannot be ignored, which could impact improvement and conservation in this population.

It is accepted that in most goat studies there are limited quantitative trait loci, however, the study provides a basis for future research in goat genomics of three provinces representing subtropical wet, arid and semi desert-adapted communal indigenous goat populations. Using medium density SNPs, selection signatures associated with adaptation to specific environmental conditions were detected. Several efforts are underway including improvements in the annotation of the goat genome assembly (Bickhart *et al*., 2017) and these developments were made possible with the release of the caprine 50K SNP chip (Tosser-Klopp *et al*., 2014; Zhong *et al*., 2023). Better management and sustainable utilization of communal indigenous goat populations will emerge from the integration of genomic information. The results of this study will advance the understanding of environmentally driven adaptation and its potential application in functional genomics and selective breeding. The results will further enhance on the design of management programs to conserve the communal indigenous goat population diversity to cope with the current and future predicted effects of climate change.

Different measures in the areas of research and animal advisory field could improve the low productivity of communal indigenous goat populations. Data of communal indigenous goat populations on their performance must be systematically collected and evaluated in order to be able to select and breed. A source of better and more regular income for farmers will always be the breeding of suitable pure or cross-bred. Another principal measure in indigenous goats' research should be targeted at aspects ranging from strengthening of local advisory services. Emphasis should be put on the design of better housing and vaccination of kids as well as formulation of low–cost feed resources. Training and provision of a goat farmers' tailor-made credit facility, which is informed by data on the communal indigenous goat population`s production cycle and the major bottlenecks are the important strategies that is required to empower the communal and subsistence farmers. To fully exploit the genetic potential of the systematically bred animals, farmers will allow the improved husbandry and breeding of communal indigenous goat populations. Hence improved goat production and contribution towards improving communal and subsistence farmer's income and food security is recommended by the study.

7.2. Recommendations

- To improve indigenous goat production, it is, therefore, critical to consider producers' socio-economic profiles.
- To facilitate the *in situ* and *ex situ* conservation and utilisation of these valuable genetic resources, it is also imperative to further characterise communal indigenous goat populations in other provinces of South Africa both phenotypically and genetically.
- The assessed phenotypic traits combined with genetic information could be a powerful tool towards the advancement of conservation and utilisation of communal indigenous goat populations.

- The level and distribution of genetic variation between South African communal indigenous goat populations using Single Nucleotide Polymorphisms require thorough investigation.

The recommendations of population types described in this study reflect only the sample set which was analysed and highly related systems and cannot be generalised across the diversity of smallholder farming as they are influenced by socio-economic parameters, feed resources and agro-ecological environment.

7.3. Policy implications

FAO and AU-IBAR have gone to great lengths to support characterisation and standardisation of FAnGR. Funding and data are becoming more accessible and the need for collaboration with other African countries cannot be ignored. Women and youth play a key role in goat production; however, challenges exist including economic/financial, social, little involvement in decision-making. Despite these challenges of cost, numerous studies have since emerged in South Africa (Mdladla *et al*., 2016, Lashmar *et al*., 2015, Monau *et al*., 2020; Magoro et al., 2022; Khowa, 2023), showing that the funding bodies realise the importance of the genetic characterisation.

Furthermore, via organized breeding methods such as the community-based breeding programs, the last few decades have seen a dramatic increase in the pace of genetic gain. Unfortunately, a reduction in genetic diversity has been accompanied by an increase in production performance (Boettcher *et al*., 2010). Therefore, conservation of indigenous goats has become an important milestone and if not given attention it can lead to an irreversible loss of adaptive genotypic and phenotypic variations in these populations. Efforts to maintain genetic diversity in the communal indigenous goat population through on-farm management are thus needed. Improvement of systems to record and monitor inbreeding may contribute to their *in-situ* conservation of communal indigenous goat populations and, in view of this, the availability of phenotypic and genomic data is a fundamental resource.

A holistic approach for a successful plan to improve communal indigenous goat production amongst poor communal and subsistence farmers with limited resources is required. In different areas of production, relevant efforts in this respect must be made from a combination of measures. The state, research community, development organizations, private sector as well as communal and subsistence farmers themselves will make up the important stakeholders that are needed. Communal indigenous goat populations could be considered as national and global public goods and their utilization be guided by national strategies. However, such national strategies should fully consider communities' interests and economic needs as goat production are the major means of livelihoods for communal and subsistence farmers.

In South Africa, the National Advisory Committee/ National Working Group for FAnGR and relevant stakeholders have succeeded in developing the National Strategy and Action Plan (NSAP) document for FAnGR. Its objectives which include; (i) To characterize FAnGR for sustainable production systems, (ii) Promote South African participation in conservation and sustainable use of FAnGR at Southern African Development Committee (SADC), African Union (AU), and international level, (iii) Establish sustainable *in situ* and *ex situ* conservation of FAnGR in scientifically sound and cost-effective breeding programmes, (iv) Support actions and initiatives concerning the conservation of FAnGR by various stakeholders, (v) Ensure that conservation of FAnGR is in harmony with the sustainable use of natural resources in response to climate change must be applied on the indigenous village goats.

To prevent the total loss of the valuable South African communal indigenous goat populations due to unforeseen natural disasters, their conservation and sustainable utilization is essential. The focus should be to conserve these local populations *in–situ* in their naturally occurring environments where they are less likely to be subject to control and loss of natural selection for survival under local conditions. The indigenous goat genetic materials must be ex *situ* conserved in the national gene bank as guided by the Strategic Plans for conservation of FAnGR. To meet conservation objectives of South African communal indigenous goat populations, a policy priority must include an approach combining threat status of breeds, their contributions to genetic diversity and rural household livelihoods (i.e. current breed merit, which includes economic or production, ecological and socio-cultural values of breeds).

When communal and subsistence farmers participate in farmers' community breeder’s programmes and farmers’ organizations, they are more likely to profit from the existing communal indigenous goat populations. This will give them an opportunity to improve the quality of their products that will come from the larger and more regular quantities of goats for sale on the market. Communal and subsistence farmers will also be in a better negotiating position, save costs, and reduce their risks and will also have a better chance of becoming suppliers for expanding supermarkets. Among other important things when developing farmers’ organizations which are not always easy will be a requirement for a great deal of commitment and the capacity to build consensus.

An important input that helps communal and subsistence farmers to improve goat production is mutual learning, as well as attendance of training courses. Infrastructure in rural areas will have to be improved in order for communal and subsistence farmers to have opportunities to produce for the market. To increase communal indigenous goat productivity, a good agricultural advisory services and veterinary services is needed. Furthermore, communal and subsistence goat farmers should also be able to participate in the market more easily and economic development should not benefit only large-scale farmers, for example, through improved micro-credit conditions, particularly for women farmers. Under fair conditions and for the preparation of communal and subsistence farmers to deal with the demands of large wholesalers such as supermarkets, public-Private Partnerships, in particular, are a promising means for integrating them into the market.

CHAPTER 8

REFERENCES

CHAPTER 8. REFERENCES

Adebayo, J. & Chineke C., 2011. Evaluation of West African dwarf goat for some qualitative Traits in Southwestern Nigeria. *African Journal of Agricultural Research* 6: 6204 – 6207.

Adedeji, T. A., Ozoje, M. O., Peters, S. O., Ojedapo, L. O., & Sanusi, O. A., 2011. Effect of coat colour and wattle genes on morphometric characteristics and scrotal dimensions in traditionally reared West African Dwarf (WAD) bucks. *International Journal of Agriculture, Environment and Biotechnology* 4(2): 157 – 162.

Ağaoağlu, O.K. & Ertuğrul, O., 2012. Assessment of genetic diversity, genetic relationship and bottleneck using microsatellites in some native Turkish goat breeds. *Small Ruminant Research* 105: 53 – 60.

Agricultural Research Council (ARC)., 2006. Genetic characterization and distances of indigenous livestock breeds. From: http://www.arc.agric.za/home.asp?pid=567 (Accessed 11 February 2023).

Ahmed, Z., Babar, M. E., Hussain, T., Nadeem, A., Awan, F. I., Wajid, A., Ali, M. M., 2014. Genetic diversity analysis of Kail sheep by using microsatellite markers. *The Journal of Animal and Plant Sciences* 24(5): 1329 – 1333.

Ai, H., Yang, B., Li, J., Xie, X., Chen, H., Ren, J., 2014. Population history and genomic signatures for high-altitude adaptation in Tibetan pigs. *BMC Genomics*. 5(1):1.

Ai, H., Huang, L., Ren, J., 2013. Genetic diversity, linkage disequilibrium and selection signatures in Chinese and Western pigs revealed by genome-wide SNP markers. *PLoS One*. 8(2): e56001.

Ajmone-Marsan, P., Colli, L., Han, J.L., 2014. The characterization of goat genetic diversity: towards a genomic approach. *Small Ruminant Research* 121: 58 – 72.

Alade, N.K., Raji, A.O. & Atiku, M.A., 2008. Determination of appropriate model for the estimation of body weight in goats. Department of Animal Science, University of Maiduguri, Maiduguri, Borno State, Nigeria, *ARPN Journal of Agricultural and Biological Science* 3(4): 51 – 57.

Alexander, D.H., Novembre, J. & Lange, K., 2009. Fast model-based estimation of ancestry in unrelated individuals. *Genome Research* 19: 1655 – 1664.

Alexandre, G. & Mandonnet, N., 2005. Goat meat production in harsh environments. *Small Ruminant Research* 60: 53 – 66.

Alvarenga, A.B., Rovadoscki, G.A., Petrini, J., Coutinho, L.L., Morota, G., Spangler, M.L., Pinto, L.F.B., Carvalho, G.G.P., Mourão, G.B., 2018. Linkage disequilibrium in Brazilian Santa Inês breed, Ovis aries. *Science Report* 8: 8851.

Anteneh, N. T., Mekala, D, G., Mnisi, P. E., Mukisira, C., Muthui, M., Murungweni, C. and Sebitloane, O., 2004. Goat Production and Livelihood Systems in Sekhukhune District of the Limpopo Province. International Centre for development-oriented Research in Agriculture (ICRA), Working Document Series 118, South Africa.

Asadollahpour, N. H., Cai, Y., Alshawi, A., Wen, J., Hussain, T., Fu, W.W., Xu, N.Y., Essa, A., Lenstra, J.A., Wang, X., Jiang, Y., 2023. Genomic analysis of indigenous goats in Southwest Asia reveals evidence of ancient adaptive introgression related to desert climate. *Zool Res* 44 (1): 18 – 27.

Avise, J. C., 2004. Molecular Markers, Natural History, and Evolution. 2nd Edn. Sunderland, MA; Oxford: Oxford University Press.

Bath, G., Van Wyk J. & Pettey, K., 2005. Control measures for some important and unusual goat diseases in southern Africa. *Small Ruminant Research* 60: 127 – 140.

Barry, D. & Godke, R., 2001. The Boer goat: The potential for cross breeding. Louisiana State University, Baton Rouge, USA. From: dnafrica@worldonline.co.za (Accessed 22 February 2016).

Barbato, M., Orozco-Terwengel, P., Tapio, M., Bruford, M.W., 2015. SNeP: A tool to estimate trends in recent efective population size trajectories using genome-wide SNP data. *Frontiers in Genetics*: 6: 109.

Belay, S., Belay, G., Nigussie, H., Ahbara, A.M., Tijjani, A., Dessie, T., Tarekegn, G.M., Jian-Lin, H., Mor, S., Woldekiros, H.S., Dobney, K., Lebrasseur, O., Hanotte, O., Mwacharo, J.M., 2024. Anthropogenic events and responses to environmental stress are shaping the genomes of Ethiopian indigenous goats. *Scientific Reports* 14:14908.

Belay, Z. & Meseretu M., 2017. On farm phenotypic characterization of indigenous goat populations in Gamo Gofa zone South Western Ethiopia. *Journal of Advanced Studies in Agricultural, Biological and Environmental Sciences (JABE)* 4 (3): 23 – 32.

Bekalu, M., Kefelegn, K., Yoseph, M., 2016. Phenotypic Characterization of Indigenous Goat Types in West Gojjam Zone, Amhara National Regional State, Ethiopia. *Journal of Biology, Agriculture and Healthcare* 6 (6): 54 – 64.

Bembridge, T. & Tapson, D., 1993. Communal livestock systems. In Maree C & Casey N H (Eds) *Livestock Production Systems, Principles and Practices.* Agri Development Foundation, Brooklyn. Page 361 – 373.

Benjelloun, B., Alberto, F. J., Streeter, I., Boyer, F., Coissac, E., Stucki, S., 2015. Characterizing neutral genomic diversity and selection signatures in indigenous populations of moroccan goats (Capra hircus) using WGS data. *Frontiers in Genetics* 6:107. DOI: 10.3389.

Benhin, J.K., 2006. Climate change and South African agriculture: Impacts and adaptation options. CEEPA discussion paper.

Berihulay, H., Islam, R., Jiang, L. & Ma, Y., 2019. Genome-Wide Linkage Disequilibrium and the Extent of Effective Population Sizes in Six Chinese Goat Populations Using a 50K Single Nucleotide Polymorphism Panel. *Animals* 9: 350; DOI:10.3390/ani9060350.

Berihulay, H., Li, Y., Liu, X., Gebreselassie, G., Islam, R., Liu, W., Jiang, L., Ma, Y., 2019a. Genetic diversity and population structure in multiple Chinese goat populations using a panel. *Animal Genetics* 50(3): 242 – 249.

Berthouly-Salazar, C., Thévenon, S., Van, T.N., Nguyen, B.T., Pham, L.D., Chi, C. V., 2012. Uncontrolled admixture and loss of genetic diversity in a local Vietnamese pig breed. *Ecology Evolution* 2: 962 – 975.

Bertolini, F., Servin, B., Talenti A., Rochat, E., Kim, E. S., Oget, C., Palhière, I., Crisà, A., Catillo, G., Steri, R., Amills, M., Colli, L., Marras, G., Milanesi, M., Nicolazzi, E., Rosen, B. D., Van Tassell, C.P., Guldbrandtsen, B., Sonstegard, T.S., Tosser-Klopp, G., Stella, A., Rothschild, M. F., Joost, S., Crepaldi, P., 2018. Signatures of selection and environmental adaptation across the goat genome post-domestication. *Genetics Selection Evolution* 50: 57 doi.org/10.1186/s12711-018-0421-y

Bester, J., Ramsay, K.A. & Scholtz, M.M., 2009. Goat farming in South Africa: Findings of a national livestock survey. *Applied Animal Husbandry and Rural Development* 2: 9 – 13.

Bickhart, D. M., Rosen, B. D., Koren, S., Sayre, B. L., Hastie, A. R., Chan, S., 2017. Single-molecule sequencing and chromatin conformation capture enable de novo reference assembly of the domestic goat genome. *Nature Genetics* 49: 643 – 650.

Biscarini, F., Cozzi, P., Gaspa, G., Marras, G., 2018. Detect runs of homozygosity and runs of heterozygosity in diploid genomes. CRAN (The Comprehensive R Archive Network). https://github.com/bioinformatics-ptp/detectRUNS/tree/master/detectRUNS. (Accessed 30 March 2023).

Blasco, A. & Toro, M.A., 2014. A short critical history of the application of genomics to animal breeding. *Livestock Science* 166: 4 – 9.

Bosse, M., Megens, H.J., Madsen, O., Paudel, Y., Frantz, L. A., Schook, L. B., 2012. Regions of homozygosity in the porcine genome: consequence of demography and the recombination landscape. *PLOS Genet* 8: e1003100. DOI: 10.1371/journal.pgen.1003100.

Braker, M.J.E., Udo, H.M.J. & Webb, E.C., 2002. Impact of intervention objectives in goat production within subsistence farming systems in South Africa. *South African Journal of Animal Science* 32: 185 – 191.

Brito, L. F., Kijas, J. W., Ventura, R. V., Sargolzaei, M., Porto-Neto, L. R., Cánovas, A., 2017. Genetic diversity and signatures of selection in various goat breeds revealed by genome-wide SNP markers. *BMC Genomics* 18:229. DOI: 10.1186/s12863-015-0220-1.

Brito, L.F., Jafarikia M., Grossi, D., Maignel, L., Sargolzaei, M. & Schenkel, F., 2014. Characterization of linkage disequilibrium and consistency of gametic phase in Canadian goats. In: Proceedings of 10th World Congress of Genetics Applied to Livestock Production 17 – 22.

Bourzat, D., Zafindrajaona, P.S., Lauvergne, J.J. & Zeuh, V., 1993. Morpho-biometrical comparison between Northern Cameroon and Chad goat. *Rev. Elev. Méd. Vét. Pays Trop* 46: 667 – 674 [in French].

Broman, K. W. & Weber, J. L., 1999. Long homozygous chromosomal segments in reference families from the centre d'étude du polymorphisme humain. *American Journal of Human Genetics* 65: 1493 – 1500.

Brown, C., Orford, M., Tzamaloukas, O., Mavrogenis, A.P. & Miltiadou, D., 2014. Assessment of inbreeding resulting from selection for scrapie resistance: a model for rare sheep breeds. *Veterinary Records* 175: 624. From: https://doi.org/10.1136/vr.102503 (Accessed 04 April 2023).

Bruford, M. W., 2015. Prospects and challenges for the conservation of farm animal genomic resources, 2015-2025. *Frontiers in Genetics* 6: 314.

Bruno-de-Sousa, C., Martinez, A.M., Ginj, a C., Santos-Silva, F., Carolino, M.I., Delgado, J.V., Gama, L.T., 2011. Genetic diversity and population structure in Portuguese goat breeds. *Livestock Science* 135: 131– 139.

Boettcher, P.J., Hoffmann, I., Baumung, R., 2014. Genetic resources and genetics for adaptation of livestock to climate change. *Frontiers in Genetics* 5: 461.

Bozgo, V., Hoda, A., Biçoku, Y. & Bajramaj, R., 2012. Visible genetic profile and genetic distances of local goat populations in Albania. *Livestock Research for Rural Development.* Volume 24, Article #49. From: http://www.lrrd.org/lrrd24/3/hoda24049.htm (Accessed 30 March 2017).

Buchmann, R. & Hazelhurst, S., 2014. Genesis Manual. Johannesburg: University of Witwatersrand.

Caballero, A., Toro, M.A., 2002. Analysis of genetic diversity for the management of conserved subdivided populations. *Conservation Genetics* 3: 289 – 299.

Calvo, S.J., Gonzáles, M.I., Ángel, P.A., Cerón-Muñoz, M.F. & Cardona-Cadavid, H., 2012. Genetic evaluation of the goat population of Antioquia, using microsatellite markers. Livestock Research for Rural Development 24; Article #82. From:
http://www.lrrd.org/lrrd24/5/gonz24082.htm (Accessed 09 January 2024).

Cam, M., Olfaz M. & Soydan, E., 2010. Possibilities of using morphometrics characteristics as a tool for body weight prediction in Turkish hair goats (Kilkeci). *Asian Journal of Animal and Veterinary Advances* 5: 52 – 59.

Capote, J., Delgado, J.V., Fresno, M., Camacho, M.E., Molina, A., 1998. Morphological variability in the Canary goat population. *Small Ruminant Research* 27: 167 – 172.

Casey N. & Van Niekerk W., 1988. The Boer goat. I. Origin, adaptability, performance testing, reproduction and milk production. *Small Ruminant Research* 1: 291 – 302.

Cañon, J., García, D., García-Atance, M.A., Obexer-Ruff, G., Lenstra, J.A., Ajmone-Marsan, P. & Dunner, S., 2006. Geographical partitioning of goat diversity in Europe and the Middle East. *Animal Genetics* 37: 327 – 334.

Cardellino, R.A. & Boyazoglu, J., 2009. Research opportunities in the field of animal genetic resources. *Livestock Science* 120: 166 – 173.

Chacón, E., La O.M., Velásquez, F.J., Pérez, E., Delgado, J.V., Cos, Y., Fonseca, Y. & Martínez, A. 2012. Validation of the racial standards of the Cuban Creole goat for its international registration. *REDVET - Revista Electrónica de Veterinaria* 13: 1– 8.

Chokoe, T. C., Matelele, T.C., Maqhashu, A., Ramukhithi, F. V., Mphahlele, T. D., Mpofu, T. J., Nephawe, K. A., Mtileni, B. 2020. Phenotypic Diversity of South African Indigenous Goat Population in Selected Rural Areas. American. *Journal of Animinal and Veterinary Science*. 15 (1): 59. 66 DOI: 10.3844/ajavsp.2020.59.66.

Colli, L., Milanesi, M., Talenti, A., Bertolini, F., Chen, M., Crisà, A., 2018. Genome-wide SNP profiling of worldwide goat populations reveals strong partitioning of diversity and highlights post-domestication migration routes. *Genetics Selection Evolution* 50:58. DOI: 10.1186/s12711-018- 0422-x.

Curik, I., Ferenčaković, M., Sölkner, J., 2014. Inbreeding and runs of homozygosity: a possible solution to an old problem. *Livestock Science* 166: 26 – 34.

Deng, T., Liang, A., Liu, J., Hua, G., Ye, T., Liu, S., 2019. Genome-Wide SNP Data Revealed the Extent of Linkage Disequilibrium, Persistence of Phase and Effective Population Size in Purebred and Crossbred Buffalo Populations. *Frontiers in Genetics* 9: 688.

Department of Agriculture, Forestry and Fisheries (DAFF)., 2017b. Economic Review of the South African Agriculture 2016/17 Directorate Statistics and Economic Analysis. Pretoria: DAFF.1.

Department of Agriculture, Forestry and Fisheries (DAFF)., 2014. Newsletter: livestock statistics, estimated livestock numbers in RSA. From: http://www.daff.gov.za/daffweb3/Resource-Centre (Accessed 13 June 2018).

Department of Agriculture, Forestry and Fisheries (DAFF)., 2021. Republic of South Africa DAFF Annual Report 2020/2021.From: http://www.daff.gov.za (Accessed 22 September 2023).

Department of Agriculture, Land Reform and Rural Development (DALRRD)., 2018. A Profile of the South African Goat Market Value Chain 2018; Department of Agriculture, Forestry and Fisheries: Pretoria, South Africa. pp. 1–30.

Delgado J.V., Barba C., Camacho M.E., Sereno F.T.P.S., Martinez A. & Vega-Pla J.L., 2001. Livestock characterisation in Spain. *AGRI* 29: 7 – 18.

Dereje, T. B., Berhanu & Aynalem, H., 2013. Morphological Characterization of Indigenous Hararghe Highland Goat Breed in Their Native Environment, West Hararghe. *Ethiopia, American - Eurasian Journal of Scientific Research* 8(2): 72 – 79.

Dong, Y., Xie, M., Jiang, Y., Xiao, N., Du, X., Zhang, W., Tosser-Klopp, G., Wang, J., Yang, S. & Liang, J., 2013. Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (Capra hircus). *Nature Biotechnology* 31:35 – 41.

Donkin EF., Ramsay K.A., van Marle-Koster E., 2006. Goat research and Development in South Africa. Unpublished.

Donkin, E.F. and Boyazoglu, P.A., 2004. Diseases and mortality of goat kids in a South African milk goat herd. *South African Journal of Animal Science* 34: 258 – 261.

Donkin, E., Stewart C., MacGregor R., Els H. & Boyazoglu P., 1992. Resistance of indigenous and crossbred goats to heartwater (*Cowdria ruminantium*). In: Recent Advances in Goat Production, V International Conference on Goats, New Delhi, 1716 – 1719.

Dossa, L.H., Rischkowsky, B., Birner, R., & Wollny, C., 2008. Socioeconomic determinants of keeping goats and sheep by rural people in southern Benin. *Agriculture and Human Values* 25: 581–592.

Dossa, L.H., Wollny, C. & Gauly, M. 2007. Smallholders' perceptions of goat farming in southern Benin and opportunities for improvement. *Tropical Animal Health and Production* 39: 49 – 57.

Dube K, Muchenye V, Mupungwa J.F., 2016. Inbreeding depression and simulation of production potential of the communally raised indigenous Xhosa lop eared goat. *Small Ruminant Research* 144: 164 – 169.

Dube, K., 2015. Characterization of goat production systems in selected coastal areas of the Eastern Cape Province, South Africa. PhD Thesis, University of Fort Hare, South Africa. From: www.netd.ac.za (Accessed 04 October 2017).

Duguma, G., Mirkena, T., Haile, A., Iniguez, L., Okeyo, A. M., Tibbo, M., Rischkowsky, B., Solkner, J., Wurzinger, M., 2010. Participatory approaches to investigate breeding objectives of livestock keepers. *Livest Res Rural Dev*. Volume 22, Article 64. From: http://www.lrrd.org/lrrd22/4/dugu22064.htm (Accessed 08 May 2023).

Du Toit, C.J.L., Van Niekerk, W.A. & Meissner, H.H., 2014. Direct greenhouse gas emissions of the South African small stock sectors. *South African Journal of Animal Science* 43: 340 – 61.

Duvel, G.H. & Afful, D.B., 1994. Human constraints in stock reduction and communal land management in a subsistence farming situation in South Africa. Research Report. South African Institute for Agricultural Extension. University of Pretoria.

Ehret, C., 1982. The first spread of food production to southern Africa. *The Archaeological and Linguistic Reconstruction of African History* 158: 182.

Elphick, R., 1985. Khoikhoi and the founding of white South Africa. Johannesburg: Ravan.

Els, F., Kotze, J.A. & Swart, H., 2004. Genetic diversity of indigenous goats in Namibia using microsatellite markers: Preliminary results. *South African Journal of Animal Science* 34 (Supplement 2): 65 – 67.

Ensminger, M.E. & Parker, R.O., 1986. Sheep and Goat Science, Fifth Edition. Danville, Illinois: The Interstate Printers and Publishers Inc.

Epstein, H., 1971. The origin of the domestic animals of Africa. Africana, New York.

Excoffier, L., Laval G. & Schneider, S., 2005. Arlequin (version 3.0): an integrated software package for population genetics data analysis. *Evolutionary Bioinformatics Online* 1: 47.

