PHENOTYPIC AND GENETIC VARIATION IN RESISTANCE TO GASTRO-INTERSTINAL NEMATODES OF GOATS IN DIFFERENT AGRO-ECOLOGICAL ZONES OF LIMPOPO PROVINCE

by

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DISSERTATION

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DEDICATION

This work is dedicated to:

The Almighty God in Great Heavens,

Both my parents Phetole and Mokgadi Mohale, my sister Maria Ngobeni for encouraging me to undertake both undergraduate and postgraduate studies. You are the rock in my life and the anchor of our family, your wishes have been fulfilled, my uncle Lordwick Raseala and brother in-law Ronny Makhurupetsi, I'm forever indebted for the encouragement and support; no matter the obstacle you gave me the courage to overcome it.

DECLARATION

I declare that the dissertation hereby submitted to the University of Limpopo, for the degree of Master of Agricultural Management (Animal Production) has not previously been submitted by me for a degree at this or any other university; that it is my own work in design and in execution and that all the material contained herein has been duly acknowledged.

…… ……...

Mohale Lekukela Bernard (Mr) Date

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ABSTRACT

The study was conducted to assess phenotypic and genotypic diversity in resistance to gastro-intestinal nematode (GIN) within communal goats in different agro-ecological zones of Limpopo province. Eighty goats were randomly sampled from Mopani = 20, Blouburg = 20, Vhembe = 20 and Capricorn = 20, representing four agro-ecological zones of Limpopo province. Frequencies and percentages of occurrence of qualitative traits and least square means (LSM) of quantitative traits were computed. Goats were characterized as multi-coloured (67.7%), black dominant coat colour (40%), flat face profile (73.8%), erect ears (68.75%), slopping rump (47.5%), no toggles (83.8%), horned (86.3%), while 71.0% and 59.4% were straight shaped and orientated backward respectively, in all agro-ecological zones. Faecal and blood samples were collected to assess the prevalence of GIN and genetic diversity of goats. The highest prevalence and abundance GIN parasites were *Haemonchus contortus* (nematode = 357.42) followed by *Fasciola hapatica* (trematode = 163) and *Moniezia* (cestodes = 121.50). The patterns of GIN prevalence varied ($P < 0.05$) across agro-ecological zones and seasons. Prevalence of *Moniezia* nematode varied ($P < 0.05$) amongst goat sexes, whilst prevalence of other GIN's did not vary ($P>0.05$). For genetic variation in GIN resistance, goats were genotyped at 15 microsatellite markers recommended by the International Society of Animal Genetics. Expected heterozygosity ($H_{E)}$ ranged from 0.69 in arid zone goat population to 0.76 in sub-humid zone goat population, while the observed heterozygosity (H_O) ranged from 0.53 in arid zone goat population to 0.60 in sub-humid zone goat population. Mean number of alleles (MNA) per population ranged from 6.13 to 7.40. Gene differentiation (F_{ST}) among populations was low (3.6%). The results revealed that genetic relationships between populations do not reflect their geographical proximity as revealed by the Nei's genetic distance results. Low heterozygosity resulted in reducing some fitness traits for GIN parasite resistance. Inbreed goats showed low internal parasite resistance across all agro-ecological zones.

Keywords: *Capra hircus,* Inbreeding co-efficient, gastro-intestinal nematodes.

LIST OF ABBREVIATIONS

AEZ	Agro-ecological zone
AnGR	Animal genetic resource
ANOVA	Analyses of variance
BD	Body Depth
BL	Body Length
CM	Centimeter
CW	Chest Width
DNA	Deoxyribonucleic acid
EDTA	Ethylenediamine tetraacetic acid
EL	Ear length
FEC	Faecal egg count
F_{IS}	Inbreeding co-efficient
F_{ST}	Fixation index
GIN	Gastro-intestinal nematodes
GLM	Generalized linear model
H_E	Expected heterozygosity
H_O	Observed heterozygosity
HW	Head width
Hz	Heterozygosity

L	Length
LSD	Least significant difference
MNA	Mean number of alleles
NA	Number of alleles
PCA	Principal Components Analysis
PCR	Polymerase chain reaction
PCV	Packed Cell Volume
PH	Potential of hydrogen
PIC	Polymorphism information content
SA	Sub-arid
SAS	Statistical Analysis System
SD	Standard deviation
SE	Standard error
SH	Sub-humid

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CHAPTER 1: GENERAL INTRODUCTION

1.1. INTRODUCTION

Goats (*Capra hircus*) are among the first farm animals to be domesticated as indicated by archaeological evidence (Ensminger & Parker, 1986). Goats play an important role in human livelihoods meeting nutritional, economic and social needs for rural households (Ruto *et al*., 2004). African indigenous goats are known for their adaptation to harsh climatic conditions, their ability to use poor quality forage and tolerance to infectious diseases and parasites as well as heat stress (Casey and Van Niekerk, 1988; Barry and Godke, 2001; Morand-Fehr *et al*., 2004; Kunene and Fossey, 2006). These traits enable them to cope with the stressful nature of vast marginal lands in the region. The African indigenous animal genetic resources were regarded as less productive, hence, subjected to replacement and crossbreeding with exotic breeds leading to genetic erosion, loss of genetic diversity and reduction of adaptive value and opportunities for efficient utilization of the existing adapted genetic resources (Ramsey *et al*., 2000; Mpofu, 2002).

African indigenous goats developed through natural selection being exposed to harsh conditions such as parasites and diseases and have variety of phenotypic traits (Mason, 1996; Alaku, 2010) and genetic diversity (Rege, 1992). One would expect these goats to be inherently resistant to gastro-intestinal nematode (GIN) infections (Waller & Thamsborg, 2004), however, indiscriminate crossbreeding and replacement of indigenous breeds with exotic breeds may have reduced this important trait and diversity. Productivity of goats in the communal farming system, which is based on the extensive system, is poor with a low weaning rate, high mortality rate and low turnover (Bembridge & Tapson, 1993). It is difficult to associate the high mortality with a single factor, as it is a combination of several factors (Webb & Mamabolo, 2004). The main causes of mortality in goats in order of importance are diseases (gastro-intestinal parasites, scabies, lung infections, abortions and heart-water), predation (Jackals, lynx, snakes and wild dogs), hostile environment and lack of technical support (Webb & Mamabolo, 2004).

A combination of phenotypic (including classical morphometric), biochemical (e.g. protein polymorphism, blood group) analysis and, molecular genetic studies using DNA information are the central sources of data on genetic relationships among varieties of breeds (Rege and Gibson, 2003). Molecular markers are more accurate and reliable than all other markers because of their dense distribution over the genome, great variation, co-dominant inheritance and easy genotyping at DNA level (Koreth *et al.*, 1996). Among the various molecular genetic markers such as Restriction Fragment Length Polymorphisms (RFLPs), Random Amplified Polymorphic DNA (RAPD) and Variable Number of Tandem Repeats (VNTRs), microsatellites (STR) are common in all eukaryotic genomes with frequencies as high as one marker per every 6 kb and easy to type via polymerase chain reaction (PCR) (Rege and Gibson, 2003).

1.2. PROBLEM STATEMENT

Goats are usually managed under extensive conditions which expose them to GIN parasites, often leading to infection, loss of production, anthelminthic drug costs and death (Ruto et al., 2004). They are more susceptible to GIN than other ruminants (Huntley *et al*., 1995). Gastro-intestinal nematode control is achieved by a combination of anthelmintic treatment (Waller & Thamsborg, 2004) and grazing management (Barger *et al*., 1994), however some researchers (Kaplan, 2004; McKellar and Jackson, 2004) have reported an increasing concern about the development of anthelmintic drug resistance in most parasite populations.

Some breeds are more resistant to GIN than others (Gruner and Cabare, 1988). Although there is a consistent pattern of responsiveness between breeds that is associated with different production characteristics, and the African indigenous goat breeds are more resistant than European breeds (Kaplan, 2004). The value of between-breed variation will come from the substitution of a susceptible breed with one having enhanced resistance (Kaplan, 2004). In most experiments, the mechanistic basis of breed differences has not been well defined (Kaplan, 2004). The first step in conservation and utilization of local genetic resources is characterization, assessing morphological and genotypical qualities among breeds (Delgado *et al*., 2001; Lanari *et al*., 2003; Mekasha, 2007;). There is currently a paucity of information on the

phenotypic and genetic variation in resistance to GIN within South African indigenous goats in different agro-ecological zones of Limpopo province.

1.3. PURPOSE OF THE STUDY

The purpose of the study was to assess phenotypic and genetic variation in GIN resistance within goats in different agro-ecological zones of Limpopo province.

The specific objectives of the study were:

i. To determine the prevalence of gastro-intestinal nematode infections in different agro-ecological zones of Limpopo province.
ii. To assess the phenotypic variations among the South African communal goat populations in different agro-ecological zones of Limpopo province.
iii. To assess the genetic diversity in gastro-intestinal nematode resistance among goat populations in different agro-ecological zones of Limpopo province.

1.4. HYPOTHESES

The hypotheses tested were that:

i. The prevalence of gastro-intestinal nematode infections differs with the agro-ecological zone in Limpopo province.
ii. There is high phenotypic variation among the South African communal goat populations in different agro-ecological zone of Limpopo.
iii. There is high genetic diversity in gastrointestinal nematode resistance among goat populations in different agro-ecological zones of Limpopo.

CHAPTER 2: LITERATURE REVIEW

2.1. INTRODUCTION

The world goat population is estimated to be 861.9 million, with the largest population in Asia (59.7%), followed by Africa (33.8%) (FAO, 2011). From a total of 351 goat breeds of the world, about 146 goat breeds are found in Asia and 59 in Africa (Devendra, 1998). Generally, goats of Africa are divided into three major types following their morphology; the long lop-eared type in north east and southern Africa, the small short-eared type dominant in eastern Africa and the dwarf short-eared type of West Africa (Rege, 1992). Intermediates morphological types are numerous. Despite the huge resource potential, production and export opportunities, goat production in Africa is relatively undeveloped.