Fatima, S., Bhonga, C.D., Ranka, D.N. & Joshi, C.G., 2008. Genetic variability and bottleneck studies in Zalawadi, Gohilwadi and Surti goat breeds of Gujarat (India) using microsatellites. *Small Ruminant Research* 77: 58 – 64.

Ferenčaković, M., Hamziæ, E., Gredler, B., Solberg, T. R., Klemetsdal, G., Curik, I., 2013. Estimates of autozygosity derived from runs of homozygosity: empirical evidence from selected cattle populations. *Journal of Animal Breeding and Genetics* 130: 286 – 293.
DOI: 10.1111/jbg.12012.

Ferenčaković, M., Hamzic, E., Gredler, B., Curik, I. & Sölkner, J., 2011. Runs of homozygosity reveal genome-wide autozygosity in the Austrian fleckvieh cattle. *Agriculturae Conspectus Scientificus* 76, 325 –328.

Frede, S., Fandrey, J., 2013. Cellular and molecular defences against hypoxia. In: Swenson ER, Bärtsch P, editors. High altitude: human adaptation to hypoxia. *New York:* Springer Press. 26
Fresco, L.O., Huizing, H., Van Keulen, H., Luning, H., Schipper, R., 1992. Land evaluation and farming system analysis for land use planning. FAO working document. Food and Agriculture Organization of the United Nation, Rome: Italy. 209.

Food and Agriculture Organization of the United Nations (FAO-UN)., 2021a. Surveying and monitoring of animal genetic resources. 7. Rome. From: http://www.fao.org/docrep/014/ba0055e/ba0055e00.htm (Accessed 14 January 2024).

Food and Agriculture Organization of the United Nations (FAO-UN)., 2021b. Molecular genetic characterization of animal genetic resources. 9. Rome. From: http://www.fao.org/docrep/014/i2413e/i2413e00.htm (Accessed 14 January 2024).

Food and Agriculture Organization of the United Nations (FAO-UN)., 2015a. "Status and trends of animal genetic resources –2014," in Fifteenth Regular Session of the Commission on Genetic Resources for Food and Agriculture, (CGRFA-15/15/Inf.18) (Rome). From: http://www.fao.org/3/a-mm278e.pdf (Accessed 06 February 2023).

Food and Agriculture Organization of the United Nations (FAO-UN)., 2015b. Draft Second Report on the State of the World's Animal Genetic Resources for Food and Agriculture (Part3), Commission on Genetic Resources for Food and Agriculture, (CGRFA-15/15/Inf.17.2) (Rome). From: http://www.fao.org/3/a-mm310e.pdf (Accessed 24 August 2023).

Food and Agriculture Organization of the United Nations (FAO-UN)., 2014. Youth and Agriculture: Key challenges and concrete solutions. Rome.

Food and Agriculture Organization of the United Nations (FAO-UN)., 2013. FAOSTAT Database, FAO, Rome, Italy. From: http://faostat3.fao.org/ (Accessed 04 April 2023).

Food and Agriculture Organization of the United Nations (FAO-UN)., 2012. Phenotypic characterization of animal genetic resources. FAO Animal Production and Health Guidelines No. 11. Rome.

Food and Agriculture Organization of the United Nations (FAO-UN)., 2007a. State of the World's Animal Genetic Resources for Food and Agriculture. Rome. From: http://www.fao.org/docrep/014/i2413e/i2413e00.htm (Accessed 24 April 2023).

Food and Agriculture Organization of the United Nations (FAO-UN)., 2007b. Global Plan of Action for Animal Genetic Resources and the Interlaken Declaration. Rome, 38 pp. From: http://www.fao.org/docrep/010/a1404e/a1404e00.htm (Accessed 04 December 2023).

Food and Agriculture Organization of the United Nations (FAO-UN)., 2000. World watch list for domestic animal diversity, 3rd edition. Rome.

Fontanesi, L., Dall'Olio, S., Beretti, F., Portolano, B. & Russo, V., 2011. Coat colours in the Massese sheep breed are associated with mutations in the agouti signalling protein (ASIP) and melanocortin 1 receptor (MC1R) genes. *Animal* 5(1): 8-17. https://doi.org/10.1017/S1751731110001382. (Accessed on March 25, 2023).

Flury, C., Tapio, M., Sonstegard, T., Drogemuller, C., Leeb, T., Simianer, H., Hanotte, O., Rieder, S., 2010. Effective population size of an indigenous Swiss cattle breed estimated from linkage disequilibrium. *Journal of Animal Breeding and Genetics* 127: 339 – 347.

Garcia-Gámez, E., Gutiérrez-Gil, B., Suarez-Vega, A., de la Fuente, L.F., Arranz, J.J., 2013. Identification of quantitative trait loci underlying milk traits in Spanish dairy sheep using linkage plus combined linkage disequilibrium and linkage analysis approaches. *Journal of Dairy Science* 96: 6059 – 6069.

Gandini, G., Oldenbroek, K., 2007. Strategies for moving from conservation to utilisation in: Oldenbroeck, K. (Ed.) Utilisation and conservation of farm animal genetic resources. Wageningen Academic Publ. pp. 55 – 74.

Garrine, C.M.L.P., 2007. Genetic characterization of indigenous goat populations of Mozambique. Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria. MSc thesis.

Gibson, J., Morton, N.E., Collins, A., 2006. Extended tracts of homozygosity in outbred human populations. *Human Molecular Genetics* 15: 789 – 795.

Ginja, C., Gama, L.T.; Martínez, A., Sevane, N., Martín-Burriel, I., Lanari, M.R., Revidatti, M.A., Aranguren-Méndez, J.A., Bedotti, D.O., Ribeiro, M.N., 2017. Genetic diversity and patterns of population structure in Creole goats from the Americas. *Animal Genetics* 48: 315 – 329.

Gizaw, S., Tegegne, A., Gebremedlin, B. and Hoekstra, D., 2010. Sheep and Goat Marketing Systems in Ethopia: Characteristics and strategies for improvement. IPMS (Improving Productivity and Market Success). *Famers project working paper* 23, ILRI (International Livestock Research Institute), Nairobi, Kenya, pp. 58.

Glowatzki-Mullis, M.L., Muntwyler, J., Baumle, E., Gaillard, C. 2008. Genetic diversity measures of Swiss goat breeds as decision-making support for conservation policy. Small Rumin. Res. 74: 202–211. DOI: 10.1016/j.smallrumres.2007.07.002.

Goddard, M., 2009. Genomic selection: prediction of accuracy and maximisation of long-term response. *Genetica* 136: 245 – 257.

González, A., Luque, M., Rodero, E., González, C., Aguilera, R., Jiménez, J., Sepúlveda, N., Bravo, S., 2011. Use of Morphometric Variables for Differentiating Spanish Hound Breeds. *International Journal of Morphology* 29: 1248 – 1255.

Groeneveld, L.F., Lenstra, J.A., Eding, H., Toro, M.A., Scherf, B., Pilling, D., Negrini, R., Finlay, E.K., Jianlin, H., Groeneveld, E., Weigend, S., 2010. The GLOBALDIV Consortium. Genetic diversity of farm animals – a review. *Animal Genetics* 41 (Suppl 1): 6 – 31.

Guo, J., Tao, H., Li, P., Li, L., Zhong, T., Wang, L., 2018. Whole-genome sequencing reveals selection signatures associated with important traits in six goat breeds. *Science Reports*. 8:10405. DOI: 10.1038/s41598-018-28719-w.

Gwaze, F.R., Chimonyo, M. & Dzama, K., 2009a. Variation in the functions of village goats in Zimbabwe and South Africa. *Tropical Animal Health and Producti*on 41: 1381 – 1391.

Gwaze, F.R., Chimonyo M. & Dzama K., 2009b. Communal goat production in Southern Africa: a review. *Tropical Animal Health and Production* 41: 1157 – 1168.

Gwaze, F.R., Chimonyo, M. & Dzama, K. 2009c. Prevalence and loads of gastrointestinal parasites of goats in the communal areas of the Eastern Cape Province of South Africa. *Small Ruminant Research* 84: 132 – 134.

Hagan J.K., Apori S.O., Bosompem M., Ankobea G. & Mawuli A., 2012. Morphological characteristics of indigenous goats in the coastal savannah and forest eco-zones of Ghana. *Journal of Animal Science Advances* 2: 813 – 821.

Hailu, D., Mieso, G., Nigatu, A., Fufa, D., Gamada, D., 2006. The effect of environmental factors on preweaning survival rate of Borana and Arsi-Bale kids. *Small Ruminant Research* 66: 291–294.

Halewood, M., Mugabe, J., 2002. Policy incentives for on-farm conservation and use of Africa's biodiversity. In: Almekinders, C.J.M. (Comp.) (Ed.), Incentive Measures for Sustainable Use and Conservation of Agrobiodiversity. Experiences and Lessons from Southern Africa. Proceedings of a Workshop, Lusaka, Zambia, 11–14 September 2001, pp. 73 – 88. From: http://www.cbd.int/doc/case-studies/inc/cs-inc-fao-incentivesagrobiodivworkshop2009-en.pdf (Accessed 22 June 2023).

Hall, S.J.G., 2004. Livestock Biodiversity, Genetic Resources for the Farming of the Future. Blackwell Science Ltd, Oxford, UK.

Hannotte, O. & Jialin, H., 2005. Genetic characterization of livestock populations and its use in conservation decision making. In J. Ruane & A. Sannino (Eds.), The role of biotechnology in exploring and protecting genetic resources (pp. 89–96). Rome.

Hammond, K. & Leitch, H. 1996. The FAO global program for the management of farm animal genetic resources. In: Miller, R., Pursel, V. and Norman, H. (Eds). Biotechnology's Role in the Genetic Improvement of Farm Animals. *American Society of Animal Science* Illinois: 24 – 42.

Harrison, R. G. & Larson, E. L., 2014. Hybridization, introgression, and the nature of species boundaries. *Journal of Heredity* 105 (Suppl): 795 – 809.

Hassen, H., Baum, M., Rischkowsky, B. & Tibbo, M., 2012. Phenotypic characterization of Ethiopian indigenous goat populations. *African Journal of Biotechnology* 11 (73): 13838 – 13846.
Hedrick, P. W., 2013. Adaptive introgression in animals: examples and comparison to new mutation and standing variation as sources of adaptive variation. *Molecular Ecology* 22: 4606 – 4618.

Herrero-Medrano, J.M., Megens, H.-J., Groenen, M.A.M., Boss, M., Pérez- Enciso, M. & Crooijmans, R.P.M.A., 2014.Whole-genome sequence Analysis reveals differences in population management and selection of European low-input pig breeds. *BMC Genomics* 15: 601.

Hoffmann, I., 2009. Open questions on poultry genetic diversity. Proc. 6th European Poultry Genetic Symposium in Poland. pp. 61–73.

Homann, S., van Rooyen, A., Moyo, T. and Nengomasha, Z., 2007. Goat production and marketing: Baseline information for semi-arid Zimbabwe. International Crops Research Institute for the Semi-Arid Tropics. From: http://www.icrisat.org/Publications-2007 (Accessed 12 April 2023).

Howrigan, D., Simonson, M. & Keller, M., 2011. Detecting autozygosity through runs of homozygosity: a comparison of three autozygosity detection algorithms. *BMC Genomics* 12: 460. DOI: 10.1186/1471-2164-12-460.

Hou, J., An, X., Li, G., Wang, Y., Song, Y., Cao, B., 2012. Exploring polymorphisms and their effects on reproductive traits of the INHA and INHβA genes in three goat breeds. *Animal Science Journal* 83: 273 – 278.

Huson, H., Sonstegard, T., Silverstein, J., Woodward-Greene, M., Masiga, C., Muchadeyi, F., Rees, J., Sayre, B., Elbetagy, A. & Rothschild, M., 2014. Genetic and phenotypic characterization of African goat populations to prioritize conservation and production efforts for small-holder farmers in Sub-Saharan africa. In: Vancouver, Canada: 10th World Congress on Genetics Applied to Livestock Production.

Iamartino, D., Bruzzone, A., Lanza, A., Blasi, M. & Pilla F., 2005. Genetic diversity of southern Italian goat populations assessed by microsatellite markers. *Small Ruminant Research* 57: 249 – 55.

Idowu, P. A. & Adelabu, O. A., 2018. An Investigation of Coat Colour Distribution of West African Dwarf Goats. *Journal of Agricultural Science* 10 (3): 228 – 236.

Islam, R., Li, Y., Liu, X., Berihulay, H., Abied, A., Gebreselassie, G., Ma, Q. & Ma, Y., 2019. Genome-Wide Runs of Homozygosity, Effective Population Size, and Detection of Positive Selection Signatures in Six Chinese Goat Breeds. *Genes* 10: 938; DOI:10.3390/genes10110938.

Jaitner, J., Sowe, J., Secka-Njie, E. and Dempfle, L., 2001. Ownership pattern and management practices of small ruminants in The Gambia — implications for a breeding programme. *Small Ruminant Research* 40:01 – 108.

Jimcy, J., Raghavan, K.C., Sujatha, K.S., 2011. Diversity of local goats in Kerala, India, based on morpho-biometric traits. *Livestock Research for Rural Development* 23:5. From:

http://www.lrrd.org/lrrd23/5/jimc23119.htm (Accessed 04 May 2023).

Joost, S., Colli, L., Baret, P.V., Garcia, J.F., Boettcher, P.J., Tixier-Boichard, M., 2010. Integrating geo-referenced multi scale and multidisciplinary data for the management of biodiversity in livestock genetic resources. *Animal Genetics* 41: 47 – 63.

Jordana, J., Ribo, O., Pelegrin, M., 1993. Analysis of genetic relationships from morphological characters in Spanish goat breeds. *Small Ruminant Research* 12: 301 – 314.

Kalinowski, S. T., 2004. Counting alleles with rarefaction: Private alleles and hierarchical sampling designs. *Conservation Genetics* 5(4): 539 – 543.
https://DOI.org/10.1023/B:COGE.0000041021.91777.1a.

Kalinowski, S. T. 2004. Counting alleles with rarefaction: private alleles and hierarchical sampling designs. *Conservation Genetics*. 5: 539 – 543.

Katongole, J.B.D., Sebolai, B., Madimabe, M.J., 1996. Morphological characterization of the Tswana goat. In: S.H.B. Lebbie and E. Kagwini (ed.) Small Ruminant Research and Development in Africa. *Proc. 3rd Biennial Conference of the African Small Ruminant Research Network, UICC, Kampala, Uganda.* 5-9 Dec. 1994. pp. 43 – 46.

Keller, M.C., Visscher, P.M., 2011. Goddard ME. Quantification of inbreeding due to distant ancestors and its detection using dense single nucleotide polymorphism data. *Genetics* 189: 237 – 249.

Khanyile, K.S., Dzomba, E.F. & Muchadeyi, F.C., 2015. Population genetic structure, linkage disequilibrium and effective population size of conserved and extensively raised village chicken populations of Southern Africa. *Frontiers in Genetics* 6: 13.

Khowa, A.A., Tsvuura, Z., Slotow, R and Kraai, M., 2023a. The utilisation of domestic goats in rural and peri-urban areas of KwaZulu-Natal, South Africa. *Trop Anim Health Prod* 55(3): 204.

DOI: 10.1007/s11250-023-03587-3.

Khowa, A.A., Tsvuura, Z., Kraai, M., 2023b. Pricing patterns of an indigenous goat in rural and urban communities in KwaZulu-Natal, South Africa. *Small Ruminant Research* 228: 107115 https://DOI.org/10.1016/j.smallrumres.2023.107115.

Kijas, J.W., Ortiz J.S., McCulloch, R., James A., Brice, B., Swain B. & Tosser - Klopp, G., 2013. Genetic diversity and investigation of polledness in divergent goat populations using 52 088 SNPs. *Animal genetics* 44: 325 – 335.

Kim, E., Elbeltagy, A., Aboul-Naga, A., Rischkowsky, B., Sayre, B., Mwacharo, J. & Rothschild, M., 2016. Multiple genomic signatures of selection in goats and sheep indigenous to a hot arid environment. *Heredity* 116: 255 – 264.

Koreth, J., O'Leary, J.J., O'D McGee, J., 1996. Microsatellites and PCR genomic analysis. *Journal of Pathology* 178: 239 – 248.

Kosgey, I.S., Rowlands, G.J., van Arendonk, J. A. M. and Baker, R.L., 2008. Small ruminant production in smallholder and pastoral/extensive farming systems in Kenya. *Small Ruminant Research* 77: 11 – 24.

Kosgey, I.S. & Okeyo, A.M. 2007. Genetic improvements of small ruminants in low-input, smallholder production systems: Technical and infrastructural issues. In: Notter, D.R., Barker, R.L., Cockett, N. (Eds.), The Outlook for Quantitative and Molecular Genetic Applications in Improving Sheep and Goats. *Small Ruminant Research* 70: 76 – 88.

Kotze, A., Grobler, J.P., van Marle-Koster, E., Jonker, T. & Dalton, D.L., 2014. The Tankwa Karoo National Park feral goat population: A unique genetic resource. *South African Journal of Animal Science* 44 (1): 43 – 48.

Kotze, A., Swart, H., Grobler, J.P., Nemaangani, A. 2004. A genetic profile of the Kalahari Red goat breed from Southern Africa. *South African Journal of Animal Science* 34: 10 – 12.

Kropff, A.S., Visser, C., Kotze, A., 2023. A homozygosity-based investigation of the South African feral Tankwa goat population. Small Ruminant Research 227: DOI.org/10.1016/j.smallrumres.2023.107086

Kraai, M., Tsvuura, Z., Khowa, A.A., 2022. The reproductive performance of goats in a South African semi-arid savanna. *J. Arid Environ* 200: 104723 https://DOI.org/10.1016/j.jaridenv.2022.104723.

Kruger, A.C & Sekele, S.S., 2013. Trends in extreme temperature indices in South Africa: 1962–2009. *Int J Climatol* 33: 661–676.

Kunene, N.W., Ceccobelli, S., Di Lorenzo, P., Hlophe, S.R., Bezuidenhout, C.C., Lasagna, E., 2014. Genetic diversity in four populations of Nguni (Zulu) sheep assessed by microsatellite analysis. *Italian Journal of Animal Science* 13: 76 – 82.

Kunene, N. & Fossey, A.**,** 2006. A survey on livestock production in some traditional areas of Northern Kwazulu Natal in South Africa. *Livestock Research for Rural Development* 18: 30 – 33.

Lanari, M.R., Taddeo, H., Domingo, E., Centeno, M.P., Gallo, L., 2003. Phenotypic differentiation of exterior traits in local Criollo goat population in Patagonia (Argentina). *Arch Tierz Dummerstorf* 46: 347 – 356.

Lashmar, S., Visser, C. & van Marle-Köster, E., 2016. SNP-based genetic diversity of South African commercial dairy and fiber goat breeds. *Small Ruminant Research* 136: 65 – 71.

Lashmar, S., Visser, C. & van Marle-Köster, E. 2015 Validation of the 50k Illumina goat SNP chip in the South African Angora goat. *South African Journal of Animal Science* 45: 56 – 59.

Lenstra, J.A., Groeneveld, L.F., Eding, H., Kantanen, J., Williams, J.L., Taberlet, P., 2012. Molecular tools and analytical approaches for the characterization of farm animal genetic diversity. *Animal Genetics* 43: 483 – 502.

Lebbie S. 2004. Goats under household conditions. *Small Ruminant Research* 51: 131 – 136.

Leutenegger, A.-L., Prum, B., Génin, E., Verny, C., Lemainque, A., Clerget-Darpoux, F., 2003. Estimation of the inbreeding coefficient through use of genomic data. *American Journal of Human Genetics* 73: 516 – 523.

Li, M., Zhao, S., Bian, C., 2002. Genetic relationships among twelve Chinese indigenous goat populations based on microsatellite analysis. *Genetics Selection Evolution* 34: 729 – 44.

Lin, B.Z., Sasazaki, S. & Mannen, H., 2010. Genetic diversity and structure in Bos Taurus and Bos indicus populations analyzed by SNP markers. *Animal Science Journal* 81: 281 – 289.

Liu, S., He, S., Chen, L., Li, W., Di, J., Liu, M., 2017. Estimates of linkage disequilibrium and effective population sizes in Chinese Merino (Xinjiang type) sheep by genome-wide SNPs. *Genes Genomics* 39: 733 – 745.

Liu, J.B., Wang, F., Lang, X. 2013. Analysis of geographic and pairwise distances among chinese cashmere goat populations. *Asian-Australasian Journal of Animal Science*. 26:323 – 233. DOI: 10.5713/ajas.2012.12500.

Luu, K., Bazin, E. & Blum, M. G. B., 2017. pcadapt: An R package to perform genome scans for selection based on principal component analysis. *Molecular Ecology Resources* 17: 67 – 77. https://DOI.org/10.1111/men.2017.17.

Madubi, M., Kifaro, G. & Petersen, P., 2000. Phenotypic characterization of three strains of indigenous goats in Tanzania. *Animal Genetic Research Info* 28: 43 – 51.

Mahan S., Semu S., Peter T. & Jongejan F., 1998. Evaluation of the MAP- 1B ELISA for Cowdriosis with Field Sera from Livestock in Zimbabwea. *Annals of the New York Academy of Sciences* 849: 259 – 261.

Mahanjana, A.M. and Cronjé, P.B., 2000. Factors affecting goat production in a communal farming system in the Eastern Cape region of South Africa. *South African Journal of Animal Science* 30 (2): 149 – 154.

Magoro, A.M., Mtileni, B., Hadebe, K., Zwane, A., 2022. Assessment of Genetic Diversity and Conservation in South African Indigenous Goat Ecotypes: A Review. *Animals* 12: 3353. https://DOI.org/10.3390/ani12233353.

Makina, S.O., Muchadeyi, F.C., Marle-Köster, E., Taylor, J.F., Makgahlela, M.L. & Maiwashe, A., 2015. Genome-wide scan for selection signatures in six cattle breeds in South Africa. *Genetics Selection Evolution* 47 (1): 92.

Mukhongo, D. M., Mwai, O., Tapio, M. & Muigai, A., 2014. Genetic diversity and population structure of the indigenous sheep in Kenya based on microsatellite analysis: Implications for their conservation. *Journal of Livestock Science* 5: 65 – 78.

Manel, S., Joost, S., Epperson, B.K., Holderegger, R., Storfer, A., Rosenberg, M.S., Scribner, K.T., Bonin, A. & Fortin, M.J., 2010. Perspectives on the use of landscape genetics to detect genetic adaptive variation in the field. *Molecular Ecology* 19: 3760 – 3772.

Manton, H., 2005. Dreams and Medicines: The Perspective of Xhosa Diviners and Novices in the Eastern Cape, South Africa. *Indo-Pacific Journal of Phenomenology* 5: 1 – 22.

Manzi, M., Rutagwenda, T., Kanuya, N. & Chatikobo, P., 2011. Phenotypic characterization of goats raised under traditional husbandry systems in Bugesera and Nyagatare districts of Rwanda. *Journal of Animal and Veterinary advances* 10 (24): 3297 – 3302.

Manunza, A., Noce, A., Serradilla, J. M., Goyache, F., Martínez, A., Capote, J., 2016. A genome-wide perspective about the diversity and demographic history of seven spanish goat breeds. *Genetics Selection and Evolution* 48:52. DOI: 10.1186/s1271 – 016 – 0229 – 6.

Mapiliyao L., 2010. Sheep production practices, flock dynamics, body condition and weight variation in two ecologically different resource poor communal farming systems. Msc Thesis. University of Fort Hare, South Africa.

Mapiye, O., Makombe, G., Mapiye, C., Dzama, K., 2018. Limitations and prospects of improving beef cattle production in the smallholder sector: a case of Limpopo Province, South Africa. *Tropical Animal Health and Production* doi: 10.1007/s11250 – 018 – 1632 – 5.

Masika, P. & Mafu, J. V., 2004. Aspects of goat farming in the communal farming systems of the central Eastern Cape, South Africa. *Small Ruminant Research* 52 (1-2): 161–164.

Mashau, T.D., 2013. Occultism in an African context: a case for the Vhavenda-speaking people of the Limpopo Province. *In die Skriflig* 41 (4): 637 − 653.

Matshaba, B., Schwalbach, L.M., Mphaphathi, M., Nemes, C., Ngwane, C., Greyling, J.P., Váradi, É. & Nedambale, T.L., 2010. *Characterization of semen from the unimproved South African indigenous goats*: *proceedings of the Second RUFORUM Biennial Meeting, held in Uganda on 20 – 24 September 2010.* Entebbe.

Marras, G., Gaspa, G., Sorbolini, S., Dimauro, C., Ajmone-Marsan, P., Valentini, A., 2015. Analysis of runs of homozygosity and their relationship with inbreeding in five cattle breeds farmed in Italy. *Animal Genetics* 46: 110–121. DOI: 10.1111/age.12259.

Marras, G., Gaspa, G., Sorbolini, S., Dimauro, C., Ajmone-Marsam, P., Valentini, A., 2014. Analysis of runs of homozygosity and their relationship with inbreeding in five cattle breeds farmed in Italy. *Animal Genetics* 46:110 –121.

Maree, C. & Plug, I., 1993. Origin of Southern African Livestock and their potential role in the industry. In Livestock Production Systems. Casey & Maree (Eds). Agri Development Foundation, Pretoria, South Africa. ISBN 0-620-17126.

Marume, U., Chimonyo, M. & Dzama, K., 2013. Some insights into the reproductive performance, selection criteria, production and market constraints in communal goat production systems of South Africa. *Scientific Research and Essays* 8: 1448 – 1458.

Martin, P. M., Palhière, I., Ricard, A., Tosser – Klopp, G., Rupp, R., 2016. Genome Wide Association Study Identifies New Loci Associated with Undesired Coat Color Phenotypes in Saanen Goats. *PLoS ONE* 11, e0152426.

Martinez, A.M., Gama, L.T., Delgado, J.V., 2015. The South Western fringe of Europe as an important reservoir of caprine biodiversity. *Genetics Selection Evolution* 47: 86.

Mastrangelo, S., Tolone, M., Sardina, M.T., Sottile, G., Sutera, A.M., 2017. Genome-wide scan for runs of homozygosity identifies potential candidate genes associated with local adaptation in Valle del Belice sheep. *Genetics Selection Evolution* 49 (1): 84. 10.1186/s12711-017-0360-z.hal-01635193.