Indigenous goat breeds constitute well over 95 % of small ruminant populations in Africa (Rege, 1992). These indigenous goat breeds are adapted to the environment and the ravages of various kinds such as drought. Their adaptive features enable them to effectively cope with the stressful nature of marginal lands (Chenyambuga, 2002). Migration to a new habitat and consequently the effect of natural and artificial selection has led to the evolution of breeds and types of goat, which differ in appearance and performance. Around 90 ‘breeds’ of African goats have been recognized using criteria as geographic distributions, ecotypes or communities-tribe ownership (Rege, 1992).

Goats (*Capra hircus*) are found in all types of environments, from arid to humid zones. They perform very well in the drier tropics, where their ability to withstand dehydration and their browsing habit enable them to survive where cattle or sheep cannot. Goats play an important role to human livelihoods meeting nutritional, economic and social needs for rural households (Ruto *et al*., 2004). There is a diverse range of indigenous goat breeds in the world, with African indigenous goats known to be genetically resistant or tolerant to disease, performing well in harsh climatic conditions and utilizing poor quality forages (Rumosa Gwaze *et al*., 2009). The main limiting factor in foraging goats is the high rate of gastrointestinal nematode infestation (Waller 1999; Kochapakdee *et al*., 2001).

2.2. DOMESTICATION OF GOATS

Domesticated animals have played a key role in human history but despite their importance, the origin of most domestic species remains poorly understood. The goat is the earliest domestic animal and possibly the first ruminant livestock, even older than cattle, after the wolf was domesticated (Hole, 1996; Uerpmann, 1996). The wild goat was present in the regions of southwest Asia during the time when agriculture was developing (Devendra and Burns, 1983). Secondly, the goat is an extremely hardy animal, hence, could have withstood the rigours of being reduced to the state of domestication better than other ruminants. Goats were primarily domesticated at first for cultural and religious purposes. (Devendra and Burns, 1983), and secondarily for meat and milk production. Domestic goats might have played a central role in the Neolithic agricultural revolution and the spread of human civilizations around the globe (Porter, 1996; Pringle, 1998).

The evidence for time and place of goat domestication is based on archaeological evidence. Domestication of goats is considered to have occurred in the mountainous area of western Asia between the 9th millennium B.C. (Epstein, 1971; Devendra and Burns, 1983). The origin of domestic goats remains uncertain and controversial, however, archaeological evidence suggests that they were probably first domesticated in the Fertile Crescent region of the Near East possibly first in the Zagros Mountains area 10,000 years ago (Zeder and Hesse, 2000). However, it has been suggested that goats could have also been domesticated outside the Zagros Mountains range. Some studies hint to a second domestication area in Sindhu valley civilization in northwest part of India (now Pakistan) from which the cashmere breeds would have originated (Devendra and Burns, 1983).

At least two wild species of *Capra* could have contributed to the gene pool of domestic goats (Clutton-Brock, 1981 and Luikart *et al.* 2001). Luikart *et al.* (2001) studied the diversity of the cytochrome gene of mitochondrial DNA (mtDNA) in Asian goats and concluded that the strongest candidate for a matriarch ancestor of domestic goats is the bezoar (*Capra aegagrus*). Furthermore, phylogeographic analysis of mtDNA revealed three highly divergent lineages (estimated divergence > 200,000 years ago) suggesting three separate maternal origins of domestic goats (Luikart *et al.* 2001).

Joshi et al. (2004) studied the mtDNA diversity of Pakistan goats, and reported four distinct mtDNA lineages termed as A, B and C (previously reported) and a new lineage D. The estimated divergence times between the most recently evolved mtDNA-lineages A and D were from 260 483 to 371 052 years ago.

They concluded that at least four different strains of wild *Capra* might have been the source of the modern domestic goats with the most likely wild ancestor being the bezoar (Harris 1961; Clutton-Brock 1981). Joshi *et al.* (2004) undertaken the investigation of 363 goats belonging to 10 different breeds from different geographic regions of India using mtDNA sequence data from hypervariable region. They found evidence for population structure and new mitochondrial DNA in Indian goats and could not reconcile the genetic diversity found within the major lineage with domestication starting 10,000 years ago from a single mtDNA ancestor.

2.3. SOCIO-ECONOMIC IMPORTANCE OF GOATS

Goat keeping has a direct economic importance to communal or rural farmers even those headed by females. The total income share from small ruminants tends to be inversely related to size of land-holding, suggesting that small ruminants are of particular importance for landless people especially for rural women (Oluwatayo and Oluwatayo, 2012). In some cultural settings, women are often not entitled to own land for instance, African rural women (such as in Nigeria, Kenya, and Tanzania) have limited access to land and receive limited land use rights from their husbands (Quisumbing *et al*., 2001). As a result, crop production provides seasonal employment; hence, rearing of small ruminants would provide an employment opportunity and income throughout the year. Sale of goat and goat products (meat, skin and milk) by farming communities is the major source of cash for purchase of clothes, grains and other essential household commodities (Deribe, 2009; Tesfaye, 2009). The purpose of keeping goats by smallholder farmers is to generate income, for labor, wage payment followed by food crop purchase, input purchase, school fees (Deribe, 2009; Tesfaye, 2009).

2.4. CHARACTERISATION OF FARM ANIMAL GENETIC RESOURCES

Characterisation is defined as the description of a character or trait of an individual. The word ‘characterise’ is also a synonym of ‘distinguish’, that is, to mark as separate or different, or to separate into kinds, classes or categories. The characterisation of genetic resources refers to the process by which populations or ecotypes are identified or differentiated. Characterisation of AnGR includes all activities associated with the identification, quantitative and qualitative description, of a breed population and the natural habitats and production systems to which they are or not adapted. The main objective of characterization is to obtain better knowledge of AnGR, their present and potential future uses for food and agriculture in defined environments, and their current state as distinct breed populations (Taberlet *et al*., 1997). The farm AnGR can either be characterized phenotypically or genetically. The breeds that are coming from industrialized countries are well-defined and phenotypically characterized. Therefore, breeds with different names may have a recent common origin, while in other cases their uniqueness has been eroded by cross-breeding (Taberlet *et al.*, 1997).

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 (Kunene, 2009). Goat biological diversity encompasses both phenotypic as well as genotypic variation (IBC, 2004). Biodiversity can be described at several levels, from phenotypic observations to molecular data.

2.5. PHENOTYPIC DIVERSITY

Phenotypic diversity of farm animal genetic resource (AnGR) is defined as the process of identifying diverse breeds/populations by unfolding their external and production characteristics in a given environment and management, and also including the social and economic factors. Phenotypic characterization has traditionally been used to characterize variations within and between species for many centuries. An organism’s phenotype is principally a manifestation of its genotype. The information generated by characterization studies is essential for planning the management of farm AnGR at local, national, regional and global levels. A good understanding of breed

characteristics is necessary to guide decision-making in livestock development and breeding programs (Taberlet *et al.*, 1997). Phenotypic characterization of livestock breeds also includes information on population size, flock size and composition, production estimates and information on the production environment and husbandry conditions, which plays an important role in trait appearance. This method provides basic evidence for the variation between and within livestock populations, which could be utilized for selection purposes (Okpeku *et al* 2002). Conservation and improved utilization of goat genetic resources has been a priority around the world.

Phenotypic characterization activities are technically and logistically challenging (Manzi *et al*., 2011). Ensuring that they are well targeted (collect data that are important to the country's priority AnGR and livestock-development activities) and are carried out in an efficient and cost-effective manner requires thorough planning and careful implementation. Valid comparisons among livestock breeds or populations, whether nationally or internationally, require the development and use of standard practices and formats for describing their characteristics. Such standards and protocols are also needed for assessing requests for the recognition of new breeds. Lack of characterization information result in underutilization of that resource, its replacement and dilution through cross breeding despite their local adaptation to prevailing environmental constraints (Manzi *et al*., 2011).

Characterization of goat breeds through phenotype, is based on the description of qualitative and quantitative traits. Qualitative traits to be recorded during phenotypic characterization of goat breeds are sex, age (dentition), coat color pattern and type, horn shape, horn and ear orientation, facial (head) and back profile, toggle/wattles, beard, and ruff. Quantitative traits include the measurements of body length, height at withers, chest girth, chest depth, shoulder point width, head length, head width, rump length, pelvic width, horn length, ear length, shin circumference and scrotum circumference for males (Okpeku *et al* 2002).

Phenotypic characters have the advantages of being easily observed and measured and usually much lower costs are incurred during phenotypic characterization compared to genetic characterization (Minelli, 1993). For these reasons, phenotypic characters have been used extensively for characterization and identification of

breeds. Phenotypic characterization is associated with the difficulty in combining different measures in order to provide a useful tool for the description of a breed. Most phenotypic characters are polygenetically inherited and most of them are influenced by environment and sometimes with strong genotype-environment interaction. Furthermore, phenotypic characters are affected by natural selection. Therefore, due to the influence of different environmental conditions and different selection pressure on different kinds of characters, interbreed phenotypic comparison is unlikely to give meaningful results.

2.6. GENETIC DIVERSITY

Biological variation is of wide occurrence in nature. Earlier work to study genetic variation of individual animals and populations employed screening of protein variants by gel electrophoresis. Polymorphism in gene products such as enzymes, blood group systems and leucocytes antigens have been used for investigating genetic diversity at the molecular level. Using protein markers, numerous studies have estimated genetic variability, gene flow and phylogenetic relationships among populations (Barbancho *et al.*, 1984; Nguyen, 1990; Pepin and Nguyen, 1994). However, these techniques lack the power to resolve the differences between closely related breeds (Meghen *et al.*, 1994; Dowling *et al.*, 1996) since a great deal of genetic variation remains undetectable by using protein markers. Moreover, the genotype frequencies estimated from protein markers may be influenced by natural selection among alleles (Alexandrino *et al.*, 1983; Pemberton *et al.*, 1988; Mopper *et al.*, 1991) making it difficult to interpret inter-population comparisons.

The goal of genetic characterisation is to determine the genetic diversity within and between breeds. The near ultimate description of an animal should be a description of the sequence of nucleotides that comprise its genome. Describing differences and similarities in the DNA of two or more populations can provide the measure of relative genetic distances of such populations from each other. The last attribute means that genetic information on rare or endangered species can be obtained without destructive sampling (Taberlet *et al.*, 1997) and it is possible to analyze DNA from extinct populations or species (Taberlet *et al.*, 1997). More recently, molecular data from DNA markers have received particular attention in the study of population variability

because of their possible use to determine the chronology of evolutionary events using neutral DNA markers.

2.7. LOSS OF GENETIC DIVERSITY IN DOMESTIC ANIMALS

Reduction in genetic diversity has been expressed primarily in terms of loss of breeds and strains/ecotypes. It is postulated that the current rate of extinction of species, breeds and strains is greater now than at any time in the past (Hammond, 1993). It is estimated that at least 30 to 40 % of all AnGR are currently at high risk of extinction (Hammond, 1994). However, adequate records do not exist to enable reliable estimates of either loss rates of the breeds or of domestic animal diversity itself. The existing data on the number of endangered breeds are likely to be underestimates of the magnitude of the problem. The loss of genetic diversity is occurring both within populations and among populations and can lead to a reduced ability to adapt to changing environments, lowering the chances of long-term persistence, lowering immunity and parasites infections.

2.7.1. GENETIC DEMOGRAPHIC BOTTLENECKS

A demographic bottleneck occurs when a large population experience a severe, temporary reduction in number due to environmental or demographic events such as natural catastrophes, which occur at unpredictable intervals including events, like drought, disease outbreak and war (Hunter, 1996). These events may kill a certain percentage of a population and, therefore, reduce the effective population size. The result is that the genetic variability of all subsequent generations is contained in the few individuals that survive the bottleneck and reproduce. Hence, some genetic diversity is lost in the process. The magnitude of the loss in diversity depends on the size of the bottleneck and the growth rate of the population afterwards (Hunter, 1996). Another demographic event that may lead to a bottleneck effect is the founder event. A founder event occurs when a few individuals of a population establish a new population. The genetic constitution of the new population depends on the genetics of the founder animals. The genetic diversity of the original larger populations is reduced because the sample of genes in the few founder animals is not likely to be representative of the original gene pool. Generally passing through a genetic bottleneck can create two problems (Carson, 1983; Baker and Moeed, 1987); a loss

of certain alleles, especially rare alleles, if no individuals possessing those alleles survive, and a reduction in the amount of variation in genetically determined characteristics due to the presence of fewer alleles and decline in heterozygosity. Bottlenecks also reduce allozyme heterozygosity. Extremely low levels of allozyme heterozygosity in broad geographical surveys imply the occurrence of one or more recent severe bottlenecks (Leberg, 1992). The overall effect of bottlenecks is the decline in fitness of the individuals in the population.

2.7.2. INBREEDING DEPRESSION

Inbreeding result from the mating of two closely related individuals. However, the degree of relationship may vary. “Close breeding” refers to the mating of very close relatives such as sibling to sibling or parent to offspring. Its probability of occurrence increases in small populations if mating occurs at random. Inbreeding allows the rare, harmful recessive alleles to become expressed in the homozygous form, with resulting harmful effects on the offspring (Selander, 1983; Charlesworth, 1987; Ralls *et al.*, 1988; Lomker and Simon, 1994) such as reduction in fertility, fecundity, offspring size, growth and survival, and physical deformities. Since inbreeding depresses reproductive fitness, it is assumed to increase the risk of extinction. This presumption is supported by correlation between extinction and inbreeding in laboratory and domestic animals (Soulé, 1980). However, gene flow from outside populations is beneficial in avoiding inbreeding and the erosion of genetic diversity (Miller and Waits, 2003).

2.7.3 HUMAN ACTIVITIES

Extinction of species, breeds and strains through human activities represents the greatest threat to genetic diversity. The major threats to genetic diversity that result from human activity are habitat destruction and degradation, pollution, introduction of exotic species, and over-exploitation (Frankham, 1994). These threats are all caused by an ever-increasing use of natural resources due to expanding human population and development of market economy. The growth of cities, factories and mines in developing countries creates a cash market for livestock products. Consequently, the traditional farmers who formerly kept animals for their own needs begin to supply the

cash market. Genetic variation is being lost as farmers in developing countries abandon their local breeds in favour of high-yielding breeds for commercial production. Even if human activities do not directly eliminate a breed or strain, loss of genetic variation is taking place as the number of individuals in populations is reduced. In the long run the population size of a breed or strain may become so small that the breed/strain is no longer viable and may eventually go extinct.

2.8. GENETIC VARIATION IN RESISTANT TO GASTRO-INTESTINAL PARASITES

Evidence for genetic variation of resistance to gastro-intestinal parasite in small stock has been demonstrated from comparisons between and within breeds (Dube *et al*., 2002). Some studies had concluded that variability in resistant within breeds may be as great as the variability between breeds (Dube *et al*., 2002). However, Dube *et al*. (2002) highlighted that there is a need for a proper interpretation of results comparing different populations (for example, breeds, strains and bloodlines), and they are also considering that the designs of most of these experiments do not take into account any confounding effect relating to the under influence of particular sires. In northeast Brazil, particularly in Ceara state, *Haemonchus contortus* is the most important dangerous parasite in goats (Gwaze *et al*., 2009). Looking at genetic diversity between and within goat breeds in northeast Brazil, Gwaze *et al* (2009) considered that a search for genetic variability in resistance to *H. contortus* might provide an option for nematodes control. Genetic variability with respect to resistant to nematodes in sheep has been well documented, and it has been observed between breeds, between sire lines within breeds and between individuals within breeds (Kumba *et al*., 2003). Such variability made Australia and New Zealand to have several sire selection programs (Mwendia., 1996).

Other studies reported on the existence of variation between individual sheep in resistance to nematode parasites, as assessed by faecal egg count (Ntonifor *at al*., 2013). There is evidence that goats are more susceptible than sheep to gastro-intestinal nematode parasites (Ntonifor *at al*., 2013). Therefore, it is expected that the reduction in productivity and financial losses would be higher in goats than in sheep. Preston and Allonby (1975) reported differences in mortality, egg counts and

nematode establishment between Saanen, East African and Galla goat breeds. Other studies also reported the variability within the Red Sokoto goat breed with respect to nematode egg counts (Bakunzi *et al.*, 2013). Based on parasitological parameters, Alpine and Saanen cross-bred kids were noticed to be more susceptible and less resistant to *Telodorsagia circumcincta* primary infection (Kumba *et al*., 2003). Mandonnet *et al*. (1996) found the sire effect on EPG (mean egg counts) from 203 six-month-old Creole kids. Kanyari (1993) classified fibre-producing male goats, exposed to natural infection, into responders and non-responders based on individual egg counts. Native goats are more resistant to trickle infection by *H. contortus* than their Anglo-Nubian crosses (Kanyari, 1993). The post-parturient rise in egg counts is higher in magnitude and more persistent in Galla does than in Small East African (Baker *et al*., 1992).

2.8.1. GENETIC DIVERSITY IN GASTRO-INTESTINAL PARASITE BETWEEN GOATS BREEDS

It has been known worldwide for many years that some breeds are more resistant to gastro-intestinal parasite than others (Mukhebi *et al*.,1985.). Although reports have shown that there is a consistent pattern of responsiveness between breeds that is associated with different production characteristics (Mukhebi *et al*.,1985.). The exotic hair-type breeds (such as the Red Maasai, Florida Native, Barbados Blackbelly and St. Croix) are more resistant than European breeds, which in turn are more resistant than breeds primarily maintained for their fine-wool production (such as the Merino and Rambouillet). The value of between-breed variation come from the substitution of a susceptible breed with one having enhanced resistance (Mukhebi *et al*., 1985). In most experiments, the mechanistic basis of breed differences has not been well-defined. However, Mukhebi *et al*. (1985) reported responses of Romney and fine-wool Merino lambs to the intestinal nematode reared and maintained in pens to standardize environmental influences and ensure acquired responses were generated to a defined parasite load. There were no differences occurred between breeds in the unvaccinated controls, but Romney lambs had significantly lower worm-egg counts in faeces (82% protection) than Merino lambs (43 % protection) after vaccination with irradiated *T. colubriformis* larvae and challenge with normal larvae. Although the report (Mukhebi *et al*.,1985) may not have satisfied the criteria of Odoi *et al*., (2007) for between-breed

comparisons, it does suggest that acquired (immunological) responses rather than innate resistance play a role in the differences observed between Romney and Merino lambs.

2.8.2. GENETIC DIVERSITY IN GASTROINTESTINAL PARASITE WITHIN GOATS BREEDS

There are number of distinct populations that exist within breeds, for example, in the Australian Merino, a number of strains have developed in response to particular environments (Odoi et al., 2007). Woolaston *et al*. (1992) examined the degree of variation in resistance to gastro-intestinal nematodes within Merino populations. In his work, lambs from over 57 bloodlines, representing each of the major strains, were artificially infected with either the *Haemonchus contortus* or *T. colubriformis* at six different locations across Australia. The results showed that most of the genetic variation (85 %) occurred within flocks, whereas variation between strains and between bloodlines within strains was small (4% and 9%, respectively). Nsoso *et al*. (2007) postulated that within-flock selection offers the greatest potential for the genetic improvement of this trait within the constraints of the existing production system.

2.9. SEASON AND SEX EFFECT ON GASTRO-INTESTINAL PARASITE PREVALENCE

Under satisfactory environmental conditions in the wet season, *H. contortus* and other nematodes larva that infect goats reach infective stages within 46 days (Nsoso *et al*., 2007). Other researchers have observed higher rate of gastro-intestinal nematode prevalence in female hosts when compared with males (Nsoso *et al*., 2007). The nematode faecal egg counts in goats was found to have a significant variation with season, warmer seasons, spring, summer and autumn having higher egg counts than the cooler winter (Nsoso *et al*., 2007). The higher incidences of FEC in the warmer seasons than in the cooler season is attributed to more conducive environmental conditions during the warmer seasons (Woolaston *et al*., 1992). The packed cell volumes were found to be significantly affected by season, Spring had the lowest PCV, winter the highest, and the other two seasons had normal values (Nsoso et al., 2007). Other studies reported the PCV range of 22-32 % in winter (Jain, 1993), indicating that the internal parasites did not have a negative impact on the goats (Woolaston *et al*.,

1992). This could indicate that this indigenous breed is able to tolerate high worm burdens. However, worm infestations can have negative effects on the hosts leading to loss in production (Woolaston *et al*., 1992).