Mastrangelo, S., Tolone, M., Di Gerlando, R., Fontanesi, L., Sardina, M.T., Portolano, B., 2016. Genomic inbreeding estimation in small populations: evaluation of runs of homozygosity in three local dairy cattle breeds. *Animal* 10:746 – 54.

Mavule, B.S., Sarti, F.M., Lasagna, E., Kunene, N. W., 2016. Morphological differentiation amongst Zulu sheep populations in KwaZulu-Natal, South Africa, as revealed by multivariate analysis. *Small Ruminant Research* 06: 001.

Mbole-Kariuki, M., Sonstegard, T., Orth A., Thumbi, S., de C Bronsvoort, B., Kiara, H., Toye, P., Conradie, I., Jennings, A. & Coetzer, K., 2014. Genome-wide analysis reveals the ancient and recent admixture history of East African Shorthorn Zebu from Western Kenya. *Heredity*. 113: 297 – 305.

McRae, K.M., McEwan, J.C., Dodds, K.G., Gemmell, N.J., 2014. Signatures of selection in sheep bred for resistance or susceptibility to gastrointestinal nematodes. *BMC Genomics*. 15(1):1.
McQuillan, R., Leutenegger, A.L, Abdel-Rahman, R., Franklin, C.S., Pericic, M., M., Barac-Lauc, L., 2008. Runs of homozygosity in European populations. *American Journal of Human Genetics* 83(3): 359 372. https://doi.org/10.1016/j.ajhg.2008.08.007 PMID: 18760389.

Mdladla, K., Dzomba, E.F. & Muchadeyi, F.C., 2018. Landscape genomics and pathway analysis to understand genetic adaptation of South African indigenous goat populations. *Heredity* 120(4): 369 – 378.

Mdladla, K., Dzomba, E.F. & Muchadeyi, F.C., 2017.Characterization of the village goat production systems in the rural communities of the Eastern Cape, KwaZulu-Natal, Limpopo and North West Provinces of South Africa. *Tropical Animal Health and Production* 49: 515 – 527.

Mdladla, K., 2016. Landscape genomic approach to investigate genetic adaptation in South African indigenous goat populations. PhD thesis. University of KwaZulu-Natal, South Africa.

Mdladla, K., Dzomba, E.F., Huson, H.J. & Muchadeyi, F.C., 2016a. Population genomic structure and linkage disequilibrium analysis of South African goat breeds using genome-wide SNP data. *Animal Genetics* 47: 471 – 482.

Mekuriaw, G., Gizaw, S., Dessie, T., Mwai, O., Djikeng, A. & Tesfaye, K. (2016). A review on current knowledge of genetic diversity of domestic goats (Capra hircus) identified by microsatellite loci: How those efforts are strong to support the breeding programs? *Journal of Life Science and Biomedicine*. 6(2), 22–32.

Mellor, J.W., Malik, S.J., 2017. The impact of growth in small commercial farm productivity on rural poverty reduction. *World Development* 91: 1-10.

Mendelsohn, R., 2003. The challenge of conserving indigenous domesticated animals. *Ecological economics* 45: 501 – 510.

Menezes M.P., Martínez A.M., Ribeiro M.N., Pimenta-Filho E.C. & Bermejo J.V.D. 2006. Caracterização genética de raças caprinas nativas Brasileiras utilizando 27 marcadores microssatélites. *Revista Brasileira de Zootecnia* 35: 1336 – 1341.

Meuwissen, T.H. & Goddard, M.E., 2007. Multipoint identity-bydescent prediction using dense markers to map quantitative trait loci and estimate effective population size. *Genetics* 176: 2551–60.

Miao, B., Wang, Z., Li, Y., 2017. Genomic analysis reveals hypoxia adaptation in the Tibetan Mastiff by introgression of the gray wolf from the Tibetan Plateau. *Molecular Biology and Evolution* 34 (3): 734 – 743.

Missohou, A., Poutya, M.R., Nenonene, A., Dayo, G.K., Ayssiwede, S.B., Talaki, E., Issa, Y. & Fane, A., 2011. Genetic diversity and differentiation in nine West African local goat breeds assessed via microsatellite polymorphism. *Small Ruminant Research* 99: 20 – 24.

Mohlatlole R.P., Dzomba E.F. & Muchadeyi F.C**.,** 2015. Addressing production challenges in goat production systems of South Africa: The genomics approach. *Small Ruminant Research* 131: 43 – 49.

Mohmmed, D., Amin, J.D., 1997. Estimating body weight from morphometric measurements of Sahel (Borno White) goats. *Small Ruminant Research* 24: 1 – 5.

Monau, P.I., Raphaka, K., Zvinorova-Chimboza, P. & Gondwe, T., 2020. Sustainable Utilization of Indigenous Goats in Southern Africa. *Diversity* 12: 20; DOI:10.3390/d12010020.

Monau, P.I., Visser, C., Nsoso, S.J., van Marle-Koster, E., 2017. A survey analysis of indigenous goat production in communal farming systems of Botswana. *Tropical Animal Health and Production* 49: 1265 –1271.

Moradi, M.H., Nejati-Javaremi, A., Moradi-Shahrbabak, M., Dodds, K.G., McEwan, J.C., 2012. Genomic scan of selective sweeps in thin and fat tail sheep breeds for identifying of candidate regions associated with fat deposition. *BMC Genomics*. 13(1):1.

Morand-Fehr, P., Boutonnet, J., Devendra, C., Dubeuf, J., Haenlein, G., Holst, P., Mowlem, L. & Capote, J., 2004. Strategy for goat farming in the 21st century. *Small Ruminant Research* 51: 175 – 183.

Morrison, J.W., 2007. A guide to the identification of the natural indigenous goats of Southern Africa. From: http://www.landbou.com/wp.../03/f2297405-a93f-4399-bdb7- 6f3de538d75d.pdf. (Accessed 20 April 2023).

Mpofu, N., 2002. Choice of genetic types for specific production environments and production systems. AGTR Case Study. Nirobi, Kenya: International Livestock Research Institute. From: http://www.hdl.handle.net/10568/3583 (Accessed 04 March 2023).

Msanga, Y.N., Mwakilembe, P.L. & Sendalo, D., 2012. The indigenous cattle of the Southern Highlands of Tanzania: Distinct phenotypic features, performance and uses. *Livestock Research and Rural Development* 110: 1 – 24.

Mthi, S., Skenjana, A., Fayemi, P. O., 2017. Characteristics of small-scale sheep production systems in some communal areas of the Eastern Cape Province, South Africa. *International Journal of Livestock Production* 8: 199 – 206.

Muema, E. K., Wakhungu, J.W., Hanotte, O. & Jianlin, H., 2009. Genetic diversity and relationship of indigenous goats of Sub-saharan Africa using microsatellite DNA markers. Livestock Research for Rural Development. Volume 21, Article #28. From: http://www.lrrd.org/lrrd21/2/muem21028.htm (Accessed 09 June 2023).

Mwacharo, J. M., Kim, E.-S., Elbeltagy, A. R., Aboul-Naga, A. M., Rischkowsky, B. A., & Rothschild, M. F., 2017. Genomic footprints of dryland stress adaptation in Egyptian fat-tail sheep and their divergence from East African and western Asia cohorts. *Scientific Reports*. 7:17647. DOI: 10.1038/s41598-017-17775-3

Nandolo, W., Mészáros, G., Banda, L.J., Gondwe, T.N., Lamuno, D., Mulindwa, H.A., Nakimbugwe, H.N., Wurzinger, M., Utsunomiya, Y.T., Woodward-Greene, M.J., Liu, M., Liu, G., Van Tassell, C.P., Curik, I, Rosen, B.D. & Sölkner, J., 2019. Timing and Extent of Inbreeding in African Goats. *Frontiers in Genetics* 10:537. DOI: 10.3389/fgene.2019.00537.

Nandolo, W., Wurzinger, M., Mészáros, G., van Tassell, C., Gondwe, T., Mulindwa, H., 2017. Estimation of inbreeding in Ethiopian goats using runs of homozygosity. *Acta Fytotech Zootech* 20: 10 – 12. DOI: 10.15414/afz.2017.20.01. 10-12.

Ncube, K., 2016. Maternal lineages and diversity of the growth hormone gene of South African goat populations. Msc dissertation. University of South Africa, South Africa.

Ndumu, D., Wurzinger, M., Baumung, R., Drucker, A., Mwai, O., Semambo, D. & Sölkner, J., 2008. Performance and fitness traits versus phenotypic appearance in the African Ankole Longhorn cattle: a novel approach to identify selection criteria for indigenous breeds. *Livestock Science* 113: 234–242.

Nguluma, A.S., Huang, Y., Zhao, Y., Chen, L., Msalya, G., Lyimo, C., Guangxin, E. & Chenyambuga, S.W., 2018. Assessment of genetic variation among four populations of Small East African goats using microsatellite markers. *South African Journal of Animal Science* 48: 117 – 127.

Nicolazzi, E.L., Caprera, A., Nazzicari, N., Cozzi, P., Strozzi, F., Lawley, C., 2015. SNPchiMpv.3: integrating and standardizing single nucleotide Polymorphism data for livestock species. *BMC Genomics* 16: 283.

Nicoloso, L., Bomba, L., Colli, L., Negrini, R., Milanesi, M., Mazza, R., Sechi, T., Frattini, S., Talenti, A. & Coizet, B., 2015. Genetic diversity of Italian goat breeds assessed with a medium-density SNP chip. *Genetics Selection Evolution* 47: 62. DOI 10.1186/s12711-015-0140-6.

Nomura, K., Ishii, K., Dadi, H., Takahashi, Y., Minezawa, M., 2012. Microsatellite DNA markers indicate three genetic lineages in East Asian indigenous goat populations. *Animal Genetics* 43: 760 – 767.

Nothnagel, M., Lu, T.T., Kayser, M., Krawczak, M., 2010. Genomic and geographic distribution of SNP-defined runs of homozygosity in Europeans. *Human Molecular Genetics* 19: 2927 – 2935.

Nsoso, S.J., Podisi, B., Otsogile, E., Mokhutshwane, B.S. & Ahmadu, B., 2004. Phenotypic characterization of indigenous Tswana goats and sheep breeds in Botswana: continuous traits. *Tropical Animal Health and Production*, 36: 789 – 800.

Nyamushamba, G. B., Mapiye, C., Tada O., Halimani, T. E., Muchenje, V., 2017. Conservation of indigenous cattle genetic resources in Southern Africa's smallholder areas: turning threats into opportunities—a review. *Asian-Australasian Journal of Animal Science* 30: 603 – 621.

Ofori, J.K. Hagan., 2021. Characteristics and trait preferences of West African Dwarf goat keepers in Ghana. T*rop. Anim. Health Prod* 53: 356.

Okpeku, M., Yakubu, A., Olusolapeters, S., Ozoje, M.O., Ikeobi, C.O., Adebambo, O.A., 2011. Application of multivariate principal component analysis to morphological characterization of indigenous goats in southern Nigeria. *Acta Agriculturae Slovenica* 98: 101 – 109.

Okourwa, M.I., 2015. Effect of coat characteristics on physiological traits and heat tolerance of West African Dwarf sheep in Southern Nigeria. *Open Journal of Animal Science* 5: 351-357. DOI: 10.4236/ojas.2015.54039.

Oldenbroek, K., 2007. Introduction. In: Oldenbroek, K. (Ed.), Utilisation and Conservation of Farm Animal Genetic Resources. Wageningen Academic Publishers, The Netherlands, pp. 13– 27.

Onzima, R.B., Upadhyay, M.R., Doekes, H.P., Brito, L.F., Bosse, M., Kanis, E., Groenen, M.A.M. & Crooijmans, R.P.M.A., 2018. Genome-Wide Characterization of Selection Signatures and Runs of Homozygosity in Ugandan Goat Breeds. *Frontiers in Genetics* 9: 318. DOI: 10.3389.

Osinowo, O.A., Buvanendram, V., Koning, N.L., 1988. A study of coat type, pigmentation and wattle incidence in Yankasa sheep and their effects on fertility and weaning weight. *Paper presented at the 13th Annual Conference of the Nig-Soc. Of Animal Prod. Held at the University of Calabar*, 20-24 March 1988: 10pp.

Ouborg, N.J, Pertoldi, C., Loeschcke, V., Bijlsma, R., Hedrick, P.W., 2010. Conservation genetics in transition to conservation genomics. *Trends Genetics* 26:177 – 87.

Ozoje, M., 2002. Incidence and relative effects of qualitative traits in West African Dwarf goat. *Small Ruminant Research* 43: 97 – 100.

Pariset, L., Joost, S., Marsan, P.A., 2009. Landscape genomics and biased F_{ST} approaches reveal single nucleotide polymorphisms under selection in goat breeds of North-East Mediterranean. *BMC Genomics*.10:1. doi: 10.1186/1471-2156-10-7.

Peacock, C., 2005. Goats—A pathway out of poverty. *Small Ruminant Research* 60: 179 – 186.

Pemberton, T.J., Absher, D., Feldman, M.W., Myers, R.M., Rosenberg, N.A., Li, J.Z., 2012. Genomic patterns of homozygosity in worldwide human populations. *American Journal of Human Genetics* 91: 275 – 292.

Peripolli, E., Stafuzza, N. B., Munari, D. P., Lima, A. L. F., Irgang, R., Machado, M. A., 2018. Assessment of runs of homozygosity islands and estimates of genomic inbreeding in Gyr (Bos indicus) dairy cattle. *BMC Genomics* 19:34. DOI: 10.1186/s12864-017-4365-3.

Pieters, A., van Marle-Koster, E., Visser, C., & Kotze, A., 2009. South African developed meat type goats: A forgotten animal genetic resource? *Animal Genetic Resources Information* 44: 33 – 44.

Pieters A., 2007. Genetic characterization of commercial goat populations in South Africa. Msc thesis. University of Pretoria, South Africa.

Purcell, S., Neale, B., Todd-Brown, K., Thomas, L., Ferreira, M.A., Bender, D., Maller, J., Sklar, P., De Bakker, P.I. & Daly, M.J., 2007. PLINK: a tool set for whole-genome association and population-based linkage analyses. *The American Journal of Human Genetics* 81: 559 – 575.

Purfield, D. C., McParland, S., Wall, E., Berry, D. P., 2017. The distribution of runs of homozygosity and selection signatures in six commercial meat sheep breeds. *PLoS One* 12: e0176780. DOI: 10.1371/journal.pone.0176780.

Purfield, D.C., Berry, D.P., McParland, S., Bradley, D.G., 2012. Runs of homozygosity and population history in cattle. *BMC Genomics* 13:70. DOI: 10.1186/1471-2156-13-70.

Qiu, Q., Zhang, G., Ma, T., Qian, W., Wang, J., Ye, Z., Cao, C., Hu, Q., Kim, J., Larkin, D.M., 2012. The yak genome and adaptation to life at high altitude. *Nature Genetics* 44(8): 946 – 949.

Riva, J., Rizzi, R., Marelli, S., Cavalchini, L.G., 2004. Body measurements in Bergamasca sheep. *Small Ruminant Research* 55: 22 – 227.

Rahmatalla, S.A., Arends, D., Reissmann, M., Ahmed, A. S., Wimmers, K., Reyer, H., Brockmann, G.A. 2018. Whole genome population genetics analysis of Sudanese goats identifies regions harboring genes associated with major traits. *BMC Genetics* 18: 92 DOI 10.1186/s12863-017-0553-z.

Reist-Marti, S.B., Simianer, H., Gibson, J., Hanotte, O., Rege, J.E.O., 2003. Weitzman's Approach and Conservation of Breed Diversity: an Application to African Cattle Breeds. *Conservation Biology* 17: 1299 – 1311.
Riva, J., Rizzi, R., Marelli, S., Cavalchini, L.G., 2004. Body measurements in Bergamasca sheep. *Small Ruminant Research* 55: 222 – 227.

Roessler, R., Drucker, A. G., Scarpa, R., Markemann, A., Lemke, U., Thuy, L.T. & Valle, Z. A., 2008. Using choice experiments to assess smallholder farmers' preferences for pig breeding traits in different production systems in North–West Vietnam. *Ecological Economics* 66 (1): 184 – 192.

Roets, M. & Kirsten, J., 2005. Commercialization of goat production in South Africa. *Small Ruminant Research* 60:187 – 195.

Rege, J. & Gibson J., 2003. Animal genetic resources and economic development: issues in relation to economic valuation. *Ecological economics* 45: 319 – 330.

Rege, J., 1994. Indigenous African small ruminants: a case for characterisation and improvement. In: *Small Ruminant Research and Development in Africa, Proceedings of the Second Biennial Conference of the African Small Ruminant Research Network*, 205 – 211.

Rewe TO, Ogore PB, Kahi AK., 2002. Integrated goat projects in Kenya: Impact on genetic improvement. In: Proceedings of the Seventh World Congress on Genetics Applied to Livestock Production, held in Montpellier, France, pp. 385 – 387.

Rumosa-Gwaze, F., 2009. Communal Production Systems of Goats Raised by Resource Poor Farmers in the Eastern Cape Province of South Africa. PhD Thesis, University of Fort Hare, Alice, South Africa. From: www.netd.ac.za. (Accessed 30 November 2023).

Sanderson, M.A., Archer, D., Hendrickson, J., Kronberg, S., Liebig, M., Nichols, K., 2013. Diversification and ecosystem services for conservation agriculture: outcomes from pastures and integrated crop-livestock systems. *Renewable Agriculture and Food Systems* 26: 129 – 144.

Sangaré, M., Pandey, V.S., 2000. Food intake, milk production and growth of kids of local goats grazing on dry season natural Sahelian rangeland in Mali. *Animal Science*. 71:165 – 173.
SAS Institute Inc., 2014. SAS/ETS User's Guide, Version 13.1, Cary, NC: SAS Institute Inc.

Schoeman, S. J., Cloete, S. W. P., Olivier, J. J., 2010. Returns on investment in sheep and goat breeding in South Africa. *Livestock. Science* 130: 70 – 82.

Scraggs, E., Zanella, R., Wojtowicz, A., Taylor, J.F., Gaskins, C.T., Reeves, J.J., 2014. Estimation of inbreeding and effective population size of full-blood Wagyu cattle registered with the American Wagyu Cattle Association. *Journal of Animal Breeding and Genetics* 131: 3 – 10.

Schulze, R.E., Hewitson, B.C., Barichievy, K.R., Tadross, MA., Kunz, R.P, Horan, M.J.C, Lumsden, T.G., 2010. Methodological approaches to assessing eco-hydrological responses to climate change in South Africa. South Africa: Water Research Commission; Report No.: Rep. 1562/1/10.

Shabalala, N. & Mosima, B., 2002. Report on the survey of large- and small-scale agriculture/Statistics South Africa. In: Statistics SA Library Cataloguing-in-Publication (CIP) Data Pretoria Statistics South Africa., South Africa.

Semakula, J., Mutetikka, D., Kugonza, R. D. and Mpairewe, D., 2010. Variability in Body Morphometric Measurements and Their Application in Predicting Live Body Weight of Mubende and Small East African Goat Breeds in Uganda. *Middle East Journal of Scientific Research* 5 (2): 98 – 105.

Serrano, M., Calvo J.H., Martinez, M., Marcos-Carcavilla, A., Cuevas, J., Gonzalez, C., Jurado, J.J. & de Tejada, P.D., 2009. Microsatellite based genetic diversity and population structure of the endangered Spanish Guadarrama goat breed. *BMC Genomics* 10: 61.

Sebei, P.J., McCrindle, C.M.E. and Webb, E.C., 2004. Factors influencing weaning percentages of indigenous goats on communal grazing. *South African Journal of Animal Science* 34 (1): 130 – 133.

Sebei P., McCrindle C. & Webb E., 2004a. An economic analysis of communal goat production. *Journal of the South African Veterinary Association* 75: 19 – 23.

Sebei, P., McCrindle, C. & Webb, E., 2004b. Factors influencing weaning percentages of indigenous goats on communal grazing. *South African Journal of Animal Science* 34: 130 – 133.

Selolo, T.C., Mashiloane, M.L., Norris, D., Ng'ambi, J.W. & Brown, D., 2015. Morphological differentiation of indigenous goats in different agro-ecological zones of Vhembe District, Limpopo Province, South Africa. *Indian Journal of Animal and Research* 49: 527 – 531.

Setlalekgomo, M. and Setlalekgomo, T., 2013. The Use of Ethnoveterinary Medicine in Goats in Lentsweletau Village in Kweneng District of Botswana. *Journal of Veterinary Advances* 3: 197 – 202.

Shi, Y. & Manley, J. L., 2007. A complex signaling pathway regulates SRp38 phosphorylation and pre-mRNA splicing in response to heat shock. *Molecular Cell* 28: 79 – 90. DOI: 10.1016/j.molcel.2007.08.028.

Shina, D., Cho, K., Park, K.D., Lee, H.J., Kim, H., 2013. Accurate estimation of effective population size in the Korean dairy cattle based on linkage disequilibrium corrected by genomic relationship matrix. *Asian-Australasia Journal of Animal Science* 26: 1672 – 1679.

Silió, L., Rodríguez, M.C., Fernández, A., Barragán, C., Benítez, R., Óvilo, C., 2013. Measuring inbreeding and inbreeding depression on pig growth from pedigree or SNP-derived metrics. *Journal of Animal Breeding and Genetics* 130: 349 – 360.

Singh, U., Deb, R., Alyethodi, R.R., Alex, R., Kumar, S., Chakraborty, S., Dhama, K. & Sharma, A., 2014. Molecular markers and their applications in cattle genetic research: A review. *BGM Genomics* 6: 49 – 58.

Simela, L. & Merkel, R., 2008. The contribution of chevon from Africa to global meat production. *Meat Science* 80: 101 – 109.

Simianer, H., Marti, S.B., Gibson, J., Hanotte, O., Rege, J.E.O., 2003. An approach to the optimal allocation of conservation funds to minimise loss of genetic diversity between livestock breeds. *Ecological economics* 45: 377 – 392.

Simonson, T.S., Yang, Y., Huff, C.D., Yun, H, Qin, G, Witherspoon, D.J., Bai, Z., Lorenzo, F.R., Xing, J., Jorde, L.B., 2010. Genetic evidence for high altitude adaptation in Tibet. *Science* 329 (5987): 72 –75.

Slayi, M., Maphosa, V., Fayemi, P.O. and Mapfumo, L., 2014. Farmers perceptions of goat kid mortality under communal farming in Eastern Cape, South Africa. *Tropical Animal Health and Production* 46: 1209 – 1215.

Sobrinho, F.A. D., Coelho, R.C., Moura, J. O., Nascimento, I.F., Bajay, M.M., Carvalho, LC.B., Britto, F.B., Sarmento, J.L.R., Azevedo, D.M.R., Mastrangelo, S., Araújo, A.M., 2024. Genomic analysis revealed hotspots of genetic adaptation and risk of disappearance in the Brazilian goat populations. *BioRxiv*. The Preprint Server for Biology: DOI.org/10.1101/2024.06.03.597192.

Sölkner, J., Nakimbugwe, H. & Valle, Z.A., 1998. Analysis of determinants for success and failure of village breeding programmes. In: Proceedings of the Sixth World Congress on Genetics applied to Livestock Production, vol. 25, Armidale, NSW, Australia, 11 – 16 January 1998. 273 – 280.

Sowande, O.S., Oyewale, B.F., Iyasere, O.S., 2009. Age and sex dependent regression models for predicting the live weight of West African dwarf goat from body measurements. *Tropical animal health production* 42: pp 969 – 975. 23.

Sponenberg, P., Martin, A., Couch, C., Beranger, J., 2019. Conservation strategies for local breed biodiversity. *Diversity* 11: 177

Sponenberg, D.P., Edmundson, L., R., 2016. Caprinasy Locales en Los Estados Unidos (Criollo and Local Goat Breeds in the USA). In Biodiversidad Caprina Iberoamericana; Vargas, J.E., Zaragoza, L., Delgado, J.V., Rodríguez, L., Eds.; University of Córdoba: Córdoba, Spain, pp. 154–170.

Stainton, J.J., Haley, C.S., Charlesworth, B., Kranis, A., Watson, K., Wiener, P., 2015. Detecting signatures of selection in nine distinct lines of broiler chickens. *Animal Genetics* 46 (1):37 – 49.

Stella, A., Nicolazzi, E.L., Van Tassell, C.P., Rothschild, M., Colli, L., Rosen, B.D. 2018. AdaptMap: exploring goat diversity and adaptation. *Genetic Selection Evolution*. https ://DOI.org/10.1186/s1271 1-018-0427-5

Sulabda, N., Susari, N.N.W., Heryani, N.L.G.S. & Puja, I.K., 2012. Genetic diversity of Gembrong Goat based on DNA microsatellite markers. *Indonesian Journal of Animal and Veterinary Science* 17: 25 – 35.

Swai, E., Mtui, P., Chang'a, A. & Machange, G., 2008. The prevalence of serum antibodies to Ehrlichia ruminantium infection in ranch cattle in Tanzania: a cross-sectional study. *Journal of the South African Veterinary Association* 79: 71 – 75.

Swai, E., Moshy, W., Mtui, P., Bwanga, S., Machange, G. & Sanka, P., 2009. Serological survey of antibodies to Ehrlichia ruminantium in small ruminants in Tanzania. *Tropical Animal Health and Production* 41: 959 – 967.

Tada, O., Muchenje, V. & Dzama, K. 2013. Preferential traits for breeding Nguni cattle in low-input in-situ conservation production systems. *SpringerPlus* 2: 195.

Tapio, M., Ozerov, M., Tapio, I., Toro, M.A., Marzanov, N., Cinkulov, M. 2010. Microsatellite-based genetic diversity and population structure of domestic sheep in northern Eurasia. *BMC Genetics* 11: 76.

Tefera, A.N., Mekala, D.G., Mnisi, P.E., Mukisira, M., Clerkson, M., Murungweni, C. & Sebitloane, O., 2004. Goat production and livelihood systems in the Sekhukhune district of the Limpopo Province, South Africa: Opportunities for commercializing goats and their by-products. Working Document Series 118.
http://search.ebscohost.com/login.aspx?direct=true&db=lah&AN= 20043182451&site=ehost-live (accessed 25 October 2024).

Tittensor, D.P., Walpole, M., Hill, S.L.L.L., Boyce, D.G., Britten, G. L., Burgess, N.D., 2014.A mid-term analysis of progress toward international biodiversity targets. *Science* 346: 241– 244.

Thaon d'Arnoldi, C. J.L., Foulley. & Ollivier, L., 1998. An overview of the Weitzman approach to diversity. *Genetics Selection Evolution* 30: 149 – 161.

Thobile, F.M., Olivia, N.M., Keabetswe, T.N., Edgar, F.D., Tlou, C.M., Farai, C.M., Khanyisile, H., 2021. Goat Farmers Production Objectives and Trait Preferences in the North West Province of South Africa: An Approach to Identify Selection Criteria for Community-Based Breeding Program. I*nt. J. Livest. Prod* 12: 64 – 75.

Traoré A., Álvarez I., Tambourá, H.H., 2009. Genetic characterisation of Burkina Faso goats using microsatellite polymorphism. *Livestock Science* 123: 322 – 328.

Traoré A., Tambourá H.H., Kabore A., Royo L.J., Fernandez I., Álvarez I., Sangare M., Bouchel D., Poivey J.P. & Francois D., 2008. Multivariate analyses on morphological traits of goats in Burkina Faso. *Archiv Tierzucht* 51: 588 – 600.

Tsegaye, D., Belay, B. & Haile A., 2013. Morphological characterization of indigenous Hararghe highland goat breeds in their native environment, West Haraghe, Ethiopia. *American-Eurasian Journal of Scientific Research* 8: 72 – 79.

Toro, M.A., Villanueva, B. & Fernandez, J., 2014.Genomics applied to management strategies in conservation programmes. *Livestock Science* 166: 48 – 53.

Toro, M.A., Fernandez, J. & Caballero, A. 2009. Molecular characterization of breeds and its use in conservation. *Livestock Science* 120: 174 – 95.

Tosser-Klopp, G., Bardou, P., Bouchez, O., Cabau, C., Crooijmans, R., Dong, Y., Donnadieu-Tonon, C., Eggen, A., Heuven, H.C. & Jamli, S., 2014. Design and characterization of a 52K SNP chip for goats. *PloS One* 9: e86227.

Vahidi, S.M.F., Tarang, A.R., Naqvi, A.N., Anbaran, M.F., Boettcher, P., Joost, S. 2014. Investigation of the genetic diversity of domestic Capra hircus breeds reared within an early goat domestication area in Iran. *Genetics Selection Evolution* 46: 27.

VanRaden, P. M., 2008. Efficient methods to compute genomic predictions. *Journal of Dairy Science* 91: 4414 – 4423.

Van Marle-Köster, E. & Visser, C., 2018. Genetic Improvement in South African Livestock: Can Genomics Bridge the Gap Between the Developed and Developing Sectors? *Frontier Genetics* 9: 331. doi: 10.3389/fgene.2018.00331

Van Niekerk, W. & Pimentel, P., 2004. Goat production in the smallholder section in the Boane district in Southern Mozambique. *South African Journal of Animal Science* 34: 123 – 125.

Van Rooyen, A. & Homann, S., 2008. Enhancing income and livelihoods through improved farmers practices on goat production and marketing: Proceedings of a workshop organized by the Goat Forum, 2 – 3 October 2007, Bulawayo, Zimbabwe: International Crops Research Institute for the Semi –Arid Tropics. 84.

Visser, C., 2019. A review on goats in southern Africa: An untapped genetic resource. *Small Ruminant Research* 176: 11 – 16.

Visser, C., 2018. Adaptation of local meat goat breeds to South African ecosystems, in Sustainable Goat Production in Adverse Environments, Vol. II, ed. Simoes J., Gutierrez C., editors. (Cham: Springer;), 67–76.

Visser, C., Lashmar, S.F., Van Marle-Koster, E., Poli, M.A. & Allain D., 2016. Genetic diversity and population structure in South African, French and Argentinian Angora Goats from genome wide SNP data. *PLoS One* 11: e0154353.

Visser, C., van Marle-Köster, E. & Friedrich, H., 2011. Parentage verification of South African Angora goats, using microsatellite markers. *South African Journal of Animal Science*. 41, 250 – 255.

Visser, C., Hefer, C.A., van Marle-Köster, E.V. & Kotze, A., 2004. Genetic variation of three commercial and three indigenous goat populations in South Africa. *South African Journal of Animal Science* 34 (Supplement 1): 24 – 27.

Waller, P.J. & Thamsborg, S.M., 2004. Nematode control in green ruminant production systems. *Trends Parasitol* 20: 493 – 497.

Wang, J., 2016. Pedigrees or markers: which are better in estimating relatedness and inbreeding coefficient? *Theoretical Population Biology* 107: 4 – 13.

Webb, E.C. and Mamabolo, M.J., 2004. Production and reproduction characteristics of South African indigenous goats in communal farming systems. *South African Journal of Animal Science* 34 (1): 236 – 239.

Weir, B.S. & Cockerham, C.C., 1984. Estimating F-statistics for the analysis of population structure. *Evolution* 1358 – 370.

Weitzman, M.L., 1992. On diversity. *Q.J. Econ* CVII: 363 – 405.

Wolfson, G.H., Vargas, E., Browne, V.A., Moore, L.G., Julian, C.G., 2017. Erythropoietin and soluble erythropoietin receptor: a role for maternal vascular adaptation to high-altitude pregnancy. *Journal of Clinical Endocrinology and Metabolism* 102(1): 242 – 250.

Xu, L., Zhao, G., Yang, L., Zhu, B., Chen, Y., Zhang, L., Gao, X., Gao, H., Liu, G.E., Li, J., 2019. Genomic Patterns of Homozygosity in Chinese Local Cattle. *Scientific Reports* 9(1): 16977. DOI: 10.1038/s41598-019-53274-3

Xu, S.-S., Gao, L., Xie, X.-L., Ren, Y.-L., Shen, Z.-Q., Wang, F., Shen, M., Eyþórsdóttir, E., Hallsson, J.H., Kiseleva, T., 2018. Genome-Wide Association Analyses Highlight the Potential for Different Genetic Mechanisms for Litter Size Among Sheep Breeds. *Frontier Genetics* 9, 118.

Xu, Q., Zhang, C., Zhang, D., Jiang, H., Peng, S., Liu, Y., Zhao, K., Wang, C., Chen, L., 2016. Analysis of the erythropoietin of a Tibetan Plateau schizothoracine fish (Gymnocypris dobula) reveals enhanced cytoprotection function in hypoxic environments. *BMC Evolutionary Biology* 16:11.

Yakubu, A., Salako, A. E., Imumorin, I. G., Ige, A. O. & Akinyemi, M. O., 2010. Discriminant analysis of morphometric differentiation in the West African Dwarf and Red Sokoto goats. *South African Journal of Animal Science* 40: 381 – 387.

Yakubu, A., Salako, A. & Imumorin, I., 2010a. Multivariate analysis of spatial patterns of morphological traits in West African Dwarf goats in three agro-ecological zones of Nigeria. *Journal of Applied Animal Research* 38: 257 – 260.

Yakubu, A., Salako, A., Imumorin, I., Ige A. & Akinyemi, M., 2010b. Discriminant analysis of orphometric differentiation in the West African Dwarf and Red Sokoto goats. *South African Journal of Animal Science* 40: 381 – 387.

Yang, J., Li, W.R., Lv, F.H., He, S.G., Tian, S.L, Peng, W.F., Sun, Y.W., Zhao, Y.X., Tu, X.L., Zhang, M., 2016. Whole-genome sequencing of native sheep provides insights into rapid adaptations to extreme environments. *Molecular Biology and Evolution* 33 (10): 2576 – 2592.

Zander, K.K., Signorello, G., De Salvo, M., Gandini, G. & Drucker, A.G., 2013. Assessing the total economic value of threatened livestock breeds in Italy: Implications for conservation policy. *Ecological Economics* 93: 219 – 229.

Zhang, C., Asadollahpour, H., Nanaei, H.A., Negari, N.J., Roudbar, M.A., Ghanatsaman, Z.A., Niyazbekova, Z., Xiaojun Yang, X., 2024. Genomic analysis uncovers novel candidate genes related to adaptation to tropical climates and milk production traits in native goats. *BMC Genomics* 25: 477. DOI: 10.1186/s12864-024-10387-y.

Zhang, Z., Ma, L., Fan, X., Wang, K., Liu, L., Zhao, Y., Zhao, Z., Zhang, H., Liang, T., Dong, W., Cai, P., Li, Y., Li, J., Zhou, S., Kang, L., 2021. Targeted sequencing identifies the genetic variants associated with high-altitude polycythemia in the Tibetan Population. *Indian J. Hematol. Blood Transfus* 38(3):1-10. DOI:10.1007/s12288-021-01474-1.

Zhang B, Chamba Y, Shang P, Wang ZX, Ma J, Wang LY, Zhang H., 2017. Comparative transcriptomic and proteomic analyses provide insights into the key genes involved in high-altitude adaptation in the Tibetan pig. *Scientific Reports* 7:3654.

Zhang, Q., Guldbrandtsen, B., Bosse, M., Lund, M. S. & Sahana, G. 2015. Runs of homozygosity and distribution of functional variants in the cattle genome. *BMC Genomics* 16:542. DOI: 10.1186/s12864-015-1715-x.

Zhao, Y.X., Yang, J., Lv, F.H., Hu, X.J., Xie, X.L., Zhang, M. 2017. Genomic reconstruction of the history of native sheep reveals the peopling patterns of nomads and the expansion of early pastoralism in East Asia. *Molecular Biology and Evolution* 34: 2380 – 2395.

Zhao, F., McParland, S., Kearney, F., Du, L., Berry, D.P. 2015. Detection of selection signatures in dairy and beef cattle using high-density genomic information. *Genetics Selection Evolution* 47(1):1–12.

Zhao, F., Wang, G., Zeng, T., Wei, C., Zhang, L., Wang, H., Zhang, S., Liu, R., Liu, Z., Du, L., 2014. Estimations of genomic linkage disequilibrium and effective population sizes in three sheep populations. *Livestock Science* 170: 22 – 29.

Zhong, T., Wang, X., Huang, C., Yang, L., Zhao, Q., Chen, X., Freitas-de-Melo, A., Zhan, S., Wang, L., Dai, D., Cao, J., Guo, J., Li, L., Zhang, H., Niu, L., 2023. A genome-wide perspective on the diversity and selection signatures in indigenous goats using 53 K single nucleotide polymorphism array. *Animal* 17: DOI.org/10.1016/j.animal.2023.100706.

Zvinorova, P. I., 2017. A Genome-Wide Association Study on Mechanisms Underlying Genetic Resistance to Gastrointestinal Parasites in Goats. Ph.D. thesis. Stellenbosch University, South Africa.

CHAPTER 9

APPENDIX

CHAPTER 9. APPENDIX

APPENDIX A: COMMUNAL INDIGENOUS GOAT POPULATIONS SURVEY QUESTIONNAIRE

CONSERVATION STRATEGIES IN SOUTH AFRICAN INDIGENOUS GOAT GENETIC RESOURCES

Department of Agriculture, Forestry and Fisheries
Directorate: Genetic Resources
Private Bag X973, Pretoria, South Africa
TEL: (+2712) 319-6220/6233; FAX: (+2712) 319-6298

INDIGENOUS GOAT GENETIC RESOURCES SURVEY

QUESTIONNAIRE

Enumerator Name ___________________ Code no. ☐ Date of interview / /

Supervisor Name _______________________________ Code no. ☐

1. **Province** Name ______________________ Code no. ☐

2. **District** Name ____________________________________ Code no. ☐

3. **Station / camp** Name ____________________________________ Code no. ☐

4. **Village (VIDCO)** Name ____________________________________ Code no. ☐

5. **Farm type** Communal ☐ Small-scale commercial ☐ Large-scale commercial ☐

6. **Major Specie** Cattle ☐ Sheep ☐ Goats ☐ Pig ☐ Poultry (Chicken/Ostrich) ☐

Others Specify_________________

7. **GPS reading** __________________ (*to be filled in later) 8*. **Household** No ☐

1. GENERAL INFORMATION

1. Interviewee ____________________

2. Household head

3. Position in household

Household head	Spouse of head	Brother	Other (specify)
Sister	Son	Daughter	

Sex of head:

Male	Female

Age (yrs)

≤ 30	31-40	41-50	Not known
51-60	61-70	> 70	

4. Ethnic Group

Name ___________________

Code ☐

5. Land holding/ farm size

Area	Units (Hectares)
Crops	
Grazing *	
Forest	
Total size	
* Other than communal	

6. Land ownership

Own	
Lease	
Communal	
Other Specify	

7. Livestock activity

Is livestock your major source Y N of income?

9. Livestock kept

(Enter number in first column and rank with 1= just important and 3 highly important)

	No.	Rank (1 – 3)
Cattle		
Sheep		
Goats		
Chickens †		
Pigs		
Donkeys		
Other (specify)		
† Adult birds only		

10 Livestock production category

	Dairy	Meat	Dual purpose
Cattle			
Sheep			
Goats			

11. Do you belong to a Y N **Farmers Union?**

If Yes Specify ______________

12. Do you belong to a producer Y N **organization?**

If Yes Specify ________________

13. Awareness regarding conservation of animal genetic resources

No knowledge		Minimal		Well informed	

14. How do you value conservation of FAnGR

Extremely important		Important		Not important	

15. Value for indigenous animals

Extremely valuable		Moderately valuable		Not valuable	

2. CASTRATION/ENTRIES/EXITS/CULLING

1. Castration

Do you castrate?

Y	N

(*Tick one or more boxes*
If yes, indicate why)

Control breeding	
Improve meat quality	
Better price	
Better draft power	
Better temperament	
Other (specify)	

And at what age?

< 3 Months	
3 – 6 Months	
6 to 12 Months	
> 12 Months	

2. Numbers of entries within last 12 months

For questions 2. and 3. first ask for information on calves and on others (i.e. weaners and adults total). Then complete individual columns for weaners and adults if known.

Weaners and Adults					
			Adults		Total
	Calves	Weaners	Males	Females	W + A
Born					
Bought					
Donated/gift*					
Exchanged/lent					
** To include bride price and dowry*					

3. Number of exits within last 12 months

Weaners and Adults					
			Adults		Total
	Calves	Weaners	Males	Females	W + A
Died					
Sold					
Donated/gift*					
Exchanged/lent					
Stolen					
Slaughtered					
** To include bride price and dowry*					

4. Sale outlet

Were animal sold in last 12 months?

Y	N

(If yes tick one)

Sold at auction	
Sold to butcher	
Sold privately	
Sold to abattoir	
Other (specify)	

5. Reason for culling/disposal (tick and rank)

Then rank top three by writing in second half of box 1 for primary reason for culling, 2 for second and 3 for third

	Males		Females	
Size				
Conformation / shape				
Colour				
Temperament				
Health				
Body condition				
Performance				
Old age				
Poor fertility				
Other (specify)				

3. PRODUCTION SYSTEM

1. System of production
(tick one or more)

Industrial/intensive	
Semi-intensive	
Extensive/pastoral	
Free range / backyard	
Other (specify)	

2. Members of household who own animals
(tick one or more)

Husband/Wife	Head/spouse together	Daughters
Spouse	Sons	Others

3. Purpose of keeping animals
Ask an open question and tick any purpose considered in first half of box - one or more boxes to be ticked.

Meat	Work/draft	Manure	Hide	Investment	Ceremonies	Other (specify) ------------------
Milk	Stud breeding	Blood	Cash / sales	Dowry	Cultural	mohair
Eggs	Feathers	wool	pelt	fat	Cashmere	

5. Members of household responsible for animal activities
(Tick as appropriate; more than one column in a row may be ticked)

	Adults		Boys	Girls	Hired Labour
	Males	Females	(<15y)	(<15y)	
1. Purchasing					
2. Selling / slaughtering					
3. Herding					
4. Breeding decisions					
5. Feeding					
6. Milking					
7. Making dairy products					
8. Selling dairy products					
9. Animal health					
Other (specify)					

6. Grazing/feeding

	Winter season	Summer season
Herded		
Paddock		
Tethered		
Stall		
Yard		
Free grazing		
Other (specify)		

6. Grazing/feeding

Are progenies grazed/fed with | Y | N | adults?

For poultry what is the method of | Incubator | Natural | **hatching**

7. Housing

	Winter season	Summer season
Kraal		
Stall/shed		
Yard		
None		
Other (specify		
Poultry Housing		
1. Run + battery		
2. Run + deep litter		
Other (specify)		

8. Materials used for housing

Materials used		**Form of housing**	
Untreated wood/bush		Roof	
Treated wood		Solid wall	
Iron sheets		Floor	
Bricks		concrete	
Mud		wooden	
Wire		Earth	
other (specify)		Other (specify)	

Are progenies housed together with adults? Y N

If animals not housed go to question 10.

10. Supplementation regime

(Tick as appropriate)

	Winter season	Summer season
Roughage/crop residue		
Minerals (salts) / vitamins		
Bought-in feed / concentrates		
None		
Other (specify)		
Poultry/ Pig Supplementation regime		
Kitchen waste		
Bought complete ration		
Home-made ration		
Crushed grain		
Whole grain		
Other (specify)		

11. How animals are watered

	Winter season	Summer season
Animals go to water		
Water is fetched/provided		
Both		

12. Distance to furthest water

	Winter season	Summer season
At household		
<1km		
1-5 km		
6-10 km		
>10 km		

13. Source of water

	Winter season	Summer season
Dam/pond		
River		
Water well		
Borehole		
Spring		
Municipal/piped		
Other (specify)		

4.PHENOTYPIC DESCRIPTION (GOAT)

1. Breed common name ________________________ **Code** (*list of breeds)*

2. Coat description	Pattern	Uniform (1-colour)		Hair	Short		Fibre type	Hair	
		Uniform (multi-coloured)			Medium			Course wool	
		Pied			Long				
		Spotted			Straight			Fine wool	
					Curly				

3. Colour *Enter number(s) from colour chart. Complete both halves of double box if animals have more than one colour, main colour first; complete first half only if uniform colour. Rank in order of frequency of colour combinations in animals.*

Rank				Rank					Rank			Rank		
Body	1			Head	1			Hoof	1		Muzzle	1		
	2				2				2			2		
	3				3				3			3		

4. Body Size

Beard	Present in all		**Toggles**	Present in all	
	Present in some			Present in some	
	Absent			Absent	

		M	F			M	F
Height	Short			**Length**	small		
	Tall				long		
	Taller				longer		

7. Profile

Face	Flat		Back	Hollow	Rump	Flat	
	Concave			Straight		Sloping	
	Convex			Long		Roofy	

8. Ears

Size	Rudimentary		Orientation	Erect	
	Medium			Lateral	
	Large			Drooping	
				forward	

9. Horns

	Males	Females						
Present in all			Shape *(1 or more ticks allowed)*	Straight		Orientation *(1 or more ticks allowed)*	Upward	
Present in some				Curved			Forward	
Absent				Lyre-shaped			Backward	
				Spiral			Lateral	
							Downward	

Numbers		M		F	Length	Rudimentary (2 cm)
	2		2			Medium (2-8 cm)
	4		4			Long (>8 cm)

11. Tail

Base	Narrow	Tapered	Yes		Curled	Yes	
	Medium		No			No	
	Wide						

12 Long hair on legs

Distribution	Present in all	
	Present in some	
	Absent	

5. BREEDING

1. Primary reason for keeping bull(s)
(Tick one)

Breeding	
Socio-cultural	
Work / draft	
Other (specify)	

2. Reason for choice of bull(s) for breeding
Tick. Then rank top three by writing in second half of box
1 for primary reason for choice, 2 for second and 3 for third

	Tick	Rank
Size		
Conformation/shape		
Colour		
Horns		
Temperament		
Performance		
Availability (no choice)		
Other (specify)		

3. Mating

Uncontrolled	
Hand mating	
Group mating	
A.I.	
Other (Specify)	

4. Source and breed(s) of bull(s) used in the herd. Breed name(s) *(specify if known – crosses can be included.)*

		Breed 1 Common Name	Code	Code	**Breed 2 Common Name**	Code	Code
Own bull (bred)							
Own bull (bought)							
Bull donated							
Bull borrowed							
A.I.							
Communal area bull							

6. HEALTH

1. Access to veterinary services

Government vet.	
Private vet.	
Veterinary drug supplier	
Extension service	
None	
Other (specify)	

External parasite control

Done when need arises	
Done routinely	
If done routinely specify how often	

Method

	(Tick)	Wint	Sum	Wint	Sum	Wint season	Sum season
		season		season			
1. None	☐						
2. Dip	☐	☐	☐	☐	☐	every ☐ weeks	every ☐ weeks
3. Spray	☐	☐	☐	☐	☐	every ☐ weeks	every ☐ weeks
4. Pour-on	☐	☐	☐	☐	☐	every ☐ weeks	every ☐ weeks
5. Hand dressing	☐	☐	☐	☐	☐	every ☐ weeks	every ☐ weeks
6. Injectables	☐	☐	☐	☐	☐	every ☐ weeks	every ☐ weeks
7. Traditional	☐	☐	☐	☐	☐	every ☐ weeks	every ☐ weeks

If traditional method specifies ____________________ Code ☐ *(to be entered from list of traditional methods)*

Other (specify)

8. ___________	☐	☐	☐	☐	☐	every ☐ weeks	every ☐ weeks

Internal parasite control

Done when need arises	
Done routinely	
If done routinely specify how often	

Method

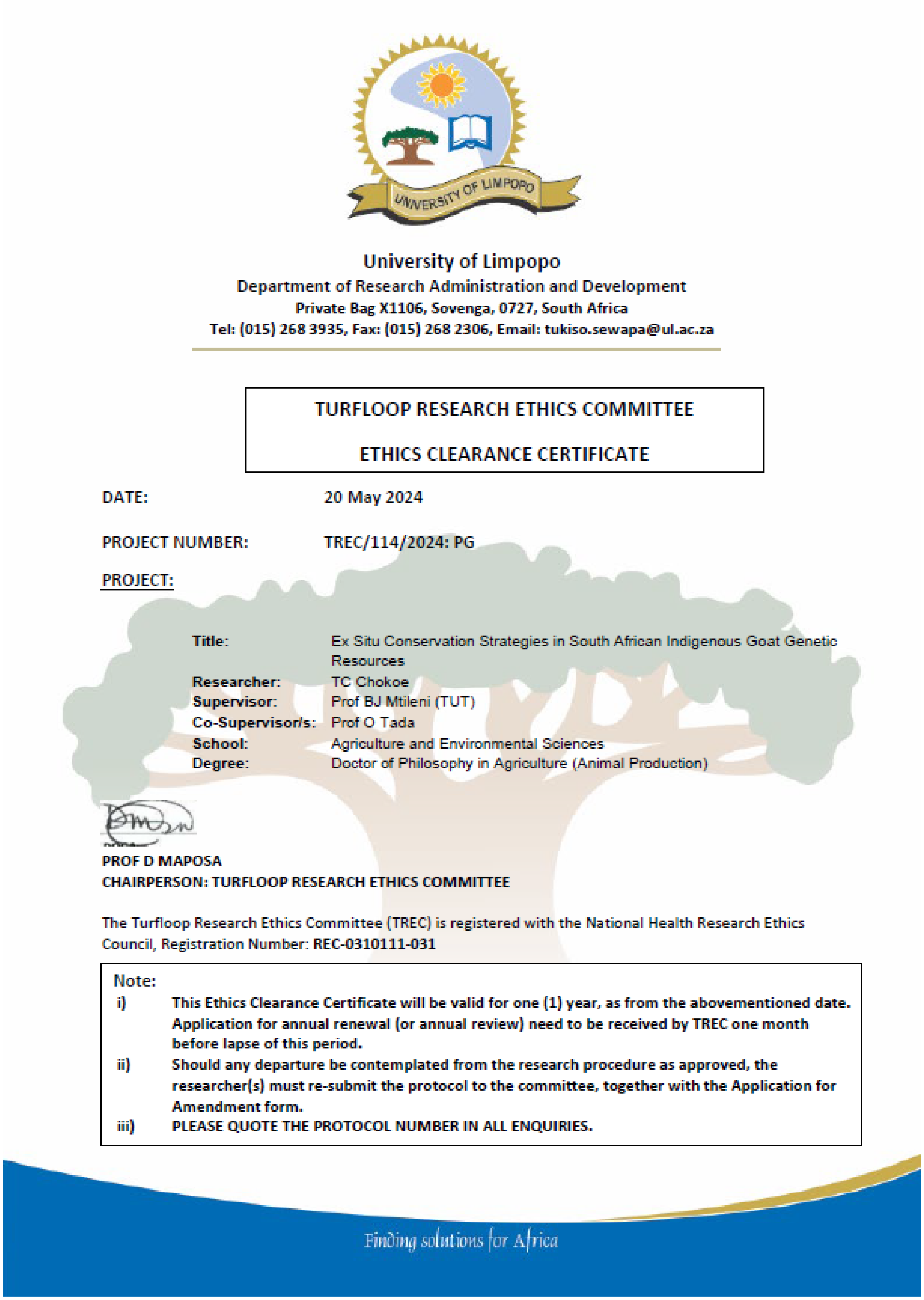
	(Tick)	Wint	Sum	Wint	Sum	Wint season	Sum season
		season		season			
1. None	☐						
2. Drench	☐	☐	☐	☐	☐	every ☐ weeks	every ☐ weeks
3. Traditional	☐	☐	☐	☐	☐	every ☐ weeks	every ☐ weeks

If traditional method specifies ____________________ Code ☐

Other (specify)

4. ___________	☐	☐	☐	☐	☐	every ☐ weeks	every ☐ weeks

APPENDIX B: TURFLOOP RESEARCH ETHICS COMMITTEE, ETHICS CLEARANCE CERTIFICATE.