2.10. ANTHELMINTIC DRUGS RESISTANT TO GASTRO-INTESTINAL PARASITE

The rate of resistance appears to vary geographically in accordance with the prevailing climate, parasite species and treatment method in the region. Although the rate of resistant strains has generally been slower in temperate zones in the northern hemisphere, the prevalence of resistance is also increasing throughout Europe (Odoi *et al*., 2007) and the rest of the world (Woolaston *et al*., 1992). Over the last few decades new and better drugs have been developed, and these is used as the only means of controlling worms in small ruminants. The use of these anthelmintic treatments has now brought the small ruminant industry to the point where parasitic nematodes have developed resistant to all of the main classes of anthelmintics and there are very limited management options available to control these parasites. Surveys in South Africa have indicated that about 90 % of small ruminant farms have strains of gastro-intestinal nematodes that are resistant to drugs from at least one of the five available anthelmintic groups. In at least two cases, resistance to all five anthelmintic groups was demonstrated (Odoi *et al*., 2007).

2.11. GEOGRAPHIC DISTRIBUTION OF GASTRO-INTESTINAL PARASITES SHOWING ANTHELMINTIC RESISTANCE

Anthelmintic resistant in the field is usually noticed when worm control policies fail dramatically. Throughout the world, resistance has been detected most commonly amongst the gastro intestinal parasite of sheep and goats, preferably *Haemonchus contortus* and *Teladorsagia circumcincta*, although parasites belonging to the *Trichostrongylus, Cooperia*, and *Nematodirus* genera have also reported to develop anthelmintic resistant (Taylor and Hunt, 1989). Drugs to which resistance has been developed and recorded in many countries throughout the world against drugs in all of the three broad-spectrum families, *avermectins* and *imidazothiazoles*, which are commonly used by the livestock industry to control nematodosis (Mukhebi *et al*.,1985).

Resistance has been recorded also in drugs with a narrower spectrum of activity such as the *salicylanilides* (Jeannin *et al.,* 1990; Scott and Armour, 1991). The major anthelmintic drugs against which has been reported include: *phenothiazine* (Mukhebi *et al*.,1985), *thiabendazole* (TBZ) and other BZs (Taylor and Hunt, 1989), *ivermectin* (IVM) (Woolaston *et al*., 1992) and *levamisole* (LEV) (Odoi *et al*., 2007). It is alarming that gastro-intestinal parasite of small ruminants have developed resistance against all major groups of anthelmintics.

2.12. FACTORS CONTRIBUTING TOWARDS DEVELOPMENT OF ANTHELMINTIC RESISTANCE

Modern anthelmintic are used at an efficiency of around 99% against susceptible strains. A small number of surviving worms, which are the most resistant component of the population, then contaminate the pasture with a majority of resistant offsprings for subsequent generations which lead to development of anthelmintic resistance due to selection pressure. The rate of development of resistance is influenced by many factors which can be classified as genetic, biological or operational. The most important are the operational factors because they can be manipulated by the farmer and form the bases of resistance management programmes. However, it is necessary to understand the genetic and biological factors in order to arrive at the correct operational procedures (Odoi *et al*., 2007). There are some other factors which can also contribute towards the development of anthelmintic resistance including introduction of resistant parasites by means of animals transported from country to country (Mukhebi *et al*.,1985) and keeping the sheep and goats together (Kumba *et al*., 2003).

CHAPTER 3: METHODOLOGY

3.1. SAMPLING

The study was conducted in communal farming systems of Limpopo province representing four agro-ecological zones: Arid zone; Semi-arid zone; Dry sub-humid zone and Humid zone (Figure 3.1).

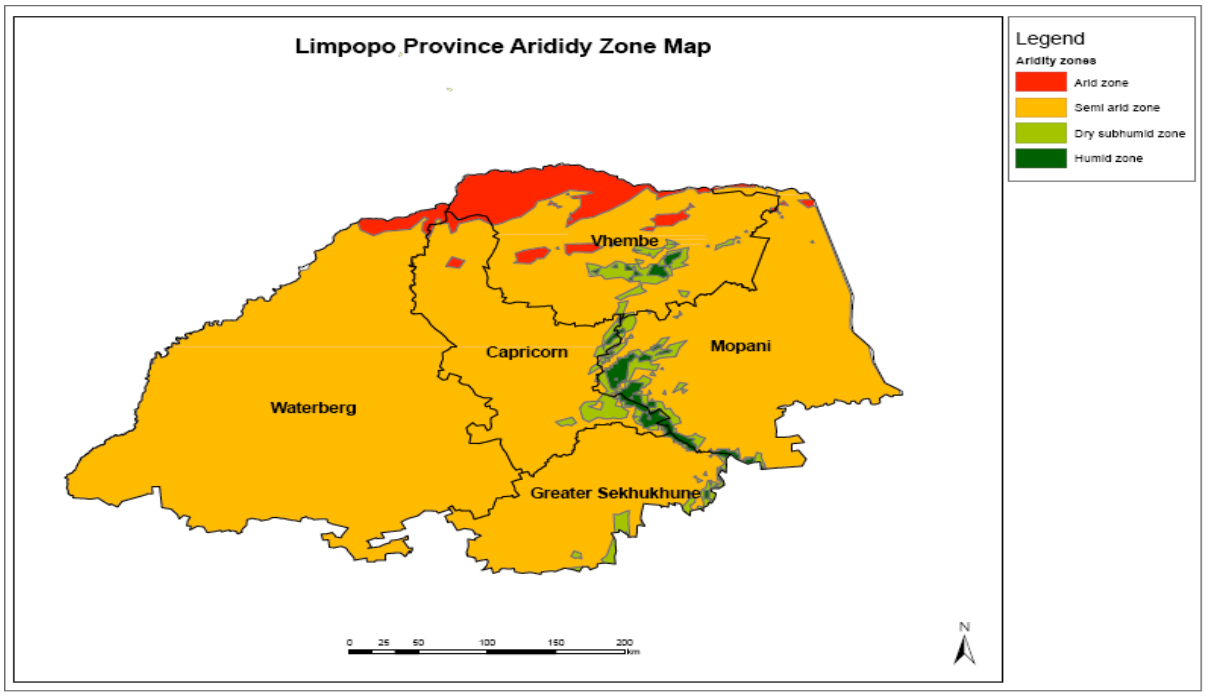

Figure 3. 1: The selected four agro-ecological zones of Limpopo Province, South Africa (Mpofu *et al.,* 2017)

Table 3. 1: Agro-ecological zones and their veld types in Limpopo Province, South Africa (Mpofu *et al*., 2016)

Eco-zone	Location	Temperature range (°C)	Veld type	Predominant grass species
Arid	Alldays	22 - 30.4	Sweet	*Cenchrus ciliaris, Panicum maximum*
	Lephalale	22.3 – 31.9	Mixed	*Aristida tranvaalenesis, Panicum maximum*
	Polokwane	19.2 - 26.6	Mixed	*Eragristis curvula, E. capensis*
Semi-Arid	Mokopane	19.8 - 27.8	Sourveld	*Eragristis curvula, E. capensis*
	Nylstroom	19.7 - 28.6	Sourveld	*Panicum maximum, Themeda triandra*
	Mookgopong	20.4 - 28.8	Sourveld	*Panicum maximum, Themeda triandra*
	Soekmekaar	19.9 - 26.9	Mixed	*Eragristis curvula, Themeda trianda*
Dry Sub-Humid	Makhado	20.2 - 27.1	Sweet	*Panicum maximum, Eragrostis Frichophora*
Humid	Tzaneen	21.9 - 29.1	Sourveld	*Cymbopogon caesius, Themeda trianda*

Table 3. 2: Number of hectares covered by each agro-ecological zone in each district of Limpopo province **(Selolo, 2014)**

District	Arid	Semi-arid	Dry Sub humid	Humid
Vhembe	508886.22	1483188.67	114843.75	27464.35
Capricorn	30.632.59	1545166.11	90103.157	34065.50
Mopani	13281.90	2200766.28	2632.45	90177.56
Greater Sekhukhune	0	1264127.93	65699.20	2074.46
Waterberg	75146.93	4864918.24	0	0

3.2. DATA COLLECTION AND ANALYSES

3.2.1. Prevalence of gastro-intestinal parasitic infestations within goats of Limpopo in different agro-ecological zones of Limpopo province

Faecal and blood samples were collected directly from the rectum and the jugular vein, respectively, by venipuncture into airtight EDTA vacutainer over four different seasons (Table 3.3). Samples were kept between 2 – 4 °C in cooler boxes prior and transported to the laboratory for further analyses. The micro tubes were placed into a haematocrit counter machine for 8 minutes for Pack Cell Volume (PCV) determination. Faecal egg counts (FEC) were determined by the modified McMaster technique, using floatation methods for nematodes (MAFF, 1986).

Table 3. 3: Classification of seasons with average rainfall in Limpopo province (Mpofu *et al*., 2016)

Season	Months	Average rainfall (mm)
Summer	November – January	467
Autumn	February – April	162
Winter	May – July	53
Spring	August – October	15.3

The FEC and PCV were subjected to ANOVA using the PROC GLM procedure of SAS (2013). The factors fitted in the model were agro-ecological zones, sex of goat and the season of sample collection. Fisher's Least Significant Difference (LSD) test was used to separate the least square means (P<0.05). The following model was used:

$Y_{ijkl} = \mu + A_j + S_J + S_k + e_{ijk}$

Where: Y_{ijk} is the response variable of FEC;

μ - Underlying constant common to all observations

A_i - Fixed effect of agro-ecological zone

S_j - Fixed effect of goat sex

S_k - The effect of the season;

e_{ijk} The random residual effect.

3.2.2. Phenotypic variations among the South African communal goat populations in different agro-ecological zones of Limpopo province

Phenotypic data were collected from 80 indigenous goat populations in four different agro-ecological zones: Arid (n=20), Semi-arid (n=20), Dry sub-humid (n=20) and Humid (n=20) of which 10 male and 10 femaleS were sampled per agro-zone in Limpopo province, South Africa. Extensive management systems were practiced, where goats foraged in communal pastures during the day and kraaled during the night. Animals of the same age were randomly selected based on sex and dentition technique supplemented with owner's information. Visual observations were made, and morphological qualitative traits were

recorded based on breed morphological descriptor list of FAO (2012) for phenotypic characterization of goats. The morphometric traits such as coat colour and pattern, presence of toggles, beard and horns, horn shape, horn size and orientation, ear size and orientation, head profile and rump shape and for quantitative, head length, head width, ear length, chest width, body length, body depth, hearth girth was measured on indigenous goat's population using plastic measuring tape.