University of Limpopo
Department of Research Administration and Development
Private Bag X1106, Sovenga, 0727, South Africa
Tel: (015) 268 3935, Fax: (015) 268 2306, Email: tukiso.sewapa@ul.ac.za

TURFLOOP RESEARCH ETHICS COMMITTEE

ETHICS CLEARANCE CERTIFICATE

DATE: 20 May 2024

PROJECT NUMBER: TREC/114/2024: PG

PROJECT:

Title:	Ex Situ Conservation Strategies in South African Indigenous Goat Genetic Resources
Researcher:	TC Chokoe
Supervisor:	Prof BJ Mtileni (TUT)
Co-Supervisor/s:	Prof O Tada
School:	Agriculture and Environmental Sciences
Degree:	Doctor of Philosophy in Agriculture (Animal Production)

PROF D MAPOSA
CHAIRPERSON: TURFLOOP RESEARCH ETHICS COMMITTEE

The Turfloop Research Ethics Committee (TREC) is registered with the National Health Research Ethics Council, Registration Number: **REC-0310111-031**

Note:
i) **This Ethics Clearance Certificate will be valid for one (1) year, as from the abovementioned date. Application for annual renewal (or annual review) need to be received by TREC one month before lapse of this period.**
ii) **Should any departure be contemplated from the research procedure as approved, the researcher(s) must re-submit the protocol to the committee, together with the Application for Amendment form.**
iii) **PLEASE QUOTE THE PROTOCOL NUMBER IN ALL ENQUIRIES.**

APPENDIX C: PER MARKER F_{ST} OF LIMPOPO VERSUS COMMERCIAL BREEDS (BOER, KALAHARI RED AND SAVANNA).

Marker	**Chromosome**	**Position**	**Overall F_{ST}**
snp28078-scaffold300-3412212	8	38197294	0.72
snp19368-scaffold1958-104157	6	8034538	0.71
snp3556-scaffold1110-106176	9	59365070	0.70
snp19366-scaffold1958-28303	6	8110392	0.69
snp28077-scaffold300-3369813	8	38154895	0.69
snp51703-scaffold760-153052	6	7438269	0.68
snp32526-scaffold371-1443673	13	39230563	0.68
snp48555-scaffold690-432877	6	104631767	0.67
snp49002-scaffold7-1603772	13	30788222	0.67
snp49005-scaffold7-1739012	13	30652982	0.66
snp14833-scaffold1599-1648545	16	48916418	0.66
snp39336-scaffold50-3297453	11	85314176	0.66
snp39334-scaffold50-3223208	11	85388421	0.66
snp834-scaffold1022-261355	24	6796728	0.65
snp6953-scaffold1255-276605	6	108237574	0.65
snp50228-scaffold717-6783091	12	27168032	0.65
snp32288-scaffold366-3374677	8	82251905	0.64
snp41147-scaffold532-2467263	26	19263257	0.64
snp35992-scaffold431-3698420	12	50165674	0.64
snp23960-scaffold2420-103083	10	95541485	0.64
snp48983-scaffold7-757999	13	31633995	0.64
snp15420-scaffold1634-771995	13	37797942	0.64
snp50237-scaffold717-7182753	12	27567694	0.63
snp12903-scaffold1499-480243	8	68047290	0.63
snp1842-scaffold1052-490895	14	68650539	0.63
snp55229-scaffold85-1952236	7	16702787	0.63
snp53804-scaffold82-4879979	2	81607276	0.63
snp28079-scaffold300-3453358	8	38238440	0.63
snp43116-scaffold572-2955845	10	93940994	0.63
snp58821-scaffold960-1070050	24	58989582	0.62
snp1880-scaffold1052-2240134	14	66901300	0.62
snp6985-scaffold1257-924855	1	102100621	0.62
snp32290-scaffold366-3455018	8	82171564	0.62
snp58911-scaffold965-310891	9	10335006	0.62
snp31039-scaffold343-1533935	10	26693103	0.62
snp47362-scaffold666-637358	5	90104066	0.62
snp29370-scaffold3175-373136	19	52139389	0.62
snp648-scaffold102-635295	24	19528727	0.62
snp28377-scaffold303-743729	19	30266065	0.62
snp34632-scaffold41-1222140	15	17526001	0.62
snp54715-scaffold837-1615921	15	55285889	0.62
snp28114-scaffold300-4928606	8	39713688	0.61
snp35943-scaffold431-1405126	12	47872380	0.61

APPENDIX C: PER MARKER F_{ST} OF LIMPOPO VERSUS COMMERCIAL BREEDS (BOER, KALAHARI RED AND SAVANNA) (Continued).

Marker	**Chromosome**	**Position**	**Overall F_{ST}**
snp28076-scaffold300-3335943	8	38121025	0.61
snp836-scaffold1022-339033	24	6719050	0.61
snp15413-scaffold1634-460263	13	37486210	0.61
snp33542-scaffold394-770559	5	42491486	0.61
snp3187-scaffold1095-4084951	12	29012392	0.61
snp46064-scaffold632-185079	18	56514202	0.61
snp13162-scaffold1502-321603	24	47347699	0.61
snp49003-scaffold7-1632946	13	30759048	0.60
snp50235-scaffold717-7093985	12	27478926	0.60
snp58317-scaffold947-1388094	10	31456656	0.60
snp12367-scaffold1466-749565	14	65955795	0.60
snp20566-scaffold2022-376531	13	15909019	0.60
snp1838-scaffold1052-332190	14	68809244	0.60
snp15611-scaffold165-866200	21	53620729	0.60
snp41697-scaffold542-2448188	15	48727568	0.60
snp46885-scaffold654-729925	3	33563672	0.60
snp55230-scaffold85-1981640	7	16673383	0.60
snp43609-scaffold582-835889	3	36349407	0.60
snp52842-scaffold792-767250	12	11056014	0.60
snp12950-scaffold1499-2536881	8	65990652	0.60
snp50200-scaffold717-5507351	12	25892292	0.60
snp43510-scaffold579-6303169	9	59516256	0.59
snp19457-scaffold1964-119046	6	7732009	0.59
snp41676-scaffold542-1367712	15	47647092	0.59
snp45014-scaffold614-1443654	2	47037815	0.59
snp39569-scaffold503-1404542	13	20260856	0.59
snp37595-scaffold460-703154	3	30903478	0.59
snp34916-scaffold416-2141525	14	56247710	0.59
snp33930-scaffold4-2005175	11	94347929	0.59
snp8838-scaffold1317-827711	7	32463717	0.59
snp41174-scaffold532-3630728	26	18099792	0.58
snp35658-scaffold43-2147682	18	22003155	0.58
snp35138-scaffold420-1629579	7	62668519	0.58
snp41396-scaffold538-519683	10	95958611	0.58
snp26382-scaffold276-3252186	1	91810480	0.58
snp44764-scaffold609-1510371	17	51120743	0.58
snp6239-scaffold122-811967	26	11805464	0.58
snp20874-scaffold205-1017491	16	46018309	0.58
snp9199-scaffold1335-368697	19	44656775	0.58
snp35576-scaffold428-3304453	17	31355361	0.58
snp45520-scaffold620-3561964	9	54754940	0.58
snp13050-scaffold150-3127888	13	49042684	0.58
snp8182-scaffold13-555106	24	18338227	0.57

APPENDIX C: PER MARKER F_{ST} OF LIMPOPO VERSUS COMMERCIAL BREEDS (BOER, KALAHARI RED AND SAVANNA) (Continued).

Marker	**Chromosome**	**Position**	**Overall F_{ST}**
snp456-scaffold1011-1028523	9	19146910	0.57
snp28075-scaffold300-3305715	8	38090797	0.57
snp85-scaffold100-265663	15	5337309	0.57
snp3704-scaffold112-1934811	16	60352587	0.57
snp51848-scaffold762-834851	27	38479358	0.57
snp17949-scaffold185-6144571	11	66914593	0.57
snp14775-scaffold1596-57767	29	1123546	0.57
snp42019-scaffold548-3435198	15	29615685	0.56
snp36098-scaffold431-8463413	12	54930667	0.56
snp32529-scaffold371-1576249	13	39097987	0.56
snp37765-scaffold464-4856841	2	97844906	0.56
snp10493-scaffold1374-422289	26	422289	0.56
snp46893-scaffold654-1069751	3	33903498	0.56
snp8967-scaffold1324-570052	9	89466032	0.56
snp10731-scaffold1380-32604	11	51251527	0.56
snp13173-scaffold1502-765308	24	47791404	0.56
snp20528-scaffold202-7032275	2	36809018	0.56
snp37590-scaffold460-483110	3	31123522	0.56
snp31096-scaffold344-349091	6	8487885	0.56
snp46124-scaffold635-161069	6	6919777	0.56
snp33893-scaffold4-320518	11	92663272	0.56
snp33894-scaffold4-349467	11	92692221	0.56
snp33895-scaffold4-413151	11	92755905	0.56
snp33896-scaffold4-444332	11	92787086	0.56
snp35989-scaffold431-3552989	12	50020243	0.56
snp50252-scaffold717-7820456	12	28205397	0.56
snp26764-scaffold281-1243900	6	35578781	0.56
snp1239-scaffold1031-974747	7	22223501	0.56
snp58818-scaffold960-916834	24	59142798	0.56
snp44200-scaffold600-944853	8	15779841	0.56
snp43599-scaffold582-381763	3	35895281	0.56
snp21586-scaffold2108-276236	3	61660450	0.56
snp28109-scaffold300-4710797	8	39495879	0.56
snp29287-scaffold316-161510	7	18816632	0.56
snp20558-scaffold2022-66896	13	16218654	0.56
snp40231-scaffold512-3206150	18	18345407	0.56
snp24361-scaffold247-7543141	11	44896274	0.55
snp1595-scaffold1045-307666	16	32863089	0.55
snp35377-scaffold425-795259	14	72578630	0.55
snp8834-scaffold1317-677468	7	32613960	0.55
snp44634-scaffold606-4621460	8	52718949	0.55
snp47353-scaffold666-240753	5	90500671	0.55
snp3330-scaffold1101-1353267	19	54763563	0.55

APPENDIX C: PER MARKER F_{ST} OF LIMPOPO VERSUS COMMERCIAL BREEDS (BOER, KALAHARI RED AND SAVANNA) (Continued).

Marker	**Chromosome**	**Position**	**Overall F_{ST}**
snp11305-scaffold1408-348781	6	6598573	0.55
snp1672-scaffold1047-1386839	3	53366887	0.55
snp39074-scaffold497-916276	8	81458724	0.55
snp33432-scaffold392-3363447	5	53357331	0.55
snp10528-scaffold1376-43622	8	74557439	0.55
snp10527-scaffold1376-6315	8	74594746	0.55
snp1230-scaffold1031-586840	7	21835594	0.55
snp14304-scaffold157-2608112	5	17079707	0.55
snp5510-scaffold1193-22066	6	4909464	0.55
snp10221-scaffold1368-562200	23	42753103	0.55
snp50006-scaffold716-1302734	7	74438604	0.55
snp50497-scaffold725-471271	9	65587263	0.55
snp11748-scaffold1433-238485	13	36787363	0.55
snp59122-scaffold97-446740	13	53896082	0.55
snp6514-scaffold1230-1489811	21	30150934	0.55
snp24826-scaffold254-1597421	7	59225637	0.54
snp49067-scaffold7-4476259	13	27915735	0.54
snp16194-scaffold1703-171177	29	39313358	0.54
snp13833-scaffold154-1698431	22	32314180	0.54
snp30545-scaffold338-88317	15	72096544	0.54
snp59985-scaffold999-128817	6	1438392	0.54
snp27752-scaffold296-1177458	24	11100851	0.54
snp12150-scaffold145-767791	1	149111957	0.54
snp56283-scaffold881-803514	13	44385209	0.54
snp39153-scaffold499-377463	23	44965669	0.54
snp11898-scaffold144-2525228	3	69128844	0.54
snp20387-scaffold202-948699	2	30725442	0.54
snp50123-scaffold717-2243748	12	22628689	0.54
snp3302-scaffold1101-14122	19	53424418	0.54
snp35884-scaffold430-6764474	2	44645817	0.54
snp26766-scaffold281-1311915	6	35646796	0.54
snp43087-scaffold572-1822323	10	92807472	0.54
snp32202-scaffold3643-393290	19	49794943	0.54
snp20495-scaffold202-5660539	2	35437282	0.54
snp19499-scaffold197-420534	1	16141683	0.54
snp35982-scaffold431-3206404	12	49673658	0.54
snp31905-scaffold356-4777048	8	103115286	0.54
snp45817-scaffold629-484215	1	26230231	0.54
snp30075-scaffold33-107046	19	40224821	0.54
snp39582-scaffold504-102451	9	2650311	0.54
snp8057-scaffold1292-81777	1	24171311	0.54
snp40203-scaffold512-1947795	18	17087052	0.54
snp8961-scaffold1324-255129	9	89151109	0.54

APPENDIX C: PER MARKER F_{ST} OF LIMPOPO VERSUS COMMERCIAL BREEDS (BOER, KALAHARI RED AND SAVANNA) (Continued).

Marker	**Chromosome**	**Position**	**Overall F_{ST}**
snp39332-scaffold50-3163935	11	85447694	0.54
snp46479-scaffold643-2604318	15	37471509	0.54
snp15280-scaffold1629-549843	4	105882800	0.54
snp34922-scaffold416-2397891	14	55991344	0.53
snp46914-scaffold654-1941821	3	34775568	0.53
snp32456-scaffold37-1565950	15	13546974	0.53
snp50230-scaffold717-6871142	12	27256083	0.53
snp6955-scaffold1255-336868	6	108297837	0.53
snp39505-scaffold501-2867382	10	17481344	0.53
snp41168-scaffold532-3374420	26	18356100	0.53
snp14431-scaffold1576-143213	20	46769865	0.53
snp10878-scaffold139-85379	15	63423240	0.53
snp1238-scaffold1031-941914	7	22190668	0.53
snp40213-scaffold512-2379007	18	17518264	0.53
snp37022-scaffold449-312721	14	32546820	0.53
snp49503-scaffold706-1271483	4	20477723	0.53
snp47067-scaffold659-724477	3	21511827	0.53
snp4403-scaffold1139-1176136	6	106240879	0.53
snp4407-scaffold1139-1327389	6	106392132	0.53
snp35475-scaffold427-2768557	9	43084391	0.53
snp26767-scaffold281-1361783	6	35696664	0.53
snp18054-scaffold185-10574388	11	62484776	0.53
snp1236-scaffold1031-862188	7	22110942	0.53
snp36101-scaffold431-8559972	12	55027226	0.53
snp3557-scaffold1110-169872	9	59301374	0.53
snp6577-scaffold1234-132552	24	58332462	0.53
snp36431-scaffold438-719115	25	20325709	0.53
snp42659-scaffold566-3436453	14	76865550	0.53
snp34912-scaffold416-1940101	14	56449134	0.53
snp28013-scaffold300-596083	8	35381165	0.53
snp25885-scaffold2674-34300	17	71715797	0.53
snp35184-scaffold421-1024790	24	29679943	0.53
snp32530-scaffold371-1615483	13	39058753	0.53
snp11110-scaffold14-1651402	14	69842396	0.53
snp31828-scaffold356-1288428	8	99626666	0.53
snp19300-scaffold1948-1484	24	7132730	0.53
snp36115-scaffold431-9087529	12	55554783	0.52
snp47142-scaffold659-3842528	3	24629878	0.52
snp46206-scaffold637-2738188	20	43361342	0.52
snp5548-scaffold1195-532765	5	40681465	0.52
snp27537-scaffold294-67724	24	7063423	0.52
snp27738-scaffold296-511801	24	11766508	0.52
snp18052-scaffold185-10505563	11	62553601	0.52

APPENDIX C: PER MARKER F_{ST} OF LIMPOPO VERSUS COMMERCIAL BREEDS (BOER, KALAHARI RED AND SAVANNA) (Continued).

Marker	**Chromosome**	**Position**	**Overall F_{ST}**
snp28291-scaffold301-2686568	2	28883680	0.52
snp46900-scaffold654-1368681	3	34202428	0.52
snp39238-scaffold5-3008760	9	86414293	0.52
snp15715-scaffold1652-331055	1	28292037	0.52
snp7319-scaffold1269-2530432	7	55126166	0.52
snp28390-scaffold303-1304573	19	30826909	0.52
snp59824-scaffold995-103773	7	32208730	0.52
snp16035-scaffold169-178962	9	8596722	0.52
snp9869-scaffold1352-1074208	6	93322577	0.52
snp35653-scaffold43-1962260	18	22188577	0.52
snp44610-scaffold606-3554272	8	51651761	0.52
snp11298-scaffold1408-66505	6	6316297	0.52
snp21207-scaffold207-4247881	17	16083382	0.52
snp43502-scaffold579-5997651	9	59821774	0.52
snp24767-scaffold253-1835132	11	90697164	0.52
snp12910-scaffold1499-866232	8	67661301	0.52
snp47899-scaffold675-1391473	3	26625734	0.52
snp12045-scaffold1444-393170	19	13540466	0.52
snp33922-scaffold4-1671582	11	94014336	0.52
snp33924-scaffold4-1773054	11	94115808	0.52
snp33925-scaffold4-1818866	11	94161620	0.52
snp2702-scaffold1077-1551097	1	17908915	0.52
snp52812-scaffold791-2229348	14	54880060	0.52
snp14834-scaffold1599-1681033	16	48948906	0.52
snp44600-scaffold606-3145331	8	51242820	0.52
snp11119-scaffold14-2120966	14	69372832	0.52
snp53546-scaffold815-140798	16	7059512	0.52
snp52256-scaffold775-15664	5	48478347	0.52
snp10373-scaffold1370-1759409	14	52329533	0.52
snp16605-scaffold175-649430	28	22448458	0.52
snp17694-scaffold1834-174736	13	1571977	0.52
snp6492-scaffold1230-528760	21	31111985	0.52
snp46120-scaffold635-31540	6	6790248	0.52
snp2712-scaffold1079-159043	7	14464313	0.52
snp4065-scaffold1128-524656	19	61389936	0.52
snp27707-scaffold2951-376219	6	112133690	0.52
snp11822-scaffold1438-1084369	1	125698770	0.52
snp32628-scaffold375-45642	17	15231350	0.52
snp59358-scaffold978-442863	8	27768276	0.52
snp21131-scaffold207-1039979	17	19291284	0.52
snp29115-scaffold312-7215702	2	58815990	0.51
snp40177-scaffold512-869116	18	16008373	0.51
snp28098-scaffold300-4261990	8	39047072	0.51

APPENDIX C: PER MARKER F_{ST} OF LIMPOPO VERSUS COMMERCIAL BREEDS (BOER, KALAHARI RED AND SAVANNA) (Continued).

Marker	**Chromosome**	**Position**	**Overall F_{ST}**
snp53770-scaffold82-3369225	2	83118030	0.51
snp45-scaffold10-301476	14	5884085	0.51
snp12219-scaffold1455-237507	8	86119415	0.51
snp48635-scaffold690-3931116	6	101133528	0.51
snp44321-scaffold603-2275617	4	13847341	0.51
snp25878-scaffold267-791378	13	35683645	0.51
snp54712-scaffold837-1472937	15	55428873	0.51
snp4870-scaffold1163-240403	19	16158606	0.51
snp16834-scaffold1762-376087	19	14211483	0.51
snp59938-scaffold998-379875	14	50190150	0.51
snp50560-scaffold727-457111	16	36354745	0.51
snp21377-scaffold2085-181875	6	9705253	0.51
snp24707-scaffold2522-205328	4	115537623	0.51
snp9278-scaffold1337-856324	14	87561818	0.51
snp6606-scaffold1236-218377	3	38821456	0.51
snp24981-scaffold257-500532	3	62176284	0.51
snp58100-scaffold94-5714186	6	68612251	0.51
snp8581-scaffold131-188064	16	58229613	0.51
snp24035-scaffold2445-61247	19	61809657	0.51
snp27044-scaffold2876-113158	4	111367291	0.51
snp18485-scaffold187-818705	15	67577635	0.51
snp49071-scaffold7-4626335	13	27765659	0.51
snp21983-scaffold2163-92927	1	148574464	0.51
snp37593-scaffold460-593855	3	31012777	0.51
snp3314-scaffold1101-583094	19	53993390	0.51
snp9474-scaffold1342-389525	22	11685228	0.51
snp15097-scaffold1612-160415	21	23284045	0.51
snp20496-scaffold202-5689643	2	35466386	0.51
snp13584-scaffold1525-1401917	24	60137790	0.51
snp6608-scaffold1236-307900	3	38910979	0.51
snp49292-scaffold703-3226008	10	11111208	0.51
snp4997-scaffold117-468425	4	45844814	0.50
snp6731-scaffold1244-1159993	1	145623967	0.50
snp48852-scaffold697-490687	12	490687	0.50
snp51851-scaffold762-973954	27	38618461	0.50
snp2980-scaffold1090-426157	14	86507117	0.50
snp24576-scaffold25-654894	8	18469829	0.50
snp37554-scaffold46-2356397	1	150963379	0.50
snp58850-scaffold962-779212	8	108461434	0.50
snp19517-scaffold197-1228293	1	16949442	0.50
snp47556-scaffold67-2509157	26	33460261	0.50
snp47926-scaffold675-2511728	3	27745989	0.50
snp1204-scaffold1030-2806089	16	40168133	0.50

APPENDIX C: PER MARKER F_{ST} OF LIMPOPO VERSUS COMMERCIAL BREEDS (BOER, KALAHARI RED AND SAVANNA) (Continued).

Marker	**Chromosome**	**Position**	**Overall F_{ST}**
snp3631-scaffold1113-569475	2	118937355	0.50
snp22448-scaffold222-592606	3	37831940	0.50
snp7559-scaffold127-7689826	2	114513193	0.50
snp43245-scaffold575-2442204	20	15338018	0.50
snp2849-scaffold1083-1170933	29	26830357	0.50
snp52100-scaffold770-280654	3	55911849	0.50
snp43678-scaffold585-2123504	8	77002820	0.50
snp18323-scaffold1859-142506	4	101116125	0.50
snp37566-scaffold46-2847203	1	150472573	0.50
snp43426-scaffold579-2901105	9	62918320	0.50
snp57337-scaffold913-116322	20	6736508	0.50
snp53148-scaffold799-4952512	29	36982332	0.50
snp23078-scaffold230-4075893	1	129115113	0.50
snp42217-scaffold552-702040	4	29001121	0.50
snp43420-scaffold579-2665013	9	63154412	0.50
snp16819-scaffold1760-792895	6	34149710	0.50
snp19565-scaffold1972-170066	8	64915462	0.50
snp10545-scaffold1376-836918	8	73764143	0.50
snp39943-scaffold51-2086104	21	43464109	0.50
snp14653-scaffold1591-11752	20	10250412	0.50
snp49562-scaffold707-984535	12	5423076	0.50
snp28378-scaffold303-778163	19	30300499	0.50
snp38265-scaffold481-1325071	12	39291905	0.50
snp5857-scaffold1205-1567307	4	104027520	0.50
snp26280-scaffold275-2529043	27	16999410	0.50
snp37877-scaffold467-324567	18	28726857	0.50
snp14229-scaffold1568-1742714	1	49698034	0.50
snp46884-scaffold654-687586	3	33521333	0.50
snp35864-scaffold430-5797314	2	43678657	0.50
snp44223-scaffold600-1806927	8	16641915	0.50
snp14830-scaffold1599-1502937	16	48770810	0.50
snp26810-scaffold2812-54948	17	71753047	0.50
snp29546-scaffold320-1004575	1	147476863	0.50
snp31410-scaffold348-473653	13	75402212	0.50
snp54085-scaffold824-508008	11	57758024	0.50
snp29097-scaffold312-6531765	2	59499927	0.50
snp22959-scaffold2290-863164	9	72698675	0.50
snp14756-scaffold1594-1418947	19	42762578	0.50
snp18964-scaffold191-352435	21	44554758	0.50
snp11368-scaffold1412-75843	20	64187922	0.50
snp29110-scaffold312-7006367	2	59025325	0.50
snp4073-scaffold1128-815079	19	61680359	0.50
snp37594-scaffold460-625087	3	30981545	0.50

APPENDIX C: PER MARKER F_{ST} OF LIMPOPO VERSUS COMMERCIAL BREEDS (BOER, KALAHARI RED AND SAVANNA) (Continued).

Marker	**Chromosome**	**Position**	**Overall F_{ST}**
snp40795-scaffold522-1640755	3	2395582	0.50
snp30977-scaffold342-657656	20	62286132	0.50
snp6928-scaffold1252-766503	2	53795934	0.50
snp56441-scaffold887-660137	11	91400365	0.50
snp15573-scaffold1648-8706	8	74609866	0.49
snp18467-scaffold187-107344	15	68288996	0.49
snp43883-scaffold593-555448	5	92956576	0.49
snp24783-scaffold2537-54961	24	46971036	0.49
snp36100-scaffold431-8526387	12	54993641	0.49
snp28961-scaffold312-1068960	2	64962732	0.49
snp45094-scaffold614-5003260	2	50597421	0.49
snp48873-scaffold698-35481	5	101043075	0.49
snp21988-scaffold2163-296961	1	148778498	0.49
snp875-scaffold1023-1092590	18	12294874	0.49
snp26087-scaffold2713-4612	28	1073340	0.49
snp19158-scaffold1927-418254	28	5836531	0.49
snp876-scaffold1023-1124568	18	12262896	0.49
snp23097-scaffold2300-636007	19	51766960	0.49
snp55800-scaffold865-861913	3	3346505	0.49
snp59349-scaffold978-75724	8	27401137	0.49
snp3650-scaffold1113-1281732	2	118225098	0.49
snp8423-scaffold1304-437108	9	71398304	0.49
snp39262-scaffold5-4037271	9	87442804	0.49
snp46918-scaffold654-2139845	3	34973592	0.49
snp30755-scaffold34-2405052	27	4053757	0.49
snp45013-scaffold614-1411491	2	47005652	0.49
snp38015-scaffold473-1602	10	724985	0.49
snp39229-scaffold5-2630513	9	86036046	0.49
snp52227-scaffold774-1069944	26	43544416	0.49
snp37581-scaffold460-60946	3	31545686	0.49
snp21985-scaffold2163-176087	1	148657624	0.49
snp25874-scaffold267-608206	13	35866817	0.49
snp51796-scaffold761-3779442	23	17788158	0.49
snp46873-scaffold654-255687	3	33089434	0.49
snp2898-scaffold1089-14390	21	7752366	0.49
snp54709-scaffold837-1316009	15	55585801	0.49
snp53120-scaffold799-3757571	29	35787391	0.49
snp27759-scaffold296-1451339	24	10826970	0.49
snp51793-scaffold761-3632159	23	17935441	0.49
snp59598-scaffold984-174399	27	1474207	0.49
snp16363-scaffold1725-377372	4	106810114	0.49
snp55890-scaffold869-872860	16	30770826	0.49
snp52683-scaffold79-643284	17	38833045	0.49

APPENDIX C: PER MARKER F_{ST} OF LIMPOPO VERSUS COMMERCIAL BREEDS (BOER, KALAHARI RED AND SAVANNA) (Continued).