Descriptive statistics were computed using FREQ procedures of SAS. To detect the statistical differences for quantitative traits, the General Linear Model Procedure (PROC GLM) of the SAS was used. Fisher's Least Significant Difference (LSD) test was used to separate the least square means (P<0.05). The following model was used:

$$Y_{ijk} = \mu + A_i + S_j + e_{ij}$$

Where:

Y_{YR} - Observations on linear body measurements
μ - Underlying constant common to all observations
A_i - Fixed effect of agro-ecological zone
S_j - Fixed effect of goat sex
e_{ij} - Random residual / error

3.2.3. Genetic variation among communal goat populations in different agro-ecological zones of Limpopo province

At least 5 ml of blood samples were collected from jugular veins of sampled populations into EDTA tubes and kept at 4^{O} C until DNA extraction. DNA was extracted from the whole blood samples using Roche High Pure PCR Template Preparation kit (Roche, USA). The concentration of the genomic DNA (gDNA) was measured using spectrophotometer (Nanodrop 2000) and purity verified by the 260/280 absorbance ratio (Thermo Fisher Scientific Inc. Waltham MA USA). Polymerase chain reaction (PCR) and genotyping 15

microsatellite markers recommended by the International Society Animal Genetics (BM1258, BM1818, CSRD247, HSC, ILSTS005, ILSTS08, ILSTS87, INRA06, INRA172, INRA23, INRA63, MAF65, OARFCB20, SRCRSP5 and SRCRSP8) were used to amplify the gDNA. These markers are endorsed for estimating genetic diversity parameters by ISAG and FAO advisory board (FAO, 2011).

A 15µl reaction was prepared with 10x buffer optimized with 50mM MgCl2 and 100mM deoxynucleotides triphosphates; 5U Bioline MyTaq DNA polymerase® (Bioline USA Inc.); 0.3µl of 10 mol/µl primers (Applied Biosystems Foster city CA USA) and 5µl of 50-100 ng of gDNA. After amplification, the PCR products were quantified using 3% agarose gel stained with ethidium bromide and visualized under a UV trans-illuminator repeatedly. The amplified products were separated using the capillary electrophoresis ABI Prism 3130XL Genetic Analyzer (Applied, Biosystems, Foster city, CA USA). The data was imported to GeneMapper1.95TM software (Applied Biosystems, Foster city, CA USA) to determine allele fragment sizes.

Microsatellite Toolkit (Park 2001) was used to estimate the basic population, genetic descriptive statistics including heterozygosity values (H_O) and (H_E), total number of alleles, mean number of alleles (MNA) and private alleles. The genetic distance among the goat populations in different AEZ of Limpopo was determined according to Nei's standards (Nei, 1987) using POPGen (Raymond and Rousset, 1995). The genetic population structure analysis of communal goat's populations was assessed using Bayesian admixture procedure implemented in STRUCTURE 2.3.4 (Pritchard *et al*., 2000).

CHAPTER 4: RESULTS

The prevalence of gastro-intestinal nematodes in the different agro-ecological zones is shown in Table 4.1. There was a significant ($P<0.05$) difference in PCV. The prevalence of *Haemonchus contortus* and *Moniezia* varies significantly ($P<0.05$) across agro-ecological zones, whilst prevalence of other GIN under study did not vary ($P>0.05$). Highest prevalence and abundance were recorded for *H. contortus* (357.42) followed by *Fascila hapatrica* (133.33) and *Moniezia* (121.50). Goats in humid zone had higher prevalence of *H. contortus* (490.63) than those in arid (366.67), semi-arid (285.71) and sub-humid (286.67), respectively. Goats in dry-sub humid zone had higher PCV (30.44) than those in arid (27.77) and humid (28.36) agro-ecological zones.

Table 4. 1: Prevalence of gastro-internal parasite (GIN) and packed cell volume (PCV+SE) in indigenous goats in different agro-ecological zones of Limpopo province

Agro-ecological zone	Gastro-intestinal parasites				Means	PCV
	H. contortus	*F. hapatrica*	*Nematoridus*	*Moniezia*		
Arid	$366.67^{ab} \pm 40.2$	$150.00^{a} \pm 66.7$	$145.45^{a} \pm 15.7$	$166.70^{a} \pm 28.9$	207.21	$27.77^{c} \pm 0.33$
Semi –arid	$285.71^{b} \pm 44.8$	$150.00^{a} \pm 0.00$	$171.43^{a} \pm 28.6$	$150.00^{b} \pm 24.5$	189.32	$29.31^{ab} \pm 0.39$
Humid	$490.63^{a} \pm 44.0$	$133.33^{a} \pm 50.0$	$177.78^{a} \pm 22.2$	$100.00^{c} \pm 33.3$	222.44	$28.36^{bc} \pm 0.45$
Dry sub-humid	$286.67^{b} \pm 47.3$	$100.00^{a} \pm 0.00$	$160.00^{a} \pm 24.45$	-	182.22	$30.44^{a} \pm 0.39$
Means	357.42	133.33	163.66	121.50		

$^{a, b, c}$ Column means with different superscripts differ significantly ($P<0.05$)

Table 4.2 shows the prevalence of gastro-intestinal nematodes in indigenous goats in different seasons. There was a significant ($P<0.05$) difference on PCV and the prevalence of *H. contortus* and *Moniezia* whilst there was no significant difference on the prevalence of *F. hapatrica* and *Nematodirus* across the different seasons. The prevalence of *H. contortus* was highest during winter (600.00), followed by autumn (435.00), and spring (430.00), whilst lowest during summer. The prevalence of *Moniezia* was higher during winter (166.70) and spring (166.70) whilst lowest during autumn (100.00).

Table 4. 2: Prevalence of gastro-internal parasite and packed cell volume (PCV + SE) in indigenous goats in different seasons of Limpopo province

Season	Gastro-intestinal parasites				Means	PCV
	H. contortus	*F. hapatrica*	*Nematodirus*	*Moniezia*		
Autumn	435.00^{a} ± 52.1	140.00^{a} ± 0.00	160.00^{a} ± 24.5	100.00^{b} ± 21.1	208.00	28.36^{b} ± 0.41
Winter	600.00^{a} ± 56.8	120.00^{a} ± 66.7	166.67^{a} ± 33.3	166.70^{a} ± 20.0	263.34	28.89^{ab} ± 0.47
Spring	430.00^{a} ± 81.7	150.00^{a} ± 66.7	133.33^{a} ± 21.1	166.70^{a} ± 28.9	220.00	28.78^{ab} ± 0.31
Summer	241.86^{b} ± 27.3	-	173.33^{a} ± 15.3	-	220.66	29.86^{a} ± 0.40

$^{a, b}$ Values within column with different superscripts differs significantly (P<0.05)

The prevalence of GIN in different sexes of indigenous goats is presented in Table 4.3 Prevalence of *Moniezia* nematodes varied ($P < 0.05$) amongst goat sexes, whilst prevalence of other GIN under study and PCV did not vary significantly ($P>0.05$). The highest prevalence of *Moniezia* was recorded in male (233.30) compared to female (100.00) goats.

Table 4. 3: Prevalence of gastro-internal parasite in different sexes of indigenous goats (SE)

Gender	Gastro-intestinal parasites				Means	PCV
	H. contortus	*F. hapatrica*	*Nematodirus*	*Moniezia*		
Male	405.66[a] ± 31.7	141.67[a] ± 66.7	178.57[a] ± 15.5	233.30[a] ± 14.9	239.63	29.15[a] ± 0.28
Female	341.03[a] ± 33.1	100.00[a] ± 0.00	150.00[a] ± 14.6	100.00[b] ± 0.00	172.86	28.79[a] ± 0.29

[a, b] Column means with different superscripts differ significantly (P<0.05)

The qualitative phenotypic traits of goats in different agro-ecological zones of Limpopo province are summarized in Table 4.4. Out of the total sampled goat population in the study area, 67.7 %, 26.1 % and 6.3 %, were multi coat coloured, uniform and spotted, respectively. Between agro-ecological zones, the observed overall coat colour patterns for both sexes were 55 % multicolour, 35 % uniform and 10 % spotted in Arid; 85% uniform, 10 % spotted and 5 % multicolour in humid; and 85 % multicolour, 10 % uniform and 5 % spotted in semi-arid; 70 % multicolour and 30 % uniform in sub humid. In the study area the dominant coat colour types were black (40 %), white (26.3 %) whilst brown and red colour both accounting 10 %, respectively with the remaining proportion being fawn (6.3 %) and grey (7.5 %). The sample population has flat head profile (73.75 %) and 63% of the population are not bearded. The proportions of goats having beard in arid, humid, semiarid and dry sub humid were 45, 30, 40 and 30 %, respectively. Most of the goats in arid, humid, semi-arid and sub humid (90, 75, 70 and 60 %, respectively) had flat face profile and about 10, 25, 40 and 40 % of these goat types were with slight concave head. However, sloping rump profile was predominant in arid (95 %) and humid (80 %) goat populations, other back profiles such as roofy and straight were also noted rarely.

Majority of goats had horns (86.3 %) and had straight (71.0 %), curved (27.5 %) and spiral (1.5 %) shape and no toggles (83.8 %). In studied populations, the horned goats accounted 80, 90, 90 and 85 % in arid, humid, semi-arid and dry sub humid goat populations, respectively. The reminder small proportion in each agro-ecological zone was polled. Regarding horn orientation: backward (59.4 %), upward (30.4 %) and lateral (10.15%) were recorded. The most dominant ear form was erect (68.8 %) and dropping (31.25 %) were observed in goat population. The largest proportion of goats (83.3, 72.2 and 52.9 %) had backward orientated horns in humid, semi-arid and sub-humid agro-ecological zones, with those in arid zone having the largest proportion (68.8 %) of upward horn orientation. The proportions of goats having erect ears in arid, humid, semiarid and dry sub humid were 90, 65, 65 and 55 %, respectively.

Table 4. 4: Qualitative traits of indigenous goats in different agro-ecological zones of Limpopo province

Trait	Attribute	Arid		Semi-arid		Humid		Sub humid		Mean %
		Freq	%	Freq	%	Freq	%	Freq	%	
Colour pattern	Uniform colour	14	35	4	10	34	85	12	30	26.07
	Multi-colour	22	55	34	85	2	5	28	70	67.68
	Spotted	4	10	2	5	4	10			6.25
Dominant colour	Black	16	40	18	45	14	35	16	40	40
	Brown	4	10	2	5	6	15	4	10	10
	White	12	30	12	40	8	20	10	25	26.25
	Grey	2	5	4	10	2	5	4	10	7.50
	Red	4	10	2	5	3	15	4	10	10
	Fawn	2	5	2	5	4	10	2	5	6.25
Face profile	Slight concave	4	10	12	30	10	25	16	40	26.25
	Flat	36	90	28	70	30	75	24	60	73.75
Rump shape	Flat	2	5	4	10	10	25	4	10	12.5
	Sloping	38	59	4	10	2	5	32	80	47.5
	Roofy			32	80	28	70	4	10	40
Beard	Absent	22	55	24	60	28	70	28	70	63.75
	Present	18	45	16	40	12	30	12	30	36.25
Toggles	Absent	36	90	32	80	36	90	30	75	83.75
	Present	4	10	8	20	4	10	10	25	16.25
Horns	Absent	8	20	4	10	4	10	6	15	13.75
	Present	32	80	36	90	36	90	34	85	86.25
Horn shape	Curved	8	35	6	16.75	12	33.33	12	35.29	27.53
	Spiral							2	5.88	1.45
	Straight	24	75	30	82.33	24	66.67	20	58.83	71.01
Horn orientation	Backward	8	25	26	72.22	30	83.33	18	52.94	59.42
	Upward	22	68.75	8	22.22	2	5.56	10	29.41	30.43
	Lateral	2	6.25	2	5.56	4	11.11	6	17.65	10.15
Ears orientation	Erect	36	90	26	65	26	65	22	55	68.75
	Dropping	4	10	4	35	14	35	18	45	31.25

Table 4. 5: Quantitative traits measurements (cm ± SE) of South African indigenous goats in different agro-ecological zones of Limpopo province

Traits	Agro-ecological zones				Means
	Arid	Semi-arid	Humid	Dry sub-humid	
Head Length	19.30^{a} ± 0.37	19.46^{a} ± 0.43	19.36^{a} ± 0.40	19.48^{a} ± 0.41	19.40 ± 0.20
Head Width	11.25^{a} ± 0.20	11.22^{a} ± 0.19	11.28^{a} ± 0.24	11.51^{a} ± 0.23	11.31 ± 0.11
Ear Length	13.58^{b} ± 0.36	14.68^{a} ± 0.35	14.33^{ab} ± 0.34	14.33^{ab} ± 0.36	14.23 ± 0.18
Chest Width	16.95^{b} ± 0.25	17.93^{a} ± 0.27	17.99^{a} ± 0.19	17.50^{a} ± 0.23	17.60 ± 0.13
Body Length	19.30^{a} ± 0.24	19.46^{a} ± 0.36	19.36^{a} ± 0.24	19.48^{a} ±0.29	66.65 ± 0.13
Body Depth	34.38^{a} ± 0.93	35.75^{a} ± 0.99	36.10^{a} ± 0.82	35.11^{a} ± 0.92	39.59 ± 4.30
Hearth Girth	78.75^{a} ± 0.47	79.33^{a} ± 0.44	79.67^{a} ± 0.35	79.34^{a} ± 0.45	79.27 ± 0.21

^{a,b} Values within row with different superscripts differ significantly ($P < 0.05$)

Table 4. 6: Effect of agro-ecological zone and sex of animals on quantitative traits measurements (cm+ SE) of South African indigenous goats

Traits	Arid		Semi-arid		Dry sub-humid		Humid	
	Male	Females	Male	Female	Male	Female	Male	Female
HL	$20.42^{a} \pm 0.47$	$18.18^{b} \pm 0.29$	$20.93^{a} \pm 0.50$	$18.00^{b} \pm 0.24$	$20.90^{a} \pm 0.44$	$18.06^{b} \pm 0.23$	$20.85^{a} \pm 0.35$	$17.87^{b} \pm 0.24$
HW	$11.87^{a} \pm 0.22$	$10.62^{b} \pm 0.20$	$11.67^{ab} \pm 0.26$	$10.78^{b} \pm 0.21$	$12.21^{a} \pm 0.27$	$10.80^{b} \pm 0.21$	$11.92^{a} \pm 0.34$	$10.63^{b} \pm 0.19$
EL	$14.56^{ab} \pm 0.35$	$12.59^{c} \pm 0.45$	$15.69^{a} \pm 0.28$	$13.67^{bc} \pm 0.45$	$15.20^{ab} \pm 0.31$	$13.45^{bc} \pm 0.53$	$14.95^{ab} \pm 0.47$	$13.71^{bc} \pm 0.41$
CW	$17.72^{bc} \pm 0.26$	$16.18^{d} \pm 0.26$	$18.81^{a} \pm 0.14$	$17.05^{cd} \pm 0.34$	$18.18^{ab} \pm 0.20$	$16.84^{cd} \pm 0.29$	$18.49^{ab} \pm 0.18$	$17.50^{bc} \pm 0.24$
BL	$66.65^{bc}d \pm 0.21$	$65.15^{e} \pm 0.27$	$68.38^{a} \pm 0.22$	$65.96^{cde} \pm 0.43$	$67.29^{abc} \pm 0.28$	$65.82^{de} \pm 0.39$	$67.57^{ab} \pm 0.23$	$66.40^{bcde} \pm 0.35$
BD	$37.45^{ab} \pm 0.23$	$31.33^{c} \pm 1.22$	$39.11^{a} \pm 0.19$	$32.41^{c} \pm 1.26$	$37.91^{ab} \pm 0.24$	$32.30^{c} \pm 1.32$	$37.40^{ab} \pm 0.87$	$34.79^{bc} \pm 1.32$
HG	$80.27^{a} \pm 0.29$	$77.23^{b} \pm 0.57$	$80.76^{a} \pm 0.15$	$77.90^{b} \pm 0.59$	$80.82^{a} \pm 0.10$	$77.86^{b} \pm 0.60$	$80.19^{a} \pm 0.30$	$79.14^{ab} \pm 0.60$

^{a,b,c,d,e} Row means with different superscripts differ significantly ($P < 0.05$).HL: Head Length; HW: Head Width; EL: Ear Length; CW: Chest Width; BL: Body Length; BD: Body Depth; Hearth Girth; LSM: Least square Means; SE: standard errors.

Least square means (LSM) agro-ecological zone, agro-ecological zone and sex, and sex effect on body weight and linear body measurements are presented in Table 4.4, 4.5 and 4.6. Sex of goats was a significant (P<0.05) source of variation for HL, HW, EL, CW, BL, BD and HG. Goats in different agro-ecological zone had a significant (P<0.05) different EL, CW, however, they had similar (P>0.05) HL, HW, BL, BD and HG (Table 3). Goat in arid zone has shorter EL and CW than those in other agro-ecological zones. All body measurements in male goats were consistently higher (P<0.05) than in female goats across all agro-ecological zones. In all the agro-ecological zones, male goats had higher linear body measurements than their female contemporaries. Overall mean of head length, head width, ear length, chest width, body length, body depth, hearth girth was 19.40, 11.31, 14.23, 17.60, 66.65, 39.59 and 79.27 cm, respectively.

Table 4. 7: Effect of sex on quantitative traits measurements (cm ± SE) of indigenous goats in Limpopo

Traits	Females	Males
Head Length	18.03^{b} ± 0.13	20.77^{a} ± 0.22
Head Width	10.71^{b} ± 0.10	11.92^{a} ± 0.14
Ear Length	13.36^{b} ± 0.23	15.10^{a} ± 0.19
Chest Width	16.89^{b} ± 0.16	18.30^{a} ± 0.12
Body Length	65.83^{b} ± 0.19	67.47^{a} ± 0.15
Body Depth	32.71^{b} ± 0.65	37.97^{a} ± 0.25
Hearth Girth	78.03^{b} ± 0.30	80.51^{a} ± 0.12

^{a,b} Row means with different superscripts differ significantly (P < 0.05)

The mean number of alleles as observed in each marker within each population is presented in Table 4.8. The highest number of alleles observed was 11 in loci HSC, MAF65 and SRCRSP5, respectively, depicting the amount of allele richness. The lowest number of alleles found were 3 in loci SRCRSP8, ILSTS87 and INRA23, showing low polymorphic information content (PIC).

Table 4. 8: Number of alleles observed in each marker within the four agro-ecological zone goat populations

Marker	Semi-arid	Sub-humid	Arid	Humid	Boar goats	Indigenous Goats
BM1258	6	4	5	6	4	8
BM1818	4	6	7	5	2	7
CSRD247	8	8	8	7	5	8
HSC	11	9	9	11	7	13
ILSTS005	4	5	5	4	4	4
ILSTS08	5	4	6	5	4	3
ILSTS87	6	6	3	5	1	7
INRA06	6	7	7	7	6	8
INRA172	9	10	7	6	2	6
INRA23	5	8	3	6	0	4
INRA63	7	8	6	6	5	4
MAF65	10	11	7	4	3	8
OARFCB20	9	9	9	8	6	7
SRCRSP5	10	11	5	9	6	6
SRCRSP8	3	5	5	6	5	5

A total number of 234 alleles detected across the 15 microsatellite markers. High gene diversity was found across the six populations with an average of 71 % heterozygosity and 6.26 alleles per locus (Table 4.9). Forty-three distinct private alleles were found, shared between the semi-arid goat population (7), sub-humid (20), arid (11) and humid (1) whilst the reference population of indigenous goat had four and Boer goats had no

private alleles found. The mean effective number of alleles, expected and observed heterozygosity over all populations were 6.26, 0.71 and 0.55, respectively.