Marker	**Chromosome**	**Position**	**Overall F_{ST}**
snp3727-scaffold112-2830032	16	61247808	0.49
snp45173-scaffold615-716066	29	4589925	0.49
snp2700-scaffold1077-1462879	1	17997133	0.49
snp27726-scaffold296-44969	24	12233340	0.49
snp27363-scaffold2909-534802	25	35883611	0.49
snp48858-scaffold697-798668	12	798668	0.48
snp47961-scaffold675-4086912	3	29321173	0.48
snp25688-scaffold2643-302205	6	100221994	0.48
snp51547-scaffold755-2025740	14	58464136	0.48
snp22557-scaffold2234-91230	28	34135143	0.48
snp39338-scaffold50-3397424	11	85214205	0.48
snp39574-scaffold503-1642278	13	20498592	0.48
snp28998-scaffold312-2532791	2	63498901	0.48
snp45115-scaffold614-5959885	2	51554046	0.48
snp59610-scaffold984-659534	27	989072	0.48
snp6919-scaffold1252-402562	2	54159875	0.48
snp11043-scaffold1397-168754	26	45044886	0.48
snp24257-scaffold247-2817828	11	40170961	0.48
snp37587-scaffold460-329756	3	31276876	0.48
snp47889-scaffold675-869966	3	26104227	0.48
snp50070-scaffold717-5767	12	20390708	0.48
snp9228-scaffold1336-706342	12	74667258	0.48
snp34910-scaffold416-1842737	14	56546498	0.48
snp13835-scaffold154-1774580	22	32238031	0.48
snp21095-scaffold2064-368839	24	33569985	0.48
snp18977-scaffold191-950185	21	45152508	0.48
snp39551-scaffold503-611213	13	19467527	0.48
snp40453-scaffold516-2219743	15	74404703	0.48
snp23676-scaffold239-1132860	25	22518599	0.48
snp35932-scaffold431-890549	12	47357803	0.48
snp1652-scaffold1047-501348	3	54252378	0.48
snp25318-scaffold261-144290	3	32631342	0.48
snp10357-scaffold1370-1004058	14	51574182	0.48
snp50994-scaffold74-20766	20	16141935	0.48
snp24971-scaffold257-12862	3	61688614	0.48
snp23088-scaffold2300-193213	19	51324166	0.48
snp36231-scaffold433-1813258	6	81547288	0.48
snp29414-scaffold318-1726074	9	52044293	0.48
snp12917-scaffold1499-1168513	8	67359020	0.48
snp59014-scaffold968-2234884	6	28316337	0.48
snp51527-scaffold755-1142258	14	59347618	0.48
snp11900-scaffold144-2597601	3	69056471	0.48
snp35175-scaffold421-690233	24	30014500	0.48

APPENDIX C: PER MARKER F_{ST} OF LIMPOPO VERSUS COMMERCIAL BREEDS (BOER, KALAHARI RED AND SAVANNA) (Continued).

Marker	**Chromosome**	**Position**	**Overall F_{ST}**
snp52795-scaffold791-1550168	14	54200880	0.48
snp41314-scaffold537-1789481	19	57420837	0.48
snp30577-scaffold339-825223	7	42226561	0.48
snp20869-scaffold205-812586	16	46223214	0.48
snp19562-scaffold1972-48462	8	64793858	0.48
snp47376-scaffold666-1300349	5	89441075	0.48
snp2080-scaffold1063-787508	8	105911235	0.48
snp42848-scaffold57-236572	15	63026815	0.48
snp31825-scaffold356-1113129	8	99451367	0.48
snp41712-scaffold543-13848	3	102804714	0.48
snp42930-scaffold57-3599324	15	59664063	0.48
snp47681-scaffold670-1271342	2	124768983	0.48

APPENDIX D: GENE AND GENE DESCRIPTIONS HARBOURING SNPS WITH $F_{ST} > 0.47$

Gene	**Gene description**
ABCD4	ATP binding cassette subfamily D member 4
ACSBG1	acyl-CoA synthetase bubblegum family member 1
ADRA1A	adrenoceptor alpha 1A
APIP	APAF1 interacting protein
APTX	aprataxin
ARFGEF3	ARFGEF family member 3
ARHGAP15	Rho GTPase activating protein 15
ARHGAP17	Rho GTPase activating protein 17
ARHGAP24	Rho GTPase activating protein 24
ARHGAP25	Rho GTPase activating protein 25
ARHGAP42	Rho GTPase activating protein 42
ASTN2	astrotactin 2
AXIN2	axin 2
BAZ1A	bromodomain adjacent to zinc finger domain 1A
BNC2	basonuclin 2
BRCA1	BRCA1 DNA repair associated
BRINP1	BMP/retinoic acid inducible neural specific 1
C8A	complement C8 alpha chain
CACNA1E	voltage-dependent R-type calcium channel subunit alpha-1E
CARF	calcium responsive transcription factor
CAST	calpastatin
CCSER1	coiled-coil serine rich protein 1
CDH20	cadherin 20
CEP112	centrosomal protein 112
CEP128	centrosomal protein 128
CFAP61	cilia and flagella associated protein 61
CNGB3	cyclic nucleotide gated channel subunit beta 3
CNTNAP5	contactin associated protein like 5
CRB2	crumbs cell polarity complex component 2
CTNNA3	catenin alpha 3
CTNND2	catenin delta 2
CUBN	cubilin
CUX1	cut like homeobox 1
DDX52	DExD-box helicase 52
DENND1A	DENN domain containing 1A
DNAH10	dynein axonemal heavy chain 10
DNAH7	dynein axonemal heavy chain 7
DNAH9	dynein axonemal heavy chain 9
DOCK7	dedicator of cytokinesis 7
DOP1A	DOP1 leucine zipper like protein A
DST	dystonin
EFCAB2	EF-hand calcium binding domain 2
EFCAB7	EF-hand calcium binding domain 7

APPENDIX D: GENE AND GENE DESCRIPTIONS HARBOURING SNPS WITH $F_{ST} > 0.47$ (Continued)

Gene	**Gene description**
EPHA5	EPH receptor A5
ESR2	estrogen receptor 2
ETFA	electron transfer flavoprotein subunit alpha
FANCA	FA complementation group A
FANCC	FA complementation group C FERM, ARH/RhoGEF and pleckstrin domain protein 1
FGGY	FGGY carbohydrate kinase domain containing
FLT1	fms related tyrosine kinase 1
FRMD4A	FERM domain containing 4A
FRMD4B	FERM domain containing 4B
GLDC	glycine decarboxylase
GLI2	GLI family zinc finger 2
GPAM	glycerol-3-phosphate acyltransferase, mitochondrial
GTF3C3	general transcription factor IIIC subunit 3
HDAC4	histone deacetylase 4
IDH3A	isocitrate dehydrogenase (NAD (+)) 3 catalytic subunit alpha
INVS	inversin
JKAMP	JNK1/MAPK8 associated membrane protein
KAT14	lysine acetyl transferase 14
KATNAL2	katanin catalytic subunit A1 like 2
LAMA2	laminin subunit alpha 2
LEXM	lymphocyte expansion molecule
LHX6	LIM homeobox 6
MALRD1	MAM and LDL receptor class A domain containing 1
MEF2C	myocyte enhancer factor 2C
MFN2	mitofusin 2
MMEL1	membrane metalloendopeptidase like 1
MORN1	MORN repeat containing 1
MORN5	MORN repeat containing 5
MRC1	mannose receptor C-type 1
MRRF	mitochondrial ribosome recycling factor
MTUS2	microtubule associated scaffold protein 2
NDST3	N-deacetylase and N-sulfotransferase 3
NFIA	nuclear factor I A
NKAIN3	sodium/potassium transporting ATPase interacting 3
NKD1	NKD inhibitor of WNT signaling pathway 1
NRG1	neuregulin 1
NUCB1	nucleobindin 1
OCLN	occludin
OGFR	opioid growth factor receptor
PALM2AKAP2	A-kinase anchoring protein 2

APPENDIX D: GENE AND GENE DESCRIPTIONS HARBOURING SNPS WITH $F_{ST} > 0.47$ (Continued)

Gene	**Gene description**
PCOLCE2	procollagen C-endopeptidase enhancer 2
PDE5A	phosphodiesterase 5A
PIK3C2G	phosphatidylinositol-4-phosphate 3-kinase catalytic subunit type 2 gamma
PRDM5	PR/SET domain 5
PRKAA2	protein kinase AMP-activated catalytic subunit alpha 2
PROSER2	proline and serine rich 2
PTPRB	protein tyrosine phosphatase receptor type B
PTPRO	protein tyrosine phosphatase receptor type O
RAPGEF2	Rap guanine nucleotide exchange factor 2
RARA	retinoic acid receptor alpha
RASAL2	RAS protein activator like 2
RASSF3	Ras association domain family member 3
RBP1	retinol binding protein 1
RNF157	ring finger protein 157
RNF17	ring finger protein 17
RNF180	ring finger protein 180
RPS6KA2	ribosomal protein S6 kinase A2
RPS6KA5	ribosomal protein S6 kinase A5
RPTOR	regulatory associated protein of MTOR complex 1
SASH1	SAM and SH3 domain containing 1secretagogin, EF-hand calcium binding protein
SEC24D	SEC24 homolog D, COPII coat complex component
SEMA5A	semaphorin 5A
SERGEF	secretion regulating guanine nucleotide exchange factor
SH2B3	SH2B adaptor protein 3
SLC17A1	solute carrier family 17 member 1
SLC2A12	solute carrier family 2 member 12
SLC2A13	solute carrier family 2 member 13
SLC39A11	solute carrier family 39 member 11
SMU1	SMU1DNA replication regulator and spliceosomal factor
SPATA1	spermatogenesis associated 1
SPATS2L	spermatogenesis associated serine rich 2 like
ST6GALNAC5	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 5
SYNPO2	synaptopodin 2
TCF7L2	transcription factor 7 like 2
THRB	thyroid hormone receptor beta
TMEM241	transmembrane protein 241
TTLL2	unc-93 homolog A
TXNDC8	thioredoxin domain containing 8
UCP2	uncoupling protein 2
UHRF2	ubiquitin like with PHD and ring finger domains 2
UPF2	UPF2 regulator of nonsense mediated mRNA decay

APPENDIX D: GENE AND GENE DESCRIPTIONS HARBOURING SNPS WITH F_{ST} > 0.47 (Continued)

Gene	**Gene description**
VWA8	von Willebrand factor A domain containing 8
WASHC5	WASH complex subunit 5
WDR63	WD repeat domain 63
WWP1	WW domain containing E3 ubiquitin protein ligase 1
XKR4	XK related 4
XYLB	xylulokinase
ZNF385B	zinc finger protein 385B
ZNF385D	zinc finger protein 385D

APPENDIX E: KEGG PATHWAYS FOR F_{ST} ANALYSIS (LIMPOPO POPULATIONS VERSUS COMMMMERCIAL BREEDS

KEGG ID	KEGG Pathaway
chx00020	Citrate cycle (TCA cycle)
chx00040	Pentose and glucuronate interconversions
chx00061	Fatty acid biosynthesis
chx00071	Fatty acid degradation
chx00230	Purine metabolism
chx00260	Glycine, serine and threonine metabolism
chx00270	Cysteine and methionine metabolism
chx00561	Glycerolipid metabolism
chx00562	Inositol phosphate metabolism
chx00564	Glycerophospholipid metabolism
chx00630	Glyoxylate and dicarboxylate metabolism
chx01100	Metabolic pathways
chx01200	Carbon metabolism
chx01212	Fatty acid metabolism
chx01230	Biosynthesis of amino acids
chx01521	EGFR tyrosine kinase inhibitor resistance
chx01522	Endocrine resistance
chx01524	Platinum drug resistance
chx02010	ABC transporters
chx03013	RNA transport
chx03015	mRNA surveillance pathway
chx03320	PPAR signaling pathway
chx03440	Homologous recombination
chx03460	Fanconi anemia pathway
chx04010	MAPK signaling pathway
chx04012	ErbB signaling pathway
chx04014	Ras signaling pathway
chx04015	Rap1 signaling pathway
chx04020	Calcium signaling pathway
chx04022	cGMP-PKG signaling pathway
chx04024	cAMP signaling pathway
chx04066	HIF-1 signaling pathway
chx04068	FoxO signaling pathway
chx04070	Phosphatidylinositol signaling system
chx04080	Neuroactive ligand
chx04114	Oocyte meiosis
chx04120	Ubiquitin mediated proteolysis
chx04141	Protein processing in endoplasmic reticulum
chx04144	Endocytosis
chx04145	Phagosome
chx04146	Peroxisome
chx04150	mTOR signaling pathway
chx04152	AMPK signaling pathway

APPENDIX E: KEGG PATHWAYS FOR F_{ST} ANALYSIS (LIMPOPO POPULATIONS VERSUS COMMMMERCIAL BREEDS (Continued)

KEGG ID	**KEGG Pathway**
chx04211	Longevity regulating pathway
chx04213	Longevity regulating pathway
chx04261	Adrenergic signaling in cardiomyocytes
chx04270	Vascular smooth muscle contraction
chx04310	Wnt signaling pathway
chx04340	Hedgehog signaling pathway
chx04360	Axon guidance
chx04371	Apelin signaling pathway
chx04390	Hippo signaling pathway
chx04510	Focal adhesion
chx04514	Cell adhesion molecules (CAMs)
chx04520	Adherens junction
chx04530	Tight junction
chx04550	Signaling pathways regulating pluripotency of stem cells
chx04610	Complement and coagulation cascades
chx04659	Th17 cell differentiation
chx04668	TNF signaling pathway
chx04670	Leukocyte transendothelial migration
chx04710	Circadian rhythm
chx04713	Circadian entrainment
chx04714	Thermogenesis
chx04722	Neurotrophin signaling pathway
chx04910	Insulin signaling pathway
chx04915	Estrogen signaling pathway
chx04916	Melanogenesis
chx04917	Prolactin signaling pathway
chx04919	Thyroid hormone signaling pathway
chx04920	Adipocytokine signaling pathway
chx04921	Oxytocin signaling pathway
chx04922	Glucagon signaling pathway
chx04928	Parathyroid hormone synthesis, secretion and action
chx04929	GnRH secretion
chx04930	Type II diabetes mellitus
chx04931	Insulin resistance
chx04934	Cushing syndrome
chx04970	Salivary secretion
chx04977	Vitamin digestion and absorption
chx05010	Alzheimer disease
chx05016	Huntington disease
chx05020	Prion diseases
chx05034	Alcoholism
chx05100	Bacterial invasion of epithelial cells
chx05132	Salmonella infection
chx05135	Yersinia infection
chx05145	Toxoplasmosis

APPENDIX E: KEGG PATHWAYS FOR F_{ST} ANALYSIS (LIMPOPO POPULATIONS VERSUS COMMMMERCIAL BREEDS (Continued)

KEGG ID	**KEGG Pathway**
chx05146	Amoebiasis
chx05152	Tuberculosis
chx05160	Hepatitis C
chx05165	Human papillomavirus infection
chx05200	Pathways in cancer
chx05202	Transcriptional misregulation in cancer
chx05203	Viral carcinogenesis
chx05206	MicroRNAs in cancer
chx05210	Colorectal cancer
chx05213	Endometrial cancer
chx05215	Prostate cancer
chx05216	Thyroid cancer
chx05217	Basal cell carcinoma
chx05219	Bladder cancer
chx05221	Acute myeloid leukemia
chx05222	Small cell lung cancer
chx05224	Breast cancer
chx05225	Hepatocellular carcinoma
chx05226	Gastric cancer
chx05322	Systemic lupus erythematosus
chx05323	Rheumatoid arthritis
chx05410	Hypertrophic cardiomyopathy (HCM)
chx05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)
chx05414	Dilated cardiomyopathy (DCM)
chx05416	Viral myocarditis
chx05418	Fluid shear stress and atherosclerosis

APPENDIX F: GENES AND GENES DESCRIPTIONS BASED ON REGIONS WITH HIGH FREQUENCY OF ROH

Gene name	**Gene description**
5S_rRNA	5S ribosomal RNA
7SK	7SK RNA
ABCA7	ATP binding cassette subfamily A member 7
ABCC5	ATP binding cassette subfamily C member 5
ABCF3	ATP binding cassette subfamily F member 3
ABHD17A	abhydrolase domain containing 17A
ABLIM3	actin binding LIM protein family member 3
ACCS	1-aminocyclopropane-1-carboxylate synthase homolog (inactive)
ACCSL	1-aminocyclopropane-1-carboxylate synthase homolog (inactive) like
ACTBL2	actin beta like 2
ADAM10	ADAM metallopeptidase domain 10
ADAMTS9	ADAM metallopeptidase with thrombospondin type 1 motif 9
ADORA2B	adenosine A2b receptor
AFAP1L1	actin filament associated protein 1 like 1
AFF4	AF4/FMR2 family member 4
AGMO	alkylglycerol monooxygenase
AGR2	anterior gradient 2, protein disulphide isomerase family member
AGR3	anterior gradient 3, protein disulphide isomerase family member
AHSP	alpha hemoglobin stabilizing protein
AK1	adenylate kinase 1
AK4	adenylate kinase 4
AK5	adenylate kinase 5
AKAP10	A-kinase anchoring protein 10
AKTIP	AKT interacting protein
ALDH1A2	aldehyde dehydrogenase 1 family member A2
ALDH3A1	aldehyde dehydrogenase 3 family member A1
ALG11	ALG11 alpha-1,2-mannosyltransferase
ALG2	ALG2 alpha-1,3/1,6-mannosyltransferase
ALG3	ALG3 alpha-1,3- mannosyltransferase
ALG6	ALG6 alpha-1,3-glucosyltransferase
ALKBH3	alkB homolog 3, alpha-ketoglutaratedependent dioxygenase
ALKBH5	alkB homolog 5, RNA demethylase
ALX4	ALX homeobox 4
ANAPC15	anaphase promoting complex subunit 15
ANGPTL2	angiopoietin like 2
ANGPTL3	angiopoietin like 3
ANK2	ankyrin 2
ANKMY2	ankyrin repeat and MYND domain containing 2
ANKRD34B	ankyrin repeat domain 34B
ANKS6	ankyrin repeat and sterile alpha motif domain containing 6
ANXA6	annexin A6
AP2M1	adaptor related protein complex 2 subunit mu 1
APC2	APC regulator of WNT signaling pathway 2
API5	apoptosis inhibitor 5
AQP9	aquaporin 9

APPENDIX F: GENES AND GENES DESCRIPTIONS BASED ON REGIONS WITH HIGH FREQUENCY OF ROH (Continued)

Gene name	**Gene description**
ARHGEF37	Rho guanine nucleotide exchange factor 37
ARID3A	AT-rich interaction domain 3A
ARL11	ADP ribosylation factor like GTPase 11
ARMC5	armadillo repeat containing 5
ARSI	arylsulfatase family member I
ARSJ	arylsulfatase family member J
ART1	ADP-ribosyltransferase 1
ASL	argininosuccinate lyase
ASPHD1	aspartate beta-hydroxylase domain containing 1
ATG4C	autophagy related 4C cysteine peptidase
ATOH1	atonal bHLH transcription factor 1
ATP5F1D	ATP synthase F1 subunit delta
ATP6V0E1	ATPase H+ transporting V0 subunit e1
ATP6V1C2	ATPase H+ transporting V1 subunit C2
ATP7B	ATPase copper transporting beta
ATP8B3	ATPase phospholipid transporting 8B3
ATP8B4	ATPase phospholipid transporting 8B4 (putative)
ATPAF2	ATP synthase mitochondrial F1 complex assembly factor 2
AUTS2	activator of transcription and developmental regulator AUTS2
AZU1	azurocidin 1
B3GNT5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5
B9D1	B9 domain containing 1
BCKDK	branched chain keto acid dehydrogenase kinase
BCL10	BCL10 immune signaling adaptor
BCL7C	BAF chromatin remodeling complex subunit BCL7C
BHLHE22	basic helix-loop-helix family member e22
BLOC1S6	biogenesis of lysosomal organelles complex 1 subunit 6
BNIP1	BCL2 interacting protein 1
BRCA2	BRCA2 DNA repair associated
BRD8	bromodomain containing 8
BTBD2	BTB domain containing 2
BTG3	BTG anti-proliferation factor 3
BZW2	basic leucine zipper and W2 domains 2
C15orf41	chromosome 10 C15orf41 homolog
C15orf48	chromosome 15 open reading frame 48
C15orf65	chromosome 15 open reading frame 65
C16orf54	chromosome 25 C16orf54 homolog
C16orf58	chromosome 25 C16orf58 homolog
C16orf87	chromosome 18 C16orf87 homolog
C19orf25	chromosome 7 C19orf25 homolog
C1orf87	chromosome 3 C1orf87 homolog
C21orf91	chromosome 1 C21orf91 homolog
C2CD4C	C2 calcium dependent domain containing 4C
C2orf50	chromosome 11 C2orf50 homolog
C2orf73	chromosome 11 C2orf73 homolog

APPENDIX F: GENES AND GENES DESCRIPTIONS BASED ON REGIONS WITH HIGH FREQUENCY OF ROH (Continued)

Gene name	**Gene description**
C3orf14	chromosome 22 C3orf14 homolog
C3orf49	chromosome 3 open reading frame 49
C3orf70	chromosome 1 C3orf70 homolog
C5orf15	chromosome 7 C5orf15 homolog
C5orf24	chromosome 7 C5orf24 homolog
C5orf47	chromosome 5 open reading frame 47
C9orf16	chromosome 11 C9orf16 homolog
CACHD1	cache domain containing 1
CALN1	calneuron 1
CAMK2A	calcium/calmodulin dependent protein kinase II alpha
CAMK2N2	calcium/calmodulin dependent protein kinase II inhibitor 2
CAMLG	calcium modulating ligand
CASP6	caspase 6
CATSPER3	cation channel sperm associated 3
CAVIN2	caveolae associated protein 2
CCDC189	coiled-coil domain containing 189
CCDC42	coiled-coil domain containing 42
CCDC69	coiled-coil domain containing 69
CCDC70	coiled-coil domain containing 70
CCDC85A	coiled-coil domain containing 85A
CCDC88A	coiled-coil domain containing 88A
CCN1	cellular communication network factor 1
CCPG1	cell cycle progression 1
CCSER1	coiled-coil serine rich protein 1
CD226	CD226 molecule
CD2BP2	CD2 cytoplasmic tail binding protein 2
CD74	CD74 molecule
CD82	CD82 molecule
CD8A	CD8a molecule
CDC23	cell division cycle 23
CDC25C	cell division cycle 25C
CDC34	cell division cycle 34
CDIPT	CDP-diacylglycerol--inositol 3-phosphatidyltransferase
CDK9	cyclin dependent kinase 9
CDKL3	cyclin dependent kinase like 3
CDKN2AIPNL	CDKN2A interacting protein N-terminal like
CDRT4	CMT1A duplicated region transcript 4
CDX1	caudal type homeobox 1
CEP152	centrosomal protein 152
CEP78	centrosomal protein 78
CFAP157	cilia and flagella associated protein 157
CFAP52	cilia and flagella associated protein 52
CFD	complement factor D
CGNL1	cingulin like 1
CHCHD5	coiled-coil-helix-coiled-coil-helix domain containing 5

APPENDIX F: GENES AND GENES DESCRIPTIONS BASED ON REGIONS WITH HIGH FREQUENCY OF ROH (Continued)

Gene name	Gene description
CHD9	chromodomain helicase DNA binding protein 9
chi-mir-101	chi-mir-101
chi-mir-125b	chi-mir-125b
chi-mir-143	chi-mir-143
chi-mir-145	chi-mir-145
chi-mir-147	chi-mir-147
chi-mir-16a	chi-mir-16a
chi-mir-216b	chi-mir-216b
chi-mir-33b	chi-mir-33b
chi-mir-582	chi-mir-582
chi-mir-99a	chi-mir-99a
CHODL	chondrolectin
CHRD	chordin
CHRM5	cholinergic receptor muscarinic 5
CHRNA10	neuronal acetylcholine receptor subunit alpha-10
CHRNA3	cholinergic receptor nicotinic alpha 3 subunit
CHRNA5	cholinergic receptor nicotinic alpha 5 subunit
CHRNB4	cholinergic receptor nicotinic beta 4 subunit
CIRBP	cold inducible RNA binding protein
CIZ1	CDKN1A interacting zinc finger protein 1
CKAP2	cytoskeleton associated protein 2
CKAP2L	cytoskeleton associated protein 2 like
CLCA1	chloride channel accessory 1
CLCA2	chloride channel accessory 2
CLCA4	chloride channel accessory 4
CLCN2	chloride voltage-gated channel 2
CLEC3A	C-type lectin domain family 3 member A
CLHC1	clathrin heavy chain linker domain containing 1
CLPB	ClpB homolog, mitochondrial AAA ATPase chaperonin
COG6	component of oligomeric golgi complex 6
COL15A1	collagen type XV alpha 1 chain
COL24A1	collagen type XXIV alpha 1 chain
COL25A1	collagen type XXV alpha 1 chain
COL6A2	collagen type VI alpha 2 chain
COPB1	coatomer protein complex subunit beta 1
COPS2	COP9 signalosome subunit 2
COPS3	COP9 signalosome subunit 3
CORO1A	coronin 1A
COX10	protoheme IX farnesyltransferase, mitochondrial
COX6A2	cytochrome c oxidase subunit 6A2, mitochondrial
CPEB4	cytoplasmic polyadenylation element binding protein 4
CRCP	CGRP receptor component
CREBRF	CREB3 regulatory factor
CRH	corticotropin releasing hormone
CRPPA	CDP-L-ribitol pyrophosphorylase A
CRSP-1	calcitonin receptor-stimulating peptide-1