Table 4. 9: Descriptive statistics for communal goat population in different agro-ecological zone of Limpopo Province

Population	N	Loci	H_E ± SD	H_O ± SD	NA ± SD	F_{IS}	Private alleles
Semi-arid	20	15	0.73 ± 0.03	0.59 ± 0.03	6.87 ± 2.50	0.19	7
Sub-humid	20	15	0.76 ± 0.03	0.60 ± 0.03	7.40 ± 2.35	0.21	20
Arid	20	15	0.69 ± 0.05	0.53 ± 0.03	6.13 ± 1.85	0.23	11
Humid	20	15	0.74 ± 0.03	0.60 ± 0.03	6.33 ± 1.88	0.20	1
Boer goats	15	14	0.65 ± 0.06	0.37 ± 0.04	4.29 ± 1.77	0.43	0
Indigenous goats	56	15	0.68 ± 0.03	0.60 ± 0.02	6.53 ± 2.47	0.12	4
Means			0.71	0.55	6.26	0.23	

H_E:Expected Heterozygosity; SD: Standard deviation; H_o: Observed Heterozygosity; NA: Number of alleles; F_{IS}: Inbreeding coefficient of individuals within a subpopulation.

The analysis of molecular variance (AMOVA) analyses for the goat population in different agro-ecological zone indicated that 95.2 % was due to difference among individuals within populations and 4.3% of the genetic variation was due to differences among populations (Table 4.10.)

Table 4. 10: AMOVA analyses for communal goat population in different agro-ecological zone of Limpopo Province

Source of variation	Sum of squares	Variance component	Percentage of variance	P value
Between population	19.560	0.10391	4.30	0.001
Within population	365.365	2.31244	95.70	0.001
Total	161	2.41635	0	0

Genetic distances between the ecotypes indicated relatively close relationships among all the populations (Table 4.11). The allele frequencies were used to determine the genetic distances between the different populations. Pairwise genetic differentiation by F_{ST} ranged from 0.023 to 0.048 and was observed that the goat populations in all agro-ecological zones had a shorter distance with the indigenous goat reference populations. The semi-arid, sub-humid had a greater genetic distance to the Boar goat reference population. However, the arid and humid goat populations had a moderate genetic distance with the Boar goat reference population.

Table 4. 11: Pair-wise population matrix of FST values between the communal goat populations in different agro-ecological zones of Limpopo Pronvince

	Semi-arid	Sub-humid	Arid	Humid	Boar goats	Indigenous Goats
Semi-arid	*****					
Sub-humid	0.027	*****				
Arid	0.033	0.045	*****			
Humid	0.023	0.038	0.048	*****		
Boar goats	0.151	0.135	0.132	0.122	*****	
Indigenous Goats	0.007	0.032	0.038	0.027	0.171	*****

Nei's genetic distance amongst populations is illustrated in Table 4.12. The genetic distance estimate of Nei's ranged from 0.060 to 0.179. Shorter distances were observed between semi-arid goat populations and humid (0.060) and followed by semi-arid and sub-humid (0.066) and semi-arid and arid (0.088). It was observed that the goat's populations in all agro-ecological zones had a shorter distance with the indigenous goat's reference populations. It was also observed that the semi-arid, sub-humid had a greater genetic distance to the Boar goat reference population. However, the arid and humid goat populations had a moderate genetic distance with the Boar goat reference population.

Table 4. 12: Nei's genetic distance (DA) of goat populations in different agro-ecological zones of Limpopo Province

	Semi-arid	Sub-humid	Arid	Humid	Boar goats	Indigenous Goats
Semi-arid	*****					
Sub-humid	0.066	*****				
Arid	0.088	0.160	*****			
Humid	0.060	0.152	0.179	*****		
Boar goats	0.770	0.610	0.528	0.505	*****	
Indigenous Goats	0.000	0.112	0.124	0.096	0.937	*****

Structure test was performed to identify which population or populations the study subjects belong to as well as group them (Figure 4.1). The K = 5 analyses revealed that all populations do not differ from each other and that the communal goat populations in particular are more closely related to the indigenous goat reference population. The structure also revealed that the communal goat's populations are admixtures.

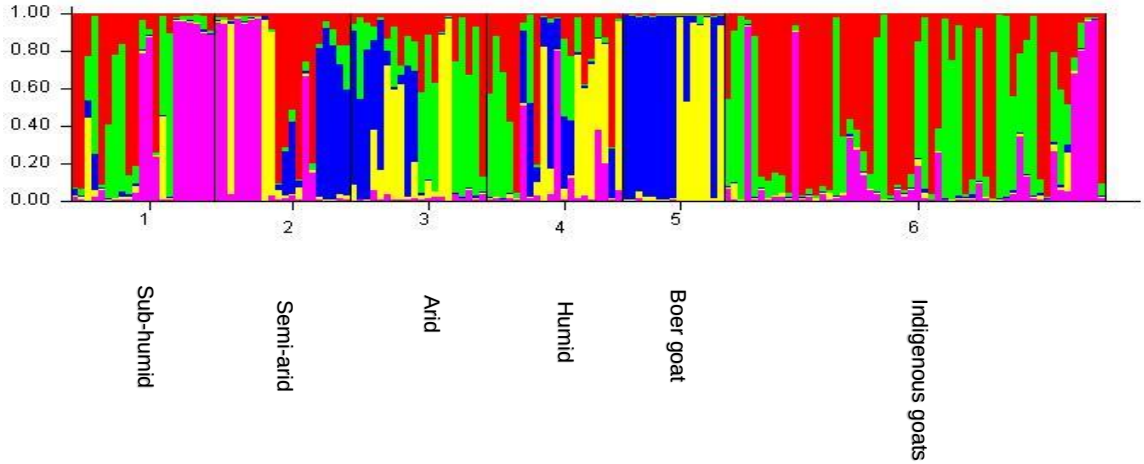

FIGURE 4. 1: Principal component analysis based on Nei's genetic distance

CHAPTER 5: DISCUSSION

The most prevalent GIN were *H. contortus* across all the agro-ecological zones. Similar reports have reported that *H. contortus* is the most important nematode that threatens the future of small stock industry (Vassilev, 1995; Tsotetsi and Mbati, 2003; Odoi *et al.,* 2007; Bakunzi *et al*., 2013; Ntonifor *et al*., 2013; Shija *et al*., 2014). Its higher prevalence could be due to the fact that they have short generational interval. Adult females had high fecundity, which can lead to rapid larval pasture contamination and associated outbreaks of haemonchosis (Roeber *et al*., 2013) and enviable developmental plasticity for adaptation or resistance to control measures (Poeschel & Todd, 1972; Kotze and Prichard, 2016). The level of FEC in the current study was low compared to report by Menkir *et al*. (2007), who reported higher values for GIN 1930 *H. contortus 320* for *Nematodirus*). This could be associated with the browsing/foraging behaviour of indigenous goats, which minimizes chances of ingesting the nematodes eggs which are found on plants closer to the ground, and access to trees or shrubs with high levels of tannins e.g. *Acacia* that has the ability to reduce levels of infection (Odoi *et al*., 2007).

The higher prevalence of *H. contortus* in humid agro-ecological zone is attributed by the fact that these areas are warm and receives enough rainfall which in turn provides suitable temperatures and moisture condition needed for gastro-intestinal nematodes fecundity and development (Menkir *et al*., 2006). The low prevalence of *Moniezia spp* and *Nematodirus* observed across all agro-ecological zones depicts that the Limpopo province is not dominated by these nematode species or goats are more resistant towards these nematode parasites as most of tropic indigenous goats being resistant to gastro-intestinal nematodes (Baker *et al*., 1998). The higher prevalence of *Moniezia spp* in arid zone than semi-arid and sub-humid zone, may be caused by the reason that arid zone experiences warm temperatures and low erratic rainfall distribution (Hunters *et al*., 1992) which is favourable for *Moniezia spp* nematodes development.

The low prevalence of *H. contortus, F. hapatica* and *Moniezia spp* gastro-intestinal nematodes were observed in dry-sub humid regions. This can be attributed by the fact that this zone is characterized by hot-dry and cool-wet seasons (Hunters *et al*., 1992) which in turn provide unconducive environment for nematode development as they need moist and warm environmental conditions for the development, survival (Donald 1968; Hansen and Perry 1994; Urquhart *et al*., 1996).

The higher level of prevalence of *H. contortus* and *Moniezia spp* observed in winter could be attributed to high rainfall received in two previous seasons (summer and autumn) therefore triggering the development of the GIN in winter season. Climatic conditions such as temperature, rainfall and soil moisture play a significant role in the epidemiology of GIN parasites from egg to mature stage (Dube *et al*., 2002; Waller and Chandrawathani, 2005; Regassa *et al*., 2006; Godara *et al*., 2014; Khanjari *et al*., 2014). Under satisfactory environmental conditions in the wet season, *H. contortus* and other nematodes larva that infect goats reach infective stages within 46 days (Magona & Musisi, 2002). However, lower prevalence of GIN reported in other seasons (summer, autumn and spring) could be attributed to the lower rainfall which was experienced during 2015 and can also be attributed to continuous access to browse forage such as *Acacia* bush which is dominant in all agro-ecological zones. Moist, warm environmental conditions are favourable for the development, survival and transmission of pre-parasitic stages of parasitic nematodes (Donald 1968; Hansen and Perry 1994; Urquhart *et al*., 1996). Therefore, the observed gradual build-up of GIN populations in the goats with greatest burdens recorded around the peaks of the rainy seasons, would be expected. Thereafter, the GIN populations declined with the lowest numbers being recorded around the middle of the dry season, indicating lower levels of larval pickup from pasture during this period.

Similar results reporting the lack of significant difference in *H. contortus* and *F. hapatica* prevalence between goat sexes were also reported by Menkir *et al*. (2007). However, most of the researchers have observed higher rate of GIN prevalence in female hosts when compared with males (Maqsood *et al*., 1996; Valcarcel and Romero, 1999; Emiru *et al*., 2013; Vieira *et al*., 2014). The prevalence of *Moniezia* parasites was found to be

significantly higher in male goats than in females and can be attributed to some physiological factors, though both sexes are exposed to similar environmental conditions (Gauly *et al*., 2006).

The higher PCV in humid zone and during summer can be associated with the lower EPG on this zone and season, respectively. Low values of PCV are commonly associated with high FEC attributed to the adult parasites sucking a substantial amount of blood from the abomasum (Baker *et al*., 2003).

The results show the presence of clear morphological variations between and within indigenous goat populations. Village/rural goat production is based mainly on unimproved indigenous goats (Bester *et al*., 2009) with large variations in morphological appearances and body size. Goat morphological variations have important socio-cultural and economic values to the rural communities and as a result, farmers have different choices for goat coat colours (Mahanjana and Cronje, 2000; Manton, 2005; Rumosa Gwaze *et al*., 2009).

The colouration pattern variations amongst the goat populations sampled with predominantly (67.68 %) multi-coloured, followed by (26.1 %) uniform colour and 6.3 % spotted coloured goats. The same coat patterns were reported for indigenous goat types from other regions of Africa (Alemayehu, 1994; Farm-Africa, 1996; Ameha, 2001; Manzi *et al*., 2011) and Syria (Hassen *et al*., 2016). Colouration could be an adaptive trait or selected through farmers' preference for a specific coat colour (Molefe, 1986; Indetie *et al*., 1998; Manzi *et al*., 2011). In contrary, South African indigenous goats in KwaZulu-Natal account to 74.5, 16.3, 3.3, and 6.0 % plain, patchy, spotted and speckled, respectively (Mdladla *et al*., 2017). The findings that the black is the dominant colour in the Limpopo province similarly to Syrian indigenous goats (Hassen *et al*., 2016), can been linked to environmental adaptation (Robertshaw, 2006; Hagan *et al*., 2012) and the demand for such colours in cultural ceremonies (Mdladla *et al*., 2017).

Most of the goat in the sampled populations have slightly flat head profile (73.8 %), similarly the largest proportion (77.2 %) of Rwandian indigenous goats have a flat head profile (Manzi *et al*., 2011). The small proportion of goats (16.25 %) had toggles, which is

in line with the findings by Manzi *et al.* (2011) who reported only 13.5 % of African goat populations have toggles. However, on contrary, the higher frequency of toggles of 36.5 % in West African Dwarf (WAD) goats were reported (Adebayo and Chineke, 2011). Mdlaldla *et al* (2017) reported the lower proportion (7.6 %) of goats with toggles in South African rural communities' goat populations. Toggles are more commonly found in dairy and pygmy goat and Spanish goats (Manzi *et al., 2011*). The different toggle proportion in the communal goats may represent some adaptive mechanisms related to milk yield as observed in Saanen goats (Yakubu *et al*., 2010). There is a taboo towards toggled communal goats (Yakubu *et al*., 2010), which could be the reason of lower proportion of toggled goats in the study site.

A higher proportion (86.3 %) of the goats are horned, while 13.8 % were polled, these are in agreements with the report by Mdlaldla *et al*. (2017) who reported that 88.1 % indigenous goats are horned whilst 11.9 % are polled in the four provinces (Eastern Cape, KwaZulu-Natal, Limpopo and North West Provinces) of South Africa. The low occurrence of polled indigenous goat populations has also been reported in Ghanaian indigenous goats (Hagan *et al*., 2012). The presence of horn is an adaptive feature to fight competitors for available resources and predators. On contrary, the frequency of polled Syrian indigenous goats is higher than horned (Hassen *et al*., 2016).

In the current study, the frequencies of bearded goats were 36.3 %, on contrary, bearded goats account to only 6 % in the Rwandian indigenous goats in Bugesera and Nyagatare Districts. The frequencies of a beard in are generally higher in rural communal goats in South Africa (Mdlaldla *et al*., 2017). Only 47.5 % of South African communal indigenous goats in Limpopo province had slopping rump, whilst 40 % had a roofy rump. Contrary to entire indigenous goat populations in Bugesera and Nyagatare Districts of Rwanda had a sloping rump. The frequencies were 60 and 40 % for small and medium ears, and 68.8 and 31.3 % erect and drooping ears, respectively. On contrary, most of the Syrian (Hassen *et al*., 2016) and Ethiopian indigenous (Alemu, 2014) goats have long and drooping ears.

Linear body measurements were different between sexes. Similarly, several reports (Aladeet *et al*., 2008; Ferek, 2008; Sowande *et al*., 2009) reported that linear body measurements are significantly influenced by sex of the animals. The findings of this study that, male goats have higher linear body measurements than their female counterpart depicts that sex is an important source of variation for indigenous goat's linear body measurements (Adeyinke, 2006; Alemayehuet *et al*., 2012). The sexual dimorphism was evident in linear body measurements of South African indigenous goats in which male goats have higher measurements than females which could be ascribed that these differences are due to differences in their endocrinological and physiological functions (Ebangi, 2000; Semakula *et al*., 2010; Mpofu *et al*., 2017). On contrary, females have higher body linear measurements than male counterpart (Alade *et al*., 2008; Sowande *et al*., 2009; Samakula *et al*., 2010; Okbeku *et al*., 2011; Moutchou *et al*., 2017).

Limitations in food quantity and quality may affect linear body measurements (Kadim *et al*., 2006). The finding that agro-ecological zones did not influence linear body measurements understudy except EL and CW depicts that even though these zones differ in their climatic conditions, veld type, mineral status of the soil, goats in these zones are able to meet their nutritional requirements ascribed to their excellent foraging abilities (Casey and Van Niekerk, 1988; Donkin, 1992; Barry and Godke, 2001; Morand-Fehr *et al*., 2004; Kunene and Fossey, 2006). Agro-ecological zone differences were not evident for various body measurements, however, these finding are in contrast with the several reports (Belete *et al*, 2013; Grum, 2010; Halima *et al*., 2012; Mahilet, 2012) that goats in different locations have different body measurements.

All the microsatellite markers tested were found to be polymorphic in all populations. For the 15 markers tested in this study, the number of alleles observed ranged from 3 to 11 which are lower than Sub-Saharan African goats (5 to 14) (Muema *et al*., 2009), Ethiopian goats (4 to 23) (Tesfaye 2004), West African Dwarf goats (4 to 21) (Mujibi, 2005) and Swiss goat breeds (3 to19) (Saitbekova *et al*., 1999). The standard error of distance estimates is reduced if microsatellite loci have less than 4 alleles per locus (Li *et al*., 2002; Yang *et al*., 1999).

The mean number of alleles and expected heterozygosities are good indicators of genetic polymorphism within breeds. The Limpopo communal goats in different agro-ecological zones had a considerable amount of within population variation based on heterozygosities and number of alleles. The mean number of alleles of communal goats ranged from 4.29 to 7.40 across agro-ecological zones. Generally, the mean number of alleles is highly dependent on the sample size because of the unique alleles in populations, which occur in low frequencies and because the number of observed alleles tends to increase depending on the population size (Garrine, 2007).

Goats in sub-humid have 7.40 mean number of alleles (MNA), similarly to the mean number of alleles of the Kalahari Red goat breed (7.77) in South Africa (Li *et al*., 2002). The mean number of alleles of Tete goats in Mozambique (5.58) (Garrine, 2007) is similar to the mean number of alleles of arid goat populations. Communal goats in arid have 6.87 mean number of alleles, similarly to the mean number of alleles of the Pafuri goat breed (6.94) in Mozambique (Garrine, 2007). The number of alleles observed in this study were similar to previous studies using similar microsatellite markers (Barker *et al*., 2001, Li *et al*., 2002,).

The expected heterozygosities (H_E) values per population were similar, ranging from 0.69 in the arid goat population, 0.73 in semi-arid, 0.74 in humid to 0.76 in sub-humid got population. Similar H_E values using microsatellite markers in diversity studies in goats were reported (Saitbekova *et al.,* 1999; Barker *et al.*, 2001) and these were lower than those reported by Li *et al*. (2002). The average observed heterozygosity (H_O) was less than expected for all populations and this could be due to segregation of non-amplifying (null) alleles, scoring bias (heterozygotes scored incorrectly), selection against heterozygotes or inbreeding. Barker *et al*. (2001) and Garrine (2007) reported similar results on indigenous South-East Asian goat and Mozambique indigenous goat populations. Genetic drift and Inbreeding depression will affect many different fitness-related traits (Li *et al*., 2002), including survival (Coltman *et al*., 1998), and parasite susceptibility (Garrine (2007). There is no evidence to suggest that goat from less

heterozygous populations had inferior immune activity. However, it is possible that other immune system components will suffer negatively from inbreeding Barker *et al*. (2001).

The prevalence of GIN varies significantly ($P<0.05$) across agro-ecological zones, depicts the importance of agro-ecological factors such as temperature, rainfall and humidity of the experimental areas to the development of nematode eggs (Menkir *et al*., 2006) There are two mechanisms that might result in low heterozygosity causing increased parasite prevalence. Inbred individuals may have low immunity, resulting in greater susceptibility to infection and, secondly, parasite infections may be able to spread faster through populations with lower genetic diversity.

The current results are consistent with the theory (Shija et al., 2014) that population genetic homogeneity leads to higher parasite prevalence. The theory assumes that host genotypes differ in their ability to resist different parasite strains and lower genetic diversity increases the probability of parasitic infection. Inbred populations were more likely to be infected with parasites especially *Haemonchus* spices these populations also had lower mean parasite abundance. This could reflect the inability of inbred goats to survive high levels of infection meaning that high loads were not observed.

CHAPTER 6: CONCLUSIONS

Haemonchus contortus was the most dominant GIN in Limpopo province. Its prevalence and intensity may affect the productivity of goats. Knowledge and understanding of the gastro-intestinal species and epidemiological parameters are important in the development of appropriate control strategies for the different areas. There was a clear morphological variation between and within communal goat populations in different agro-ecological zones of Limpopo province. Some of the traits (e.g. coat colour) have important socio-cultural and economic values to the rural communities and may also reflect the adaptive fitness under extensive foraging systems or selected through farmers' preference for a specific coat colour. The microsatellite markers used were useful and informative for studying the genetic diversity and genetic structures of populations. The genetic diversity of the goat populations in different agro-ecological zones was low, as indicated by the Nei's genetic distance, mean number of alleles and expected heterozygosities observed for the populations. Low genetic diversity in populations is associated with a higher prevalence of parasites. This supports theories that suggest population genetic homogeneity enables parasites to spread to higher prevalence. Inbreeding negatively affects a range of fitness traits in goats. The control measures of GIN's should be implemented in all seasons. It is recommended that further studies on genetic characterization should be conducted in different agro-ecological zone of Limpopo and farmers should be advised to reduce inbreeding.

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