APPENDIX F: GENES AND GENES DESCRIPTIONS BASED ON REGIONS WITH HIGH FREQUENCY OF ROH (Continued)

Gene name	**Gene description**
CRSP-2	calcitonin receptor-stimulating peptide-2
CSF1R	colony stimulating factor 1 receptor
CSNK1A1	casein kinase 1 alpha 1
CSNK1G2	casein kinase 1 gamma 2
CTF1	cardiotrophin 1
CTNNA1	catenin alpha 1
CTXN2	cortexin 2
CXADR	CXADR Ig-like cell adhesion molecule
CXCL14	C-X-C motif chemokine ligand 14
CYP2R1	vitamin D 25-hydroxylase
CYP2U1	cytochrome P450 2U1
CYP7B1	25-hydroxycholesterol 7-alpha-hydroxylase
CYS1	cystin 1
DAZAP1	DAZ associated protein 1
DCAF10	DDB1 and CUL4 associated factor 10
DCTN4	dynactin subunit 4
DCTPP1	dCTP pyrophosphatase 1
DDAH1	dimethylarginine dimethylaminohydrolase 1
DDHD1	DDHD domain containing 1
DDX46	DEAD-box helicase 46
DHRS12	dehydrogenase/reductase 12
DHRS7C	dehydrogenase/reductase 7C
DIP2A	disco interacting protein 2 homolog A
DIPK2A	divergent protein kinase domain 2A
DKK2	dickkopf WNT signaling pathway inhibitor 2
DNAAF4	dynein axonemal assembly factor 4
DNAJB4	DnaJ heat shock protein family (Hsp40) member B4
DNAJB5	DnaJ heat shock protein family (Hsp40) member B5
DNAJC5B	DnaJ heat shock protein family (Hsp40) member C5 beta
DOC2A	double C2 domain alpha
DOCK7	dedicator of cytokinesis 7
DOK4	docking protein 4
DOK6	docking protein 6
DPH6	diphthamine biosynthesis 6
DPM2	dolichyl-phosphate mannosyltransferase subunit 2, regulatory
DPYSL3	dihydropyrimidinase like 3
DRC3	dynein regulatory complex subunit 3
DRG2	developmentally regulated GTP binding protein 2
DTWD1	DTW domain containing 1
DUOX1	dual oxidase 1
DUOX2	dual oxidase 2
DUOXA1	dual oxidase maturation factor 1
DUOXA2	dual oxidase maturation factor 2
DVL3	dishevelled segment polarity protein 3
E2F6	E2F transcription factor 6

APPENDIX F: GENES AND GENES DESCRIPTIONS BASED ON REGIONS WITH HIGH FREQUENCY OF ROH (Continued)

Gene name	**Gene description**
EBPL	EBP like
ECE2	endothelin converting enzyme 2
EFCAB7	EF-hand calcium binding domain 7
EFEMP1	EGF containing fibulin extracellular matrix protein 1
EFNA2	ephrin A2
EGR1	early growth response 1
EHHADH	enoyl-CoA hydratase and 3-hydroxyacyl CoA dehydrogenase
EIF2AK3	eukaryotic translation initiation factor 2 alpha kinase 3
EIF2B5	eukaryotic translation initiation factor 2B subunit epsilon
EIF4G1	eukaryotic translation initiation factor 4 gamma 1
ELANE	elastase, neutrophil expressed
ELOVL6	ELOVL fatty acid elongase 6
EMC4	ER membrane protein complex subunit 4
EMC7	ER membrane protein complex subunit 7
EML6	EMAP like 6
ENG	endoglin
EPHB3	EPH receptor B3
EPN2	epsin 2
ERGIC1	endoplasmic reticulum-golgi intermediate compartment 1
ERP44	endoplasmic reticulum protein 44
ETF1	eukaryotic translation termination factor 1
ETFA	electron transfer flavoprotein subunit alpha
ETNPPL	ethanolamine-phosphate phospho-lyase
EXOSC3	exosome component 3
EXT2	exostosin glycosyltransferase 2
FABP1	fatty acid binding protein 1
FAM102A	family with sequence similarity 102 member A
FAM124A	family with sequence similarity 124 member A
FAM131A	family with sequence similarity 131 member A
FAM13B	family with sequence similarity 13 member B
FAM151B	family with sequence similarity 151 member B
FAM174C	family with sequence similarity 174 member C
FAM214B	family with sequence similarity 214 member B
FAM53C	family with sequence similarity 53 member C
FAM83G	family with sequence similarity 83 member G
FANCG	FA complementation group G
FAT2	FAT atypical cadherin 2
FBLL1	fibrillarin like 1
FBN1	fibrillin 1
FBXL19	F-box and leucine rich repeat protein 19
FBXO10	F-box protein 10
FBXO22	F-box protein 22
FBXO25	F-box protein 25
FBXO38	F-box protein 38
FBXO5	F-box protein 5

APPENDIX F: GENES AND GENES DESCRIPTIONS BASED ON REGIONS WITH HIGH FREQUENCY OF ROH (Continued)

Gene name	**Gene description**
FERMT2	fermitin family member 2
FEZF2	FEZ family zinc finger 2
FGF22	fibroblast growth factor 22
FGF7	fibroblast growth factor 7
FGGY	FGGY carbohydrate kinase domain containing
FKTN	fukutin
FLII	FLII actin remodeling protein
FMN1	formin 1
FOXE1	forkhead box E1
FOXI3	forkhead box I3
FOXO1	forkhead box O1
FPGS	folylpolyglutamate synthase
FRMPD1	FERM and PDZ domain containing 1
FRY	FRY microtubule binding protein
FSD1L	fibronectin type III and SPRY domain containing 1 like
FSTL3	follistatin like 3
FSTL4	follistatin like 4
FSTL5	follistatin like 5
FTCD	formimidoyltransferase cyclodeaminase
FTO	FTO alpha-ketoglutarate dependent dioxygenase
FUS	FUS RNA binding protein
G3BP1	G3BP stress granule assembly factor 1
GABBR2	gamma-aminobutyric acid type B receptor subunit 2
GABPB1	GA binding protein transcription factor subunit beta 1
GALK2	galactokinase 2
GALNT12	polypeptide N-acetylgalactosaminyltransferase 12
GALNT17	polypeptide N-acetylgalactosaminyltransferase 17
GAMT	guanidinoacetate N-methyltransferase
GAPT	GRB2 binding adaptor protein, transmembrane
GAPVD1	GTPase activating protein and VPS9 domains 1
GARNL3	GTPase activating Rap/RanGAP domain like 3
GATM	glycine amidinotransferase
GDF9	growth differentiation factor 9
GDPD3	glycerophosphodiester phosphodiesterase domain containing 3
GFRA3	GDNF family receptor alpha 3
GID4	GID complex subunit 4 homolog
GIPC2	GIPC PDZ domain containing family member 2
GLB1L3	beta-galactosidase-1-like protein 3
GLP2R	glucagon like peptide 2 receptor
GLRA1	glycine receptor alpha 1
GM2A	GM2 ganglioside activator
GPBP1	GC-rich promoter binding protein 1
GPT2	glutamic--pyruvic transaminase 2
GPX3	glutathione peroxidase 3
GPX4	glutathione peroxidase 4

APPENDIX F: GENES AND GENES DESCRIPTIONS BASED ON REGIONS WITH HIGH FREQUENCY OF ROH (Continued)

Gene name	**Gene description**
GREB1	growth regulating estrogen receptor binding 1
GRHPR	glyoxylate and hydroxypyruvate reductase
GRIA1	glutamate ionotropic receptor AMPA type subunit 1
GRID2	glutamate ionotropic receptor delta type subunit 2
GRIN3B	glutamate ionotropic receptor NMDA type subunit 3B
GRPEL2	GrpE like 2, mitochondrial
HADH	hydroxyacyl-CoA dehydrogenase
HCN2	hyperpolarization activated cyclic nucleotide gated potassium and sodium channel 2
HDC	histidine decarboxylase
HEMGN	hemogen
HIRIP3	HIRA interacting protein 3
HMGXB3	HMG-box containing 3
HNRNPA0	heterogeneous nuclear ribonucleoprotein A0
HOOK1	hook microtubule tethering protein 1
HPCAL1	hippocalcin like 1
HS3ST3B1	heparan sulfate glucosamine 3-O-sulfotransferase 3B1
HSD17B12	hydroxysteroid 17-beta dehydrogenase 12
HSD3B7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7
HSPA5	heat shock protein family A (Hsp70) member 5
HSPA9	heat shock protein family A (Hsp70) member 9
HTR4	5-hydroxytryptamine receptor 4
HYKK	hydroxylysine kinase
IGFBPL1	insulin like growth factor binding protein like 1
IL17B	interleukin 17B
IL18BP	interleukin 18 binding protein
IL1A	interleukin 1 alpha
IL1B	interleukin 1 beta
IL1F10	interleukin 1 family member 10
IL1RN	interleukin 1 receptor antagonist
IL27	interleukin 27
IL36A	interleukin-36 alpha
IL36G	interleukin-36 gamma
IL36RN	interleukin 36 receptor antagonist
IMMT	inner membrane mitochondrial protein
INO80E	INO80 complex subunit E
INPPL1	inositol polyphosphate phosphatase like 1
INSC	INSC spindle orientation adaptor protein
INTS6	integrator complex subunit 6
INVS	inversin
IPCEF1	interaction protein for cytohesin exchange factors 1
IREB2	iron responsive element binding protein 2
IRX3	iroquois homeobox 3
IRX5	iroquois homeobox 5
ISL2	ISL LIM homeobox 2

APPENDIX F: GENES AND GENES DESCRIPTIONS BASED ON REGIONS WITH HIGH FREQUENCY OF ROH (Continued)

Gene name	Gene description
ITGAD	integrin alpha-D
ITGAL	integrin subunit alpha L
ITGAM	integrin subunit alpha M
JADE2	jade family PHD finger 2
JAK1	Janus kinase 1
JAKMIP2	janus kinase and microtubule interacting protein 2
KANK4	KN motif and ankyrin repeat domains 4
KAT8	lysine acetyltransferase 8
KCNF1	potassium voltage-gated channel modifier subfamily F member 1
KCNRG	potassium channel regulator
KCNT2	potassium sodium-activated channel subfamily T member 2
KCTD13	potassium channel tetramerization domain containing 13
KCTD7	potassium channel tetramerization domain containing 7
KDM3A	lysine demethylase 3A
KDM3B	lysine demethylase 3B
KHDRBS3	KH RNA binding domain containing, signal transduction associated 3
KIF20A	kinesin family member 20A
KIF22	kinesin family member 22
KL	klotho
KLF11	Kruppel like factor 11
KLF16	Kruppel like factor 16
KLF4	Kruppel like factor 4
KLHL24	kelch like family member 24
KLHL3	kelch like family member 3
KPNA3	karyopherin subunit alpha 3
KRCC1	lysine rich coiled-coil 1
LAMTOR1	late endosomal/lysosomal adaptor, MAPK and MTOR activator 1
LCN2	lipocalin 2
LEAP2	liver enriched antimicrobial peptide 2
LECT2	leukocyte cell derived chemotaxin 2
LEF1	lymphoid enhancer binding factor 1
LHFPL6	LHFPL tetraspan subfamily member 6
LIPC	lipase C, hepatic type
LIPH	lipase H
LLGL1	LLGL scribble cell polarity complex component 1
LMX1B	LIM homeobox transcription factor 1 beta
LPCAT4	lysophosphatidylcholine acyltransferase 4
LPIN1	lipin 1
LRIT3	leucine rich repeat, Ig-like and transmembrane domains 3
LRRC4C	leucine rich repeat containing 4C
LRRC72	leucine rich repeat containing 72
LRRC75A	leucine rich repeat containing 75A
LRRTM2	leucine rich repeat transmembrane neuronal 2
LRSAM1	leucine rich repeat and sterile alpha motif containing 1
LSS	lanosterol synthase

APPENDIX F: GENES AND GENES DESCRIPTIONS BASED ON REGIONS WITH HIGH FREQUENCY OF ROH (Continued)

Gene name	**Gene description**
MAB21L1	mab-21 like 1
MACROH2A1	core histone macro-H2A.1
MAF	MAF bZIP transcription factor
MAGEF1	MAGE family member F1
MAGI1	membrane associated guanylate kinase, WW and PDZ domain containing 1
MAP3K1	mitogen-activated protein kinase kinase kinase 1
MAP3K13	mitogen-activated protein kinase kinase kinase 13
MAP6D1	MAP6 domain containing 1
MAPK3	mitogen-activated protein kinase 3
MAPK7	mitogen-activated protein kinase 7
MAPKAP1	MAPK associated protein 1
MAZ	MYC associated zinc finger protein
MBD3	methyl-CpG binding domain protein 3
MCF2L2	MCF.2 cell line derived transforming sequence-like 2
MCM3AP	minichromosome maintenance complex component 3 associated protein
MCOLN2	mucolipin 2
MCOLN3	mucolipin 3
MCUB	mitochondrial calcium uniporter dominant negative beta subunit
MED16	mediator complex subunit 16
MED9	mediator complex subunit 9
MEIS2	Meis homeobox 2
MELK	maternal embryonic leucine zipper kinase
MEOX2	mesenchyme homeobox 2
Metazoa_SRP	Metazoan signal recognition particle RNA
MEX3D	mex-3 RNA binding family member D
MFAP4	microfibril associated protein 4
MFSD6L	major facilitator superfamily domain containing 6 like
MIDN	midnolin
MIEF2	mitochondrial elongation factor 2
MIER2	MIER family member 2
MIER3	MIER family member 3
MIGA1	mitoguardin 1
MIR1224	microRNA mir-1224
MIR129	microRNA mir-129
MIR15A	microRNA mir-15a
MIR216A	microRNA 216a
MIR30D	microRNA mir-30d
MIR378	microRNA mir-378
MIR628	microRNA mir-628
MIR874	microRNA mir-874
MIRLET7C	microRNA let-7c
MISP	mitotic spindle positioning
MNS1	meiosis specific nuclear structural 1
MRPL35	mitochondrial ribosomal protein L35
MRPS31	mitochondrial ribosomal protein S31

APPENDIX F: GENES AND GENES DESCRIPTIONS BASED ON REGIONS WITH HIGH FREQUENCY OF ROH (Continued)

Gene name	**Gene description**
MSH3	mutS homolog 3
MTFR1	mitochondrial fission regulator 1
MTIF2	mitochondrial translational initiation factor 2
MTRF1L	mitochondrial translational release factor 1 like
MVB12B	multivesicular body subunit 12B
MVP	major vault protein
MYBL1	MYB proto-oncogene like 1
MYEF2	myelin expression factor 2
MYH10	myosin heavy chain 10
MYH2	myosin heavy chain 2
MYH3	myosin-3
MYH4	myosin-4
MYH8	myosin heavy chain 8
MYLK3	myosin light chain kinase 3
MYLPF	myosin light chain, phosphorylatable, fast skeletal muscle
MYO15A	myosin XVA
MYO1B	myosin IB
MYOT	myotilin
MYOZ3	myozenin 3
N4BP2L1	NEDD4 binding protein 2 like 1
NABP1	nucleic acid binding protein 1
NAIF1	nuclear apoptosis inducing factor 1
NANS	N-acetylneuraminate synthase
NBEA	neurobeachin
NCBP1	nuclear cap binding protein subunit 1
NCOR1	nuclear receptor corepressor 1
NDST1	N-deacetylase and N-sulfotransferase 1
NDUFS7	NADH:ubiquinone oxidoreductase core subunit S7
NEDD4	NEDD4 E3 ubiquitin protein ligase
NEK3	NIMA related kinase 3
NEK5	NIMA related kinase 5
NETO2	neuropilin and tolloid like 2
NEUROG1	neurogenin 1
NEXN	nexilin F-actin binding protein
NFIA	nuclear factor I A
NIBAN2	niban apoptosis regulator 2
NKX2-5	NK2 homeobox 5
NKX3-2	NK3 homeobox 2
NME5	NME/NM23 family member 5
NMUR2	neuromedin U receptor 2
NOL10	nucleolar protein 10
NOP10	NOP10 ribonucleoprotein
NR4A3	nuclear receptor subfamily 4 group A member 3
NRG4	neuregulin 4
NRON	non-coding repressor of NFAT

APPENDIX F: GENES AND GENES DESCRIPTIONS BASED ON REGIONS WITH HIGH FREQUENCY OF ROH (Continued)

Gene name	**Gene description**
NSG2	neuronal vesicle trafficking associated 2
NT5DC4	5'-nucleotidase domain containing 4
NT5M	5',3'-nucleotidase, mitochondrial
NTN1	netrin 1
NTSR2	neurotensin receptor 2
NUDT7	nudix hydrolase 7
NUMA1	nuclear mitotic apparatus protein 1
NUP98	nucleoporin 98
NUPR1	nuclear protein 1, transcriptional regulator
NUPR2	nuclear protein 2, transcriptional regulator
ODF2L	outer dense fiber of sperm tails 2 like
ODF3L2	outer dense fiber of sperm tails 3 like 2
OPRM1	opioid receptor mu 1
OR4K15	olfactory receptor family 4 subfamily K member 15
OR4N5	olfactory receptor 4N5
ORAI3	ORAI calcium release-activated calcium modulator 3
ORC6	origin recognition complex subunit 6
PAGR1	PAXIP1 associated glutamate rich protein 1
PALM	paralemmin
PAPSS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1
PATJ	PATJ crumbs cell polarity complex component
PAX5	paired box 5
PAX8	paired box 8
PBX3	PBX homeobox 3
PCBD2	pterin-4 alpha-carbinolamine dehydratase 2
PCBP3	poly(rC) binding protein 3
PCSK4	proprotein convertase subtilisin/kexin type 4
PCYOX1L	prenylcysteine oxidase 1 like
PDE2A	phosphodiesterase 2A
PDE3B	phosphodiesterase 3B
PDE4D	phosphodiesterase 4D
PDE6A	phosphodiesterase 6A
PDE7A	phosphodiesterase 7A
PDGFRB	platelet derived growth factor receptor beta
PDIA6	protein disulfide isomerase family A member 6
PDS5B	PDS5 cohesin associated factor B
PEAK1	pseudopodium enriched atypical kinase 1
PEMT	phosphatidylethanolamine N-methyltransferase
PGAP2	post-GPI attachment to proteins 2
PGBD2	piggyBac transposable element derived 2
PGM1	phosphoglucomutase 1
PHF24	PHD finger protein 24
PHKB	phosphorylase kinase regulatory subunit beta
PHKG1	phosphorylase kinase catalytic subunit gamma 1
PHKG2	phosphorylase kinase catalytic subunit gamma 2

APPENDIX F: GENES AND GENES DESCRIPTIONS BASED ON REGIONS WITH HIGH FREQUENCY OF ROH (Continued)

Gene name	**Gene description**
PHOX2A	paired like homeobox 2A
PIGB	phosphatidylinositol glycan anchor biosynthesis class B
PIGL	phosphatidylinositol glycan anchor biosynthesis class L
PIGO	phosphatidylinositol glycan anchor biosynthesis class O
PIK3R5	phosphoinositide-3-kinase regulatory subunit 5
PIK3R6	phosphoinositide-3-kinase regulatory subunit 6
PIP5KL1	phosphatidylinositol-4-phosphate 5-kinase like 1
PITX1	paired like homeodomain 1
PKD2L2	polycystin 2 like 2, transient receptor potential cation channel
PLA2G12A	phospholipase A2 group XIIA
PLD6	phospholipase D family member 6
PLK2	polo like kinase 2
PLPP2	phospholipid phosphatase 2
PLPPR3	phospholipid phosphatase related 3
PMP22	peripheral myelin protein 22
PNPT1	polyribonucleotide nucleotidyltransferase 1
POFUT2	protein O-fucosyltransferase 2
POLR1A	RNA polymerase I subunit A
POLR1B	RNA polymerase I subunit B
POLR1E	RNA polymerase I subunit E
POLR2C	RNA polymerase II subunit C
POLR2E	RNA polymerase II subunit E
POLR2H	RNA polymerase II subunit H
POLR2M	RNA polymerase II subunit M
POLRMT	RNA polymerase mitochondrial
PPARGC1B	PPARG coactivator 1 beta
PPP2CA	protein phosphatase 2 catalytic subunit alpha
PPP4C	protein phosphatase 4 catalytic subunit
PPP4R3B	protein phosphatase 4 regulatory subunit 3B
PPP6C	protein phosphatase 6 catalytic subunit
PRICKLE2	prickle planar cell polarity protein 2
PRMT2	protein arginine methyltransferase 2
PRPSAP2	phosphoribosyl pyrophosphate synthetase associated protein 2
PRR14	proline rich 14
PRSS36	serine protease 36
PRSS53	serine protease 53
PRSS57	serine protease 57
PRSS8	serine protease 8
PRTG	protogenin
PRTN3	proteinase 3
PSAT1	phosphoserine aminotransferase 1
PSD4	pleckstrin and Sec7 domain containing 4
PSMA1	proteasome 20S subunit alpha 1
PSMA4	proteasome 20S subunit alpha 4
PSMD2	proteasome 26S subunit, non-ATPase 2

APPENDIX F: GENES AND GENES DESCRIPTIONS BASED ON REGIONS WITH HIGH FREQUENCY OF ROH (Continued)

Gene name	Gene description
PSMD6	proteasome 26S subunit, non-ATPase 6
PSPH	phosphoserine phosphatase
PSTPIP1	proline-serine-threonine phosphatase interacting protein 1
PTBP1	polypyrimidine tract binding protein 1
PTCD3	pentatricopeptide repeat domain 3
PTGES2	prostaglandin E synthase 2
PTGFR	prostaglandin F receptor
PTPRG	protein tyrosine phosphatase receptor type G
PTRH1	peptidyl-tRNA hydrolase 1 homolog
PWWP3A	PWWP domain containing 3A, DNA repair factor
PYCARD	apoptosis-associated speck-like protein containing a CARD
PYGO1	pygopus family PHD finger 1
QPRT	quinolinate phosphoribosyltransferase
R3HDM4	R3H domain containing 4
RAB28	RAB28, member RAS oncogene family
RAB3C	RAB3C, member RAS oncogene family
RABEPK	Rab9 effector protein with kelch motifs
RAD23B	RAD23 homolog B, nucleotide excision repair protein
RAI1	retinoic acid induced 1
RALGPS1	Ral GEF with PH domain and SH3 binding motif 1
RARS1	arginyl-tRNA synthetase 1
RASD1	ras related dexamethasone induced 1
RASGRF2	Ras protein specific guanine nucleotide releasing factor 2
RAVER2	ribonucleoprotein, PTB binding 2
RBL2	RB transcriptional corepressor like 2
RBM22	RNA binding motif protein 22
RCBTB1	RCC1 and BTB domain containing protein 1
RCN2	reticulocalbin 2
RCVRN	recoverin
REEP1	receptor accessory protein 1
REEP2	receptor accessory protein 2
REEP6	receptor accessory protein 6
REXO1	RNA exonuclease 1 homolog
RFC3	replication factor C subunit 3
RFX7	regulatory factor X7
RGS17	regulator of G protein signaling 17
RHOG	ras homolog family member G
RMND5A	required for meiotic nuclear division 5 homolog A
RNASEH2B	ribonuclease H2 subunit B
RNF103	charged multivesicular body protein 3
RNF112	ring finger protein 112
RNF121	ring finger protein 121
RNF126	ring finger protein 126
RNF38	ring finger protein 38
RNF40	ring finger protein 40

APPENDIX F: GENES AND GENES DESCRIPTIONS BASED ON REGIONS WITH HIGH FREQUENCY OF ROH (Continued)

Gene name	**Gene description**
ROCK2	Rho associated coiled-coil containing protein kinase 2
ROR1	receptor tyrosine kinase like orphan receptor 1
RPGRIP1L	RPGRIP1 like
RPIA	ribose 5-phosphate isomerase A
RPL12	ribosomal protein L12
RPL26L1	ribosomal protein L26 like 1
RRAS2	RAS related 2
RRH	retinal pigment epithelium-derived rhodopsin homolog
RRM2	ribonucleotide reductase regulatory subunit M2
RRS1	ribosome biogenesis regulator 1 homolog
RTN4	reticulon 4
RTTN	rotatin
RUNX1	RUNX family transcription factor 1
RYR3	ryanodine receptor 3
S100B	S100 calcium binding protein B
SAR1B	secretion associated Ras related GTPase 1B
SBNO2	strawberry notch homolog 2
SCAMP4	secretory carrier membrane protein 4
SCAPER	S-phase cyclin A associated protein in the ER
SCGB3A2	secretoglobin family 3A member 2
SEC24A	SEC24 homolog A, COPII coat complex component
SEC24B	SEC24 homolog B, COPII coat complex component
SECISBP2L	SECIS binding protein 2 like
SELENOF	selenoprotein F
SEMA6D	semaphorin 6D
SENP2	SUMO specific peptidase 2
SEPTIN1	septin 1
SEPTIN14	septin 14
SERPINE3	serpin family E member 3
SETD1A	SET domain containing 1A, histone lysine methyltransferase
SETD9	SET domain containing 9
SETDB2	SET domain bifurcated histone lysine methyltransferase 2
SEZ6L2	seizure related 6 homolog like 2
SGF29	SAGA complex associated factor 29
SGMS2	sphingomyelin synthase 2
SH2D3C	SH2 domain containing 3C
SH3BP5L	SH3 binding domain protein 5 like
SH3GLB1	SH3 domain containing GRB2 like, endophilin B1
SH3TC2	SH3 domain and tetratricopeptide repeats 2
SHC4	SHC adaptor protein 4
SHCBP1	SHC binding and spindle associated 1
SHF	Src homology 2 domain containing F
SHMT1	serine hydroxymethyltransferase 1
SHROOM1	shroom family member 1
SIL1	SIL1 nucleotide exchange factor

APPENDIX F: GENES AND GENES DESCRIPTIONS BASED ON REGIONS WITH HIGH FREQUENCY OF ROH (Continued)

Gene name	Gene description
SKP1	S-phase kinase associated protein 1
SLC12A1	solute carrier family 12 member 1
SLC12A6	solute carrier family 12 member 6
SLC19A1	solute carrier family 19 member 1
SLC20A1	solute carrier family 20 member 1
SLC24A5	solute carrier family 24 member 5
SLC25A15	solute carrier family 25 member 15
SLC25A25	solute carrier family 25 member 25
SLC25A48	solute carrier family 25 member 48
SLC26A2	solute carrier family 26 member 2
SLC27A2	solute carrier family 27 member 2
SLC28A2	solute carrier family 28 member 2
SLC2A8	solute carrier family 2 member 8
SLC30A4	solute carrier family 30 member 4
SLC36A1	proton-coupled amino acid transporter 1
SLC36A2	solute carrier family 36 member 2
SLC36A3	proton-coupled amino acid transporter 3
SLC44A1	solute carrier family 44 member 1
SLC47A1	solute carrier family 47 member 1
SLC47A2	solute carrier family 47 member 2
SLC5A10	solute carrier family 5 member 10
SLC5A2	solute carrier family 5 member 2
SLC66A3	solute carrier family 66 member 3
SLC6A7	solute carrier family 6 member 7
SLC9A9	solute carrier family 9 member A9
SMAD5	SMAD family member 5
SMCR8	SMCR8-C9orf72 complex subunit
SMIM3	small integral membrane protein 3
SMIM32	small integral membrane protein 32
SMYD1	SET and MYND domain containing 1
SNORA62	small nucleolar RNA SNORA62/SNORA6 family
SNORA63	small nucleolar RNA SNORA63
SNORA65	small nucleolar RNA, H/ACA box 65
SNORA70	small nucleolar RNA SNORA70
SNORA71	small nucleolar RNA SNORA71
SNORA72	small nucleolar RNA SNORA72
SNORA80B	small nucleolar RNA, H/ACA box 80B
SNORD14	small nucleolar RNA SNORD14
SNORD31	small nucleolar RNA SNORD31
SNORD49A	small nucleolar RNA, C/D box 49A
SNORD49B	small nucleolar RNA, C/D box 49B
SNORD63	small nucleolar RNA SNORD63
SNORD65	small nucleolar RNA, C/D box 65
SNORD66	small nucleolar RNA, C/D box 66
SNORD94	small nucleolar RNA, C/D box 94

APPENDIX F: GENES AND GENES DESCRIPTIONS BASED ON REGIONS WITH HIGH FREQUENCY OF ROH (Continued)

Gene name	Gene description
SNTN	sentan, cilia apical structure protein
SORD	sorbitol dehydrogenase
SOSTDC1	sclerostin domain containing 1
SOX6	SRY-box transcription factor 6
SPARC	secreted protein acidic and cysteine rich
SPATA5L1	spermatogenesis associated 5 like 1
SPATC1L	spermatogenesis and centriole associated 1 like
SPECC1	cytospin-B
SPINK1	serine peptidase inhibitor, Kazal type
SPINK5	serine protease inhibitor Kazal-type 5
SPINK6	serine protease inhibitor Kazal-type 6
SPINK7	serine peptidase inhibitor, Kazal type 7 (putative)
SPINK9	serine peptidase inhibitor, Kazal type 9
SPOCK1	SPARC (osteonectin), cwcv and kazal like domains proteoglycan 1
SPRYD7	SPRY domain containing 7
SPTBN1	spectrin beta, non-erythrocytic 1
ST3GAL1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1
ST6GALNAC4	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 4
STARD13	StAR related lipid transfer domain containing 13
STC2	stanniocalcin 2
STIM1	stromal interaction molecule 1
STK11	serine/threonine kinase 11
STOML2	stomatin like 2
STX17	syntaxin 17
STX1B	syntaxin 1B
STX4	syntaxin 4
STX8	syntaxin 8
STXBP1	syntaxin binding protein 1
SYDE2	synapse defective Rho GTPase homolog 2
SYNPO	synaptopodin
SYNPR	synaptoporin
TAF1B	TATA-box binding protein associated factor, RNA polymerase I subunit B
TAL2	TAL bHLH transcription factor 2
TAOK2	TAO kinase 2
TBC1D10B	TBC1 domain family member 10B
TBC1D2	TBC1 domain family member 2
TBX6	T-box transcription factor 6
TCF12	transcription factor 12
TCF3	transcription factor 3
TCF7	transcription factor 7
TCOF1	treacle ribosome biogenesis factor 1
TDRD7	tudor domain containing 7
TDRP	testis development related protein
TEKT3	tektin 3
TENM2	teneurin-2

APPENDIX F: GENES AND GENES DESCRIPTIONS BASED ON REGIONS WITH HIGH FREQUENCY OF ROH (Continued)

Gene name	**Gene description**
TEX37	testis expressed 37
TEX9	testis expressed 9
TGFB1I1	transforming growth factor beta 1 induced transcript 1
TGFBI	transforming growth factor beta induced
TGFBR1	transforming growth factor beta receptor 1
THEG	theg spermatid protein
THNSL2	threonine synthase like 2
THOC7	THO complex 7
THPO	thrombopoietin
THSD1	thrombospondin type 1 domain containing 1
TIFAB	TIFA inhibitor
TIGD6	tigger transposable element derived 6
TLCD3B	TLC domain containing 3B
TLE1	transducin-like enhancer protein 1
TM2D1	TM2 domain containing 1
TMEFF2	transmembrane protein with EGF like and two follistatin like domains 2
TMEM259	transmembrane protein 259
TMEM266	transmembrane protein 266
TMEM38B	transmembrane protein 38B
TMOD1	tropomodulin 1
TMPRSS15	transmembrane serine protease 15
TMX3	thioredoxin related transmembrane protein 3
TNIP1	TNFAIP3 interacting protein 1
TOM1L2	target of myb1 like 2 membrane trafficking protein
TOP3A	DNA topoisomerase III alpha
TOR2A	torsin family 2 member A
TP53I11	tumor protein p53 inducible protein 11
TPGS1	tubulin polyglutamylase complex subunit 1
TPST1	tyrosylprotein sulfotransferase 1
TRIM13	tripartite motif containing 13
TRIM14	tripartite motif containing 14
TRIM55	tripartite motif containing 55
TRIM72	tripartite motif containing 72
TRMO	tRNA methyltransferase O
TRMT10B	tRNA methyltransferase 10B
TRPC3	transient receptor potential cation channel subfamily C member 3
TRPC7	transient receptor potential cation channel subfamily C member 7
TRPV2	transient receptor potential cation channel subfamily V member 2
TSPAN18	tetraspanin 18
TSPAN3	tetraspanin 3
TSTD2	thiosulfate sulfurtransferase like domain containing 2
TTC16	tetratricopeptide repeat domain 16
TTC17	tetratricopeptide repeat domain 17
TTC19	tetratricopeptide repeat domain 19
TTL	tubulin tyrosine ligase

APPENDIX F: GENES AND GENES DESCRIPTIONS BASED ON REGIONS WITH HIGH FREQUENCY OF ROH (Continued)

Gene name	**Gene description**
TXNDC15	thioredoxin domain containing 15
U1	U1 spliceosomal RNA
U2	U2 spliceosomal RNA
U4	U4 spliceosomal RNA
U5	U5 spliceosomal RNA
U6	U6 spliceosomal RNA
U8	U8 small nucleolar RNA
UBB	ubiquitin B
UBE2B	ubiquitin conjugating enzyme E2 B
UBE2Q2	ubiquitin conjugating enzyme E2 Q2
UBE2U	ubiquitin conjugating enzyme E2 U
ULK2	unc-51 like autophagy activating kinase 2
UQCRQ	cytochrome b-c1 complex subunit 8
USP1	ubiquitin specific peptidase 1
USP25	ubiquitin specific peptidase 25
USP43	ubiquitin specific peptidase 43
USP8	ubiquitin specific peptidase 8
VAT1L	vesicle amine transport 1 like
VCP	valosin containing protein
VCPIP1	valosin containing protein interacting protein 1
VDAC1	voltage dependent anion channel 1
VKORC1L1	vitamin K epoxide reductase complex subunit 1 like 1
VPS35	VPS35 retromer complex component
VPS36	vacuolar protein sorting 36 homolog
VPS8	VPS8 subunit of CORVET complex
VWA5B2	von Willebrand factor A domain containing 5B2
VXN	vexin
WDFY2	WD repeat and FYVE domain containing 2
WDR18	WD repeat domain 18
WDR63	WD repeat domain 63
WNT8A	Wnt family member 8A
WWC1	WW and C2 domain containing 1
XPA	XPA, DNA damage recognition and repair factor
YBEY	ybeY metalloendoribonuclease
YEATS2	YEATS domain containing 2
YPEL3	yippee like 3
ZAR1L	zygote arrest 1 like
ZBTB34	zinc finger and BTB domain containing 34
ZBTB43	zinc finger and BTB domain containing 43
ZBTB5	zinc finger and BTB domain containing 5
ZCCHC10	zinc finger CCHC-type containing 10
ZCCHC7	zinc finger CCHC-type containing 7
ZFAT	zinc finger and AT-hook domain containing
ZFYVE16	zinc finger FYVE-type containing 16
ZG16	zymogen granule protein 16

APPENDIX F: GENES AND GENES DESCRIPTIONS BASED ON REGIONS WITH HIGH FREQUENCY OF ROH (Continued)

Gene name	**Gene description**
ZNF287	zinc finger protein 287
ZNF300	zinc finger protein 300
ZNF462	zinc finger protein 462
ZNF48	zinc finger protein 48
ZNF624	zinc finger protein 624
ZNF646	zinc finger protein 646
ZNF668	zinc finger protein 668
ZNF672	zinc finger protein 672
ZNF689	zinc finger protein 689
ZNF692	zinc finger protein 692
ZNF768	zinc finger protein 768
ZNF771	zinc finger protein 771
ZNF79	zinc finger protein 79
ZNHIT6	zinc finger HIT-type containing 6
ZSWIM7	zinc finger SWIM-type containing 7

APPENDIX G: KEGG PATHWAYS OF GENES IN THE ROH ISLANDS FOR FREE STATE AND GAUTENG POPULATIONS

KEGG ID	**KEGG Pathways**
chx00010	Glycolysis / Gluconeogenesis
chx00030	Pentose phosphate pathway
chx00040	Pentose and glucuronate interconversions
chx00051	Fructose and mannose metabolism
chx00052	Galactose metabolism
chx00062	Fatty acid elongation
chx00071	Fatty acid degradation
chx00100	Steroid biosynthesis
chx00120	Primary bile acid biosynthesis
chx00130	Ubiquinone and other terpenoid-quinone biosynthesis
chx00140	Steroid hormone biosynthesis
chx00190	Oxidative phosphorylation
chx00220	Arginine biosynthesis
chx00230	Purine metabolism
chx00240	Pyrimidine metabolism
chx00250	Alanine
chx00260	Glycine
chx00261	Monobactam biosynthesis
chx00280	Valine
chx00310	Lysine degradation
chx00330	Arginine and proline metabolism
chx00340	Histidine metabolism
chx00350	Tyrosine metabolism
chx00360	Phenylalanine metabolism
chx00380	Tryptophan metabolism
chx00410	beta-Alanine metabolism
chx00450	Selenocompound metabolism
chx00480	Glutathione metabolism
chx00500	Starch and sucrose metabolism
chx00510	N-Glycan biosynthesis
chx00512	Mucin type O-glycan biosynthesis
chx00513	Various types of N-glycan biosynthesis
chx00514	Other types of O-glycan biosynthesis
chx00515	Mannose type O-glycan biosynthesis
chx00520	Amino sugar and nucleotide sugar metabolism
chx00533	Glycosaminoglycan biosynthesiskeratan sulfate
chx00534	Glycosaminoglycan biosynthesisheparan sulfate / heparin
chx00561	Glycerolipid metabolism
chx00562	Inositol phosphate metabolism
chx00563	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis
chx00564	Glycerophospholipid metabolism
chx00565	Ether lipid metabolism
chx00590	Arachidonic acid metabolism
chx00591	Linoleic acid metabolism
chx00592	alpha-Linolenic acid metabolism

APPENDIX G: KEGG PATHWAYS OF GENES IN THE ROH ISLANDS FOR FREE STATE AND GAUTENG POPULATIONS (Continued)

KEGG ID	KEGG Pathways
chx00600	Sphingolipid metabolism
chx00601	Glycosphingolipid biosynthesislacto and neolacto series
chx00603	Glycosphingolipid biosynthesisglobo and isoglobo series
chx00604	Glycosphingolipid biosynthesisganglio series
chx00620	Pyruvate metabolism
chx00630	Glyoxylate and dicarboxylate metabolism
chx00640	Propanoate metabolism
chx00650	Butanoate metabolism
chx00670	One carbon pool by folate
chx00730	Thiamine metabolism
chx00750	Vitamin B6 metabolism
chx00760	Nicotinate and nicotinamide metabolism
chx00790	Folate biosynthesis
chx00830	Retinol metabolism
chx00920	Sulfur metabolism
chx00980	Metabolism of xenobiotics by cytochrome P450
chx00982	Drug metabolismcytochrome P450
chx00983	Drug metabolismother enzymes
chx01040	Biosynthesis of unsaturated fatty acids
chx01100	Metabolic pathways
chx01210	2-Oxocarboxylic acid metabolism
chx01212	Fatty acid metabolism
chx01230	Biosynthesis of amino acids
chx01521	EGFR tyrosine kinase inhibitor resistance
chx01522	Endocrine resistance
chx01523	Antifolate resistance
chx01524	Platinum drug resistance
chx02010	AB
chx03008	Ribosome biogenesis in eukaryotes
chx03010	Ribosome
chx03013	RNA transport
chx03015	mRNA surveillance pathway
chx03018	RNA degradation
chx03020	RNA polymerase
chx03030	DNA replication
chx03040	Spliceosome
chx03050	Proteasome
chx03060	Protein export
chx03320	PPAR signaling pathway
chx03420	Nucleotide excision repair
chx03430	Mismatch repair
chx03440	Homologous recombination
chx03460	Fanconi anemia pathway
chx04010	MAPK signaling pathway
chx04012	ErbB signaling pathway

APPENDIX G: KEGG PATHWAYS OF GENES IN THE ROH ISLANDS FOR FREE STATE AND GAUTENG POPULATIONS (Continued)

KEGG ID	**KEGG Pathways**
chx04014	Ras signaling pathway
chx04015	Rap1 signaling pathway
chx04022	cGMP-PKG signaling pathway
chx04024	cAMP signaling pathway
chx04061	Viral protein interaction with cytokine and cytokine receptor
chx04064	NF-kappa B signaling pathway
chx04066	HIF-1 signaling pathway
chx04068	FoxO signaling pathway
chx04070	Phosphatidylinositol signaling system
chx04071	Sphingolipid signaling pathway
chx04072	Phospholipase D signaling pathway
chx04080	Neuroactive ligand-receptor interaction
chx04114	Oocyte meiosis
chx04115	p53 signaling pathway
chx04120	Ubiquitin mediated proteolysis
chx04130	SNARE interactions in vesicular transport
chx04136	Autophagyother
chx04137	Mitophagyanimal
chx04140	Autophagyanimal
chx04141	Protein processing in endoplasmic reticulum
chx04142	Lysosome
chx04144	Endocytosis
chx04145	Phagosome
chx04146	Peroxisome
chx04150	mTOR signaling pathway
chx04151	PI3K-Akt signaling pathway
chx04152	AMPK signaling pathway
chx04210	Apoptosis
chx04211	Longevity regulating pathway
chx04213	Longevity regulating pathwaymultiple species
chx04216	Ferroptosis
chx04217	Necroptosis
chx04261	Adrenergic signaling in cardiomyocytes
chx04270	Vascular smooth muscle contraction
chx04310	Wnt signaling pathway
chx04330	Notch signaling pathway
chx04340	Hedgehog signaling pathway
chx04350	TGF-beta signaling pathway
chx04360	Axon guidance
chx04370	VEGF signaling pathway
chx04371	Apelin signaling pathway
chx04380	Osteoclast differentiation
chx04390	Hippo signaling pathway
chx04392	Hippo signaling pathwaymultiple species

APPENDIX G: KEGG PATHWAYS OF GENES IN THE ROH ISLANDS FOR FREE STATE AND GAUTENG POPULATIONS (Continued)

KEGG ID	**KEGG Pathways**
chx04510	Focal adhesion
chx04520	Adherens junction
chx04530	Tight junction
chx04540	Gap junction
chx04550	Signaling pathways regulating pluripotency of stem cells
chx04611	Platelet activation
chx04612	Antigen processing and presentation
chx04620	Toll-like receptor signaling pathway
chx04621	NOD-like receptor signaling pathway
chx04622	RIG-I-like receptor signaling pathway
chx04630	JAK-STAT signaling pathway
chx04640	Hematopoietic cell lineage
chx04650	Natural killer cell mediated cytotoxicity
chx04657	IL-17 signaling pathway
chx04658	Th1 and Th2 cell differentiation
chx04659	Th17 cell differentiation
chx04660	T cell receptor signaling pathway
chx04662	B cell receptor signaling pathway
chx04664	Fc epsilon RI signaling pathway
chx04666	Fc gamma R-mediated phagocytosis
chx04668	TNF signaling pathway
chx04670	Leukocyte transendothelial migration
chx04714	Thermogenesis
chx04720	Long-term potentiation
chx04721	Synaptic vesicle cycle
chx04722	Neurotrophin signaling pathway
chx04723	Retrograde endocannabinoid signaling
chx04724	Glutamatergic synapse
chx04726	Serotonergic synapse
chx04727	GABAergic synapse
chx04728	Dopaminergic synapse
chx04730	Long-term depression
chx04740	Olfactory transduction
chx04742	Taste transduction
chx04744	Phototransduction
chx04750	Inflammatory mediator regulation of TRP channels
chx04810	Regulation of actin cytoskeleton
chx04910	Insulin signaling pathway
chx04911	Insulin secretion
chx04912	GnRH signaling pathway
chx04914	Progesterone-mediated oocyte maturation
chx04915	Estrogen signaling pathway
chx04916	Melanogenesis
chx04917	Prolactin signaling pathway
chx04918	Thyroid hormone synthesis

APPENDIX G: KEGG PATHWAYS OF GENES IN THE ROH ISLANDS FOR FREE STATE AND GAUTENG POPULATIONS (Continued)

KEGG ID	**KEGG Pathways**
chx04919	Thyroid hormone signaling pathway
chx04920	Adipocytokine signaling pathway
chx04921	Oxytocin signaling pathway
chx04922	Glucagon signaling pathway
chx04923	Regulation of lipolysis in adipocytes
chx04924	Renin secretion
chx04925	Aldosterone synthesis and secretion
chx04926	Relaxin signaling pathway
chx04928	Parathyroid hormone synthesis
chx04929	GnRH secretion
chx04930	Type II diabetes mellitus
chx04931	Insulin resistance
chx04932	Non-alcoholic fatty liver disease (NAFLD)
chx04933	AGE-RAGE signaling pathway in diabetic complications
chx04935	Growth hormone synthesis
chx04940	Type I diabetes mellitus
chx04960	Aldosterone-regulated sodium reabsorption
chx04961	Endocrine and other factor-regulated calcium reabsorption
chx04962	Vasopressin-regulated water reabsorption
chx04970	Salivary secretion
chx04971	Gastric acid secretion
chx04972	Pancreatic secretion
chx04974	Protein digestion and absorption
chx04975	Fat digestion and absorption
chx04976	Bile secretion
chx04977	Vitamin digestion and absorption
chx04978	Mineral absorption
chx05010	Alzheimer disease
chx05012	Parkinson disease
chx05014	Amyotrophic lateral sclerosis (ALS)
chx05016	Huntington disease
chx05017	Spinocerebellar ataxia
chx05020	Prion diseases
chx05031	Amphetamine addiction
chx05032	Morphine addiction
chx05033	Nicotine addiction
chx05034	Alcoholism
chx05100	Bacterial invasion of epithelial cells
chx05132	Salmonella infection
chx05133	Pertussis
chx05134	Legionellosis
chx05135	Yersinia infection
chx05140	Leishmaniasis
chx05143	African trypanosomiasis
chx05144	Malaria

APPENDIX G: KEGG PATHWAYS OF GENES IN THE ROH ISLANDS FOR FREE STATE AND GAUTENG POPULATIONS (Continued)

KEGG ID	KEGG Pathways
chx05145	Toxoplasmosis
chx05146	Amoebiasis
chx05150	Staphylococcus aureus infection
chx05152	Tuberculosis
chx05160	Hepatitis
chx05161	Hepatitis B
chx05162	Measles
chx05163	Human cytomegalovirus infection
chx05164	Influenza A
chx05165	Human papillomavirus infection
chx05166	Human T-cell leukemia virus 1 infection
chx05167	Kaposi sarcoma-associated herpesvirus infection
chx05168	Herpes simplex virus 1 infection
chx05169	Epstein-Barr virus infection
chx05170	Human immunodeficiency virus 1 infection
chx05200	Pathways in cancer
chx05202	Transcriptional misregulation in cancer
chx05203	Viral carcinogenesis
chx05205	Proteoglycans in cancer
chx05206	MicroRNAs in cancer
chx05211	Renal cell carcinoma
chx05212	Pancreatic cancer
chx05213	Endometrial cancer
chx05214	Glioma
chx05215	Prostate cancer
chx05216	Thyroid cancer
chx05217	Basal cell carcinoma
chx05218	Melanoma
chx05219	Bladder cancer
chx05221	Acute myeloid leukemia
chx05223	Non-small cell lung cancer
chx05224	Breast cancer
chx05225	Hepatocellular carcinoma
chx05226	Gastric cancer
chx05235	PD-L1 expression and PD-1 checkpoint pathway in cancer
chx05321	Inflammatory bowel disease (IBD)
chx05322	Systemic lupus erythematosus
chx05323	Rheumatoid arthritis
chx05332	Graft-versus-host disease
chx05340	Primary immunodeficiency
chx05412	Arrhythmogenic right ventricular cardiomyopathy (ARV
chx05416	Viral myocarditis
chx05418	Fluid shear stress and atherosclerosis

APPENDIX H: PUBLICATIONS

Utilisation of Genome-Wide SNP Data Revealed Genetic Diversity in South African Indigenous Goat Population.

T.C. Chokoe[1,2], O. Tada[1], K. Mdladla-Hadebe[3], F. Muchadeyi[3], E. Dzomba[4], T.C. Matelele[1], T.D. Mphahlele[1], T.J. Mpofu[5], K.A. Nephawe[5] and B.J. Mtileni[5]

[1]Farm Animal Genetic Resources; Genetic Resources, Department of Agriculture, Land Reform and Rural Development, Private bag X 973, Pretoria, 0001, South Africa, [2]School of Agriculture & Environmental Sciences, Private bag X 1106, University of Limpopo, Sovenga,Polokwane, 0727,South Africa, [3]Agricultural Research Council-Biotechnology Platform, Private Bag X5, Onderstepoort, Pretoria, 0110, South Africa, [4]Discipline of Genetics, University of Kwazulu-Natal, Private BagX 01, Scottsville, 3209, South Africa. [5]Faculty of Science, Department of Animal Science, Private Bag X680, Tshwane University of Technology, Pretoria, 0001, South Africa

TlouC@dalrrd.gov.za
tlouamin@gmail.com

Background: Genome-wide assessments of the genetic landscape of Farm Animal Genetic Resources (FAnGR) are key to developing sustainable breed improvements. Understanding the FAnGR adaptation to different environments and supporting their conservation programs from community initiative to national policymakers is very important.

Aim: The aim of the study was to investigate the genetic diversity and population structure of communal indigenous goat populations from four provinces of South Africa.

Hypothesis: The diversity of indigenous goat populations can be determined by using genome-wide SNP markers.

Methodology: Communal indigenous goat populations from the Free State (FS) (n = 24), Gauteng (GP) (n = 28), Limpopo (LP) (n = 30), and North West (NW) (n = 35) provinces were genotyped using the Illumina Goats SNP50 BeadChip. An Illumina Goats SNP50 BeadChip data from commercial meat-type breeds: Boer (n = 33), Kalahari Red (n = 40), and Savanna (n = 31) were used in this study as reference populations.

Results and Discussion: The H_o revealed that the genetic diversity of a population ranged between 0.39 ± 0.11 H_o in LP to 0.42 ± 0.09 H_o in NW. Analysis of molecular variance revealed variations of 3.39% ($p < 0.0001$) and 90.64% among and within populations, respectively. The first two Principal Component Analysis (PCAs) revealed a unique Limpopo population separated from GP, FS, and NW communal indigenous goat populations with high levels of admixture with commercial goat populations. There were unique populations of Kalahari and Savanna that were observed and mixed individuals. Marker F_{ST} (Limpopo versus commercial goat populations) revealed 442 outlier single nucleotide polymorphisms (SNPs) across all chromosomes, and the SNP with the highest F_{ST} value ($F_{ST} = 0.72$; chromosome 8) was located on the *UHRF2* gene. Population differentiation tests (PCAdapt) revealed PC2 as optimal and five outlier SNPs were detected on chromosomes 10, 15, 20, and 21.

Conclusion/recommendations: The study revealed that the SNPs identified by the first two principal components show high F_{ST} values in LP communal goat populations and allowed us to identify candidate genes which can be used in the development of breed selection programs to improve this unique LP population and other communal goat population of FS, GP, and NW, and find genetic factors contributing

to the adaptation to harsh environments. Effective management and utilization of South African communal indigenous goat populations is important, and effort should be made to maintain unique genetic resources for conservation